

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 18:57:17 ; Search time 163.56 Seconds
(without alignments)
3.585 Million cell updates/sec

Title: US-09-016-061-48
Perfect score: 52
Sequence: 1 GTTFSSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_63:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	86.5	94	2 S14580	Ig heavy chain V r
2	41	78.8	97	2 S26890	Ig heavy chain V r
3	40	76.9	113	2 S26468	Ig heavy chain V r
4	40	76.9	117	1 HVMS34	Ig heavy chain pre
5	40	76.9	121	2 D27888	Ig heavy chain V r
6	40	76.9	124	2 C27888	Ig heavy chain V r
7	39	75.0	548	2 S38864	Ig epsilon chain C
8	38	73.1	40	2 S33406	Ig heavy chain V r
9	38	73.1	83	2 C25913	Ig heavy chain V r
10	38	73.1	98	2 S26891	Ig heavy chain V r
11	38	73.1	108	2 PH0248	Ig heavy chain V r
12	38	73.1	108	2 PH1006	Ig heavy chain V r
13	38	73.1	114	1 AVDGGM	Ig heavy chain V r
14	38	73.1	117	1 HVMS84	Ig heavy chain pre
15	38	73.1	117	2 PL0249	Ig heavy chain V r
16	38	73.1	117	2 PL0252	Ig heavy chain V r
17	38	73.1	119	2 F27888	Ig heavy chain V r
18	38	73.1	122	2 E27888	Ig heavy chain V r
19	38	73.1	138	2 S09258	Ig heavy chain V r
20	37	71.2	92	2 S56009	Ig heavy chain var
21	37	71.2	92	2 S56008	Ig heavy chain var
22	37	71.2	97	1 HVMS91	Ig heavy chain V r
23	37	71.2	97	2 PH0872	Ig heavy chain V r
24	37	71.2	98	2 S26889	Ig heavy chain V r
25	37	71.2	100	2 D48223	Ig heavy chain V r
26	37	71.2	102	2 S14581	Ig heavy chain V r
27	37	71.2	108	2 PH1648	Ig heavy chain V r
28	37	71.2	108	2 PH1011	Ig heavy chain V r
29	37	71.2	109	2 PH1649	Ig heavy chain V r
30	37	71.2	111	2 PH1659	Ig heavy chain V r

```
31 37 71.2 111 2 S40090 Ig heavy chain - m
32 37 71.2 111 2 PH1007 Ig heavy chain V r
33 37 71.2 112 2 S26327 Ig heavy chain V r
34 37 71.2 112 2 PH1647 Ig heavy chain V r
35 37 71.2 113 2 S25571 Ig heavy chain V r
36 37 71.2 117 1 H3HU26 Ig heavy chain pre
37 37 71.2 117 2 A45953 Ig heavy chain pre
38 37 71.2 117 2 B34964 Ig heavy chain pre
39 37 71.2 117 2 S34012 Ig heavy chain V r
40 37 71.2 118 2 S31121 Ig heavy chain - h
41 37 71.2 119 2 C36005 Ig heavy chain V r
42 37 71.2 119 2 D36005 Ig heavy chain V r
43 37 71.2 119 2 S31107 Ig heavy chain - h
44 37 71.2 119 2 S31108 Ig heavy chain - h
45 37 71.2 120 2 S48798 Ig heavy chain V r
```

ALIGNMENTS

RESULT 1

```
S14580
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S14580
R:Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A:Description: Natural polyreactive antibodies differ from Ag-induced antibodies in V
A:Reference number: S14484
A:Accession: S14580
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-94 <CHE>
A:Cross-references: EMBL:X58652; NID:g51293; PIDN:CAAA1509.1; PID:g51294
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>
```

Query Match 86.5%; Score 45; DB 2; Length 94;
Best Local Similarity 90.0%; Pred. No. 0.054;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10

Db 18 GTTFSSYDMS 27

RESULT 2

```
S26890
Ig heavy chain V region (DP-48) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26890
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups o
A:Reference number: S26885; MUID:93021117
A:Accession: S26890
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <TOM>
A:Cross-references: EMBL:F12348; NID:g32916; PIDN:CAA78218.1; PID:g32917
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>
```

Query Match 78.8%; Score 41; DB 2; Length 97;
Best Local Similarity 88.9%; Pred. No. 0.34;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 9
Db 26 GTTFSSYDM 34

RESULT 3

Ig heavy chain V region - mouse
A:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26468

R:Kavalet, J.
submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26468

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <NAV>

A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 40; DB 2; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.64;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
Db 22 GFATSSYDMS 31

RESULT 4

Ig heavy chain precursor V region (345) - mouse
A:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
C:Accession: JT0502

R:Levy, N.S.; Malpietro, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A:Reference number: JT0501; MUID:89279149

A:Accession: JT0502

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A:Note: this sequence belongs to the VH7183 subfamily

C:Superfamily: Immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:41-115/Disulfide bonds: #status predicted

Query Match 76.9%; Score 40; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.66;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
Db 45 GFATSSYDMS 54

RESULT 5

Ig heavy chain V region (H37-60) - mouse
A:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C:Accession: D27888

R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to
A:Reference number: A91043; MUID:86300658

A:Accession: D27888

A:Molecule type: DNA

A:Residues: 1-121 <CAT>

A:Experimental source: strain Balb/c

A:Note: this sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 40; DB 2; Length 121;
Best Local Similarity 80.0%; Pred. No. 0.68;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
Db 26 GFATSSYDMS 35

RESULT 6

Ig heavy chain V region (H37-62) - mouse
A:Species: Mus musculus (house mouse)

C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C:Accession: C27888

R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to

A:Reference number: A91043; MUID:86300658

A:Accession: C27888

A:Molecule type: DNA

A:Residues: 1-124 <CAT>

A:Experimental source: strain Balb/c

A:Note: this sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.9%; Score 40; DB 2; Length 124;
Best Local Similarity 80.0%; Pred. No. 0.7;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
Db 26 GFATSSYDMS 35

RESULT 7

Ig epsilon chain C region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S38864

R:Kipp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL Data Library, November 1993

A:Description: Combination of a defined specificity and desired isotype by cloning of

A:Reference number: S38864

A:Accession: S38864

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-548 <KIP>

A:Cross-references: EMBL:Z27397; NID:g416537; PIDN:CAA81788.1; PID:g940782

C:Superfamily: immunoglobulin homology

F:353-421/Domain: immunoglobulin homology <IMM>

Query Match 75.0%; Score 39; DB 2; Length 548;


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Best Local Similarity 80.0%; Pred. No. 5.4;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
Db 26 GLTFSSYGMS 35

RESULT 8
S33406
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 17-Jul-1998
C:Accession: S33406
R:Kettleborough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.M.
Eur. J. Immunol. 23, 206-211, 1993
A:Title: Optimization of primers for cloning libraries of mouse immunoglobulin genes usi
A:Reference number: S33391; MUID:93122092
A:Accession: S33406
A:Molecule type: mRNA
A:Residues: 1-40 <KET>
A:Cross-references: EMBL:X73009
A:Experimental source: strain BALB/c
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-40/Domain: immunoglobulin homology (fragment) <IMM>

Query Match 73.1%; Score 38; DB 2; Length 40;
Best Local Similarity 80.0%; Pred. No. 0.52;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
Db 26 GFTFSSYTMS 35

RESULT 9
C25913
Ig heavy chain V region (BFL14) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 16-Aug-1996
C:Accession: C25913
R:Lawler, A.M.; Lin, P.S.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 84, 2454-2458, 1987
A:Title: Adult B-cell repertoire is biased toward two heavy-chain variable-region genes
A:Reference number: A94148; MUID:87175692
A:Accession: C25913
A:Molecule type: DNA
A:Residues: 1-83 <LAW>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 73.1%; Score 38; DB 2; Length 83;
Best Local Similarity 80.0%; Pred. No. 1.1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
Db 11 GFTFSSYGMS 20

RESULT 10
S26891
Ig heavy chain V region (DP-58) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26891
R:Tominson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of v
A:Reference number: S26885; MUID:93021117

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A:Accession: S26891
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12358; NID:g32935; PIDN:CAA78228.1; PID:g32936
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 73.1%; Score 38; DB 2; Length 98;
Best Local Similarity 70.0%; Pred. No. 1.4;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
Db 26 GFTFSSYEMN 35

RESULT 11
PL0248
Ig heavy chain V region (anti-DNA, DP12VH) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C:Accession: PL0248
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A:Reference number: PL0231; MUID:90111618
A:Accession: PL0248
A:Molecule type: mRNA
A:Residues: 1-108 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-24/Region: framework 1
F:9-92/Domain: immunoglobulin homology <IMM>
F:25-29/Region: complementarity-determining 1
F:30-43/Region: framework 2
F:44-60/Region: complementarity-determining 2
F:61-92/Region: framework 3
F:93-99/Region: complementarity-determining 3
F:100-108/Region: framework 4

Query Match 73.1%; Score 38; DB 2; Length 108;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
Db 20 GFTFSSYTMS 29

RESULT 12
PH1006
Ig heavy chain V region (clone 202.33) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1006
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444
A:Accession: PH1006
A:Molecule type: mRNA
A:Residues: 1-108 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:10-93/Domain: immunoglobulin homology <IMM>

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Query Match      73.1%; Score 38; DB 2; Length 108;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
Db 21 GTTFSSYGMS 30

RESULT 13
AVDGGM
Ig heavy chain V region (Gom) - dog
C:Species: Canis lupus familiaris (dog)
C:Date: 31-May-1979 #sequence_revision 31-May-1979 #text_change 31-Mar-1997
C:Accession: A02067
R:Wasserman, R.L.; Capra, J.D.
Biochemistry 16, 3160-3168, 1977
A:Title: Primary structure of the variable regions of two canine immunoglobulin heavy chain
A:Reference number: A90403; MUID:77242268
A:Accession: A02067
A:Molecule type: protein
A:Residues: 1-114 <WAS>
C:Comment: This chain was isolated from a myeloma protein.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
F:22-96/Disulfide bonds: #status predicted

Query Match      73.1%; Score 38; DB 1; Length 114;
Best Local Similarity 77.8%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 9
Db 26 GTTFSGYDM 34

RESULT 14
HWMS84
Ig heavy chain precursor V region (5-84) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
C:Accession: J0505
R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
A:Reference number: J0501; MUID:89279149
A:Accession: J0505
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-117 <LEV>
A:Experimental source: strain BALB/cJ
A:Note: This sequence belongs to the VH7183 subfamily
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIC>
F:20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:41-115/Disulfide bonds: #status predicted

Query Match      73.1%; Score 38; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
Db 45 GTTFSSYTMS 54

RESULT 15
PL0249
Ig heavy chain V region (anti-DNA, 3E12VH) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C:Accession: PL0249
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A:Reference number: PL0231; MUID:90111618
A:Accession: PL0249
A:Molecule type: mRNA
A:Residues: 1-117 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-30/Region: framework 1
F:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:36-49/Region: framework 2
F:50-66/Region: complementarity-determining 2
F:67-98/Region: framework 3
F:99-108/Region: complementarity-determining 3
F:109-117/Region: framework 4

Query Match      73.1%; Score 38; DB 2; Length 117;
Best Local Similarity 80.0%; Pred. No. 1.6;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
Db 26 GTTFSSYTMS 35

Search completed: May 27, 2000, 19:26:37
Job time: 1760 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:50:48 ; Search time 69.28 Seconds
(without alignments)
4.396 Million cell updates/sec

Title: US-09-016-061-48
Perfect score: 52
Sequence: 1 GTTFSSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	76.9	117	1 HV55_MOUSE	P18526 mus musculus
2	38	73.1	114	1 HV01_CANFA	P01784 canis famill
3	38	73.1	117	1 HV54_MOUSE	P18525 mus musculus
4	37	71.2	97	1 HV56_MOUSE	P18527 mus musculus
5	37	71.2	117	1 HV3C_HUMAN	P01764 homo sapien
6	36	69.2	117	1 HV53_MOUSE	P18524 mus musculus
7	35	67.3	117	1 HV52_MOUSE	P06327 mus musculus
8	35	67.3	117	1 HV59_MOUSE	P18530 mus musculus
9	35	67.3	569	1 AMY_STRVL	P22998 streptomyc
10	34	65.4	114	1 HV00_MOUSE	P01741 mus musculus
11	34	65.4	527	1 YC43_SCHPO	O14057 schizosacch
12	34	65.4	641	1 FIB2_PETMA	P33573 petromyzon
13	34	65.4	703	1 CDGT_BACS2	P31746 bacillus sp
14	34	65.4	704	1 CDGT_BACOH	P27036 bacillus oh
15	33	63.5	115	1 HV3D_HUMAN	P01765 homo sapien
16	33	63.5	650	1 RAE1_RAT	P37727 rattus norv
17	33	63.5	710	1 CDGT_THETU	P26827 thermoanaer
18	33	63.5	1024	1 RIP3_MOUSE	P97434 mus musculus
19	33	63.5	2211	1 FA5_BOVIN	Q28107 bos taurus
20	32	61.5	314	1 RHRA_RHIME	Q92366 rhizobium m
21	32	61.5	441	1 DNB2_ADEG1	O64759 avian adeno
22	32	61.5	444	1 CIAH_STRPN	O54955 streptococc
23	32	61.5	576	1 RIC1_RICCO	P02879 ricinus com
24	31	59.6	116	1 HV1A_RABIT	P01826 oryctolagus
25	31	59.6	117	1 HV2B_RABIT	P01828 oryctolagus
26	31	59.6	120	1 HV3E_HUMAN	P01766 homo sapien
27	31	59.6	121	1 HV3J_HUMAN	P01771 homo sapien
28	31	59.6	326	1 YQBQ_BACSU	P45950 bacillus su
29	31	59.6	391	1 Y534_METJA	Q57954 methanococc
30	31	59.6	401	1 ODO2_RICPR	Q92d44 rickettsia
31	31	59.6	409	1 ODO2_FUGRU	Q90512 fugu rubrip
32	31	59.6	442	1 ODO2_RAT	O01205 rattus norv
33	31	59.6	453	1 ODO2_HUMAN	P36957 homo sapien
34	31	59.6	463	1 ODO2_YEAST	P19262 saccharomyc

35	31	59.6	589	1 RESE_BACSU	P35164 bacillus su
36	31	59.6	685	1 CRPI_PERAM	Q25641 periplaneta
37	31	59.6	711	1 CDGT_BACST	P31797 bacillus st
38	31	59.6	742	1 PURL_BACSU	P12042 bacillus su
39	31	59.6	902	1 YC47_SCHPO	O14053 schizosacch
40	31	59.6	923	1 PH87_YEAST	P25360 saccharomyc
41	31	59.6	995	1 YIQ9_YEAST	P40442 saccharomyc
42	31	59.6	997	1 YPX2_CAEEL	Q20256 caenorhabdi
43	30	57.7	114	1 HV3B_HUMAN	P01763 homo sapien
44	30	57.7	117	1 HV03_CARAU	P19180 carassius a
45	30	57.7	117	1 HV58_MOUSE	P18529 mus musculu

ALIGNMENTS

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RESULT 1
HV55_MOUSE
ID HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 345 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS; THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; J05052; HVMS34.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 58 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 49380B4627ACA99A CRC64;

```

Query Match 76.9%; Score 40; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.26;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
+ + + + + + + + + +
Db 45 GFAFSSYDMS 54

```

RESULT 2
HV01_CANFA
ID HV01_CANFA STANDARD; PRT; 114 AA.
AC P01784;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION GOM.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RP SEQUENCE.

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RX MEDLINE: 77242268.
RA Wasserman R.L., Capra J.D.;
RT "Primary structure of the variable regions of two canine
RL immunoglobulin heavy chains.";
RL Biochemistry 16:3160-3168(1977).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR: A02067; AVDGGM.
DR PFAM: PF00047; ig: 1.
KW Immunoglobulin V region.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12430 MW; BLD4745D2C4E13C4 CRC64;

Query Match 73.1%; Score 38; DB 1; Length 114;
Best Local Similarity 77.8%; Pred. No. 0.64;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 9
Db 26 GITFGYDM 34

RESULT 3
HV54_MOUSE
ID HV54_MOUSE STANDARD; PRT; 117 AA.
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 5-84 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/CJ;
RX MEDLINE: 89279149.
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: J70505; HVMS84.
DR PFAM: PF00047; ig: 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 19
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 73.1%; Score 38; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.66;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
Db 45 GTTFSSYDMS 54

RESULT 4
HV56_MOUSE
ID HV56_MOUSE STANDARD; PRT; 97 AA.
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)

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DE IG HEAVY CHAIN V REGION 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/CJ;
RX MEDLINE: 89279149.
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: J70504; HVMS91.
DR PFAM: PF00047; ig: 1.
KW Immunoglobulin V region.
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB333FF55DA893 CRC64;

Query Match 71.2%; Score 37; DB 1; Length 97;
Best Local Similarity 80.0%; Pred. No. 0.85;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
Db 26 GTTFSSYAMS 35

RESULT 5
HV3C_HUMAN
ID HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION VH26 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 81101090.
RA Matthysens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
RT heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: J00236; AAA53516.1; -.
DR EMBL: M35415; AAA58735.1; -.
DR PIR: A02047; H3HU26.
DR PFAM: PF00047; ig: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 71.2%; Score 37; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 1;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
Db 1 | | | | | | | |

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Db 45 GTTFSSYAMS 54

RESULT 6

HV53_MOUSE
ID HV53_MOUSE STANDARD; PRT; 117 AA.
AC P18524; IG HEAVY CHAIN V REGION RF.
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION RF PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0503; HVMSRF.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION RF.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 58 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 69 85 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 69.2%; Score 36; DB 1; Length 117;

Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10

Db 45 GTTFSSYMS 54

RESULT 7

HV52_MOUSE
ID HV52_MOUSE STANDARD; PRT; 117 AA.
AC R06327; IG HEAVY CHAIN V REGION RF.
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION VH558 A1/A4 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE; 85099340.
RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
unrearranged VH gene segments.";
RL Cell 40:271-281(1985).
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CC EMBL; M13787; AAA38499.1; -.

DR PIR; AQ0209; HVMSA1.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 58 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 69 85 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 67.3%; Score 35; DB 1; Length 117;

Best Local Similarity 60.0%; Pred. No. 2.6;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10

Db 45 GTTFSSYDIN 54

RESULT 8

HV59_MOUSE
ID HV59_MOUSE STANDARD; PRT; 117 AA.
AC P18530;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 7-39 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0507; HVMS39.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 7-39.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 58 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 69 85 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;

Query Match 67.3%; Score 35; DB 1; Length 117;

Best Local Similarity 70.0%; Pred. No. 2.6;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10

Db 45 GTTFSSYNGMS 54

RESULT 9

AMY_STRVL
ID AMY_STRVL STANDARD; PRT; 569 AA.

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AC 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE ALPHA-AMYLASE PRECURSOR (EC 3.2.1.1) (1,4-ALPHA-D-GLUCAN
DE GLUCANOHYDROLASE).
DE AML.
GN Streptomyces violaceus (Streptomyces venezuelae).
OS Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 15068;
RX MEDLINE; 89232724.
RA Virolle M.-J., Long C.M., Chang S., Bibb M.J.;
RT "Cloning, characterisation and regulation of an alpha-amylase gene
RT from Streptomyces venezuelae.";
RL Gene 74:321-334 (1988).
CC -!- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-ALPHA-GLUCOSIDIC
CC LINKAGES IN OLIGOSACCHARIDES AND POLYSACCHARIDES.
CC -!- INDUCTION: BY MALTOSE, AND REPRESSION BY GLUCOSE.
CC -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
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CC -----
DR EMBL; M25263; AAB36561.1; -.
DR PIR; JS0101; JS0101.
DR HSSP; P00690; LOSE.
DR PFAM; PF00128; alpha-amylase; 1.
DR PFAM; PF00686; CBD_4; 1.
DR PRINTS; PR00110; ALPHAAMYLASE.
KW Hydrolase; Glycosidase; Carbohydrate metabolism; Signal.
FT SIGNAL 1 28
FT CHAIN 29 569
FT ACT_SITE 205 205 BY SIMILARITY.
FT ACT_SITE 209 209 BY SIMILARITY.
FT ACT_SITE 296 296 BY SIMILARITY.
SQ SEQUENCE 569 AA; 60637 MW; 14CA5BD56720043 CRC64;

Query Match 67.3%; Score 35; DB 1; Length 569;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYD 8
Db 132 GTSFSKYD 139

RESULT 10
ID HV00_MOUSE STANDARD; PRT; 114 AA.
AC P01741.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 21-JUL-1986 (Rel. 01, Last annotation update)
DE IG HEAVY CHAIN V REGION (ANTI-ARSONATE ANTIBODY).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RC STRAIN-A/J;
RX MEDLINE; 79195438.
RA Capra J.D., Nisonoff A.;
RT "Structural studies on induced antibodies with defined idiotypic

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RT specificities. VII. The complete amino acid sequence of the heavy
RT chain variable region of anti-p-azophenylarsenate antibodies from A/J
RT mice bearing a cross-reactive idiotype.";
RL J. Immunol. 123:279-284 (1979).
CC -!- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF
CC THE IGG1 SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V
CC REGION SEQUENCE.
CC PIR; A02022; GIMSAA.
DR PIR; A02022; GIMSAA.
DR PFAM; PF00047; ig; 1.
KW Immunoglobulin V region; Antiarsonate antibody.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12555 MW; 99DD8F0B6A69F4BE CRC64;

Query Match 65.4%; Score 34; DB 1; Length 114;
Best Local Similarity 66.7%; Pred. No. 4.1;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 9
Db 26 GYTFFSYEL 34

RESULT 11
YC43_SCHPO STANDARD; PRT; 527 AA.
ID YC43_SCHPO
AC O14057;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE HYPOHETICAL 58.0 KD PROTEIN C1672.03C IN CHROMOSOME III.
GN SPCC1672.03C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
OC Schizosaccharomycetaceae; Schizosaccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-972;
RA Hilbert H., Duesterhoeft A., Wood V., Rajandream M.A., Barrell B.G.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE ATZ/TRZ FAMILY.
CC -----
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CC -----
DR EMBL; AL031324; CAA20441.1; -.
KW Hypothetical protein; Hydrolase.
SQ SEQUENCE 527 AA; 58047 MW; 23D9A3F1117601C1 CRC64;

Query Match 65.4%; Score 34; DB 1; Length 527;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTFSSY 7
Db 132 GTTFASY 138

RESULT 12
FIB2_PETMA STANDARD; PRT; 641 AA.
ID FIB2_PETMA
AC P33573;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE FIBRINOGEN ALPHA-2 CHAIN PRECURSOR.
OS Petromyzon marinus (Sea lamprey).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Cephalaspidomorphi;
 RN Petromyzontiformes; Petromyzontidae; Petromyzon.
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RX MEDLINE; 92196058.
 RA Pan Y., Doolittle R.F.;
 RT "cDNA sequence of a second fibrinogen alpha chain in lamprey: an
 RT archetypal version alignable with full-length beta and gamma
 chains";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2066-2070(1992).
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 CC POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 CC AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 CC (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 CC THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CC CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 CC RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT. THE SOFT CLOT IS
 CC CONVERTED INTO THE HARD CLOT BY FACTOR XIII WHICH CATALYZES THE
 CC EPSTILON-(GAMMA-GLUTAMYL)LYSINE CROSS-LINKING BETWEEN GAMMA CHAINS
 CC (STRONGER) AND BETWEEN ALPHA CHAINS (WEAKER) OF DIFFERENT
 CC MONOMERS.
 CC -!- SIMILARITY: ITS N-TERMINAL HALF IS HOMOLOGOUS TO THE ALPHA CHAINS,
 CC WHILE ITS C-TERMINAL HALF IS HOMOLOGOUS TO THE C-TERMINI OF THE
 CC BETA AND THE GAMMA CHAINS.
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 CC -----
 CC EMBL; M84565; AAA73183.1; -;
 DR EMBL; M84482; AAA49264.1; -;
 DR PIR; S27940; S27940.
 DR HSSP; P02671; 1FZD.
 DR PROSITE; PS00514; FIBRIN_AG_C_DOMAIN; 1.
 DR PFAM; PF00147; fibrinogen_C; 1.
 KW Blood coagulation; Plasma; Signal; Repeat.
 FT SIGNAL 1 23 POTENTIAL.
 FT PEPTIDE 24 31 FIBRINOPEPTIDE A (BY SIMILARITY).
 FT CHAIN 32 64 FIBRINOGEN ALPHA-2 CHAIN.
 FT SITE 31 32 CLEAVAGE (BY THROMBIN; RELEASE
 FT FIBRINOPEPTIDE A).
 FT DOMAIN 293 316 SER-RICH.
 FT DISULFID 45 45 INTERCHAIN (WITH THE ALPHA CHAIN)
 FT (BY SIMILARITY).
 FT DISULFID 54 54 INTERCHAIN (WITH THE BETA CHAIN)
 FT (BY SIMILARITY).
 FT DISULFID 63 63 INTERCHAIN (WITH THE GAMMA CHAIN)
 FT (BY SIMILARITY).
 FT DISULFID 67 67 INTERCHAIN (WITH THE BETA CHAIN)
 FT (BY SIMILARITY).
 FT DISULFID 179 179 INTERCHAIN (WITH THE GAMMA CHAIN)
 FT (BY SIMILARITY).
 FT DISULFID 183 183 INTERCHAIN (WITH THE BETA CHAIN)
 FT (BY SIMILARITY).
 FT DISULFID 404 435 BY SIMILARITY.
 FT DISULFID 571 584 BY SIMILARITY.
 FT CARBOHYD 271 271 POTENTIAL.
 FT CARBOHYD 397 397 POTENTIAL.
 FT CARBOHYD 458 458 POTENTIAL.
 SQ SEQUENCE 641 AA; 70756 MW; CA991A8DD698BFB5 CRC64;

Query Match 65.4%; Score 34; DB 1; Length 641;
 Best Local Similarity 75.0%; Pred. No. 27;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYD 8
 Db 553 GMTFSTVD 560

RESULT 13
 CDGT_BACS2
 ID CDGT_BACS2 STANDARD; PRT; 703 AA.
 AC P31746;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE CYCLOMALTODEXTRIN GLUCANOTRANSFERASE PRECURSOR (EC 2.4.1.19)
 DE (CYCLODEXTRIN-GLYCOSYLTRANSFERASE) (CGTASE).
 GN CGT.
 OS Bacillus sp. (strain 1-1).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-52.
 RA Schmid G., Englbrecht A., Schmid D.;
 RT "Cloning and nucleotide sequence of a cyclodextrin glycosyltransferase
 RT gene from the alkalophilic Bacillus 1-1";
 RL (in) Huber O., Szejtli J. (eds.);
 RL Proceedings of the fourth international symposium on cyclodextrins,
 RL pp.71-76, Kluwer Academic Publishers, Dordrecht and Boston (1988).
 CC -!- CATALYTIC ACTIVITY: DEGRADE STARCH TO CYCLODEXTRINS BY FORMATION
 CC OF A 1,4'-ALPHA-D-GLUCOSIDIC BOND.
 CC -!- COFACTOR: BINDS TWO CALCIUM IONS.
 CC -!- SUBUNIT: MONOMER.
 CC -!- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
 CC IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
 CC IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
 CC ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
 CC ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
 CC MALTOOLIGOSACCHARIDE PRODUCED.
 CC -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
 CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
 CC PIR; S26399; ALBSX1.
 DR HSSP; P31797; ICYG.
 DR PFAM; PF00128; alpha-amylase; 1.
 DR PFAM; PF00686; CBD.4; 1.
 KW Transferase; Glycosyltransferase; Calcium; Signal.
 FT SIGNAL 1 29
 FT CHAIN 30 703 CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
 FT DOMAIN 30 160 A1.
 FT DOMAIN 161 224 B.
 FT DOMAIN 225 428 A2.
 FT DOMAIN 429 516 C.
 FT DOMAIN 517 600 D.
 FT DOMAIN 601 703 E.
 FT DISULFID 68 75 BY SIMILARITY.
 FT ACT_SITE 251 251 BY SIMILARITY.
 FT ACT_SITE 279 279 BY SIMILARITY.
 FT ACT_SITE 350 350 BY SIMILARITY.
 SQ SEQUENCE 703 AA; 78663 MW; 4D973FB21D0D9B0A CRC64;

Query Match 65.4%; Score 34; DB 1; Length 703;
 Best Local Similarity 70.0%; Pred. No. 30;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 Db 202 GTDFSSYEDS 211

RESULT 14
 CDGT_BACOH
 ID CDGT_BACOH STANDARD; PRT; 704 AA.
 AC P27036;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)


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DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CYCLOMALTODEXTRIN GLUCANOTRANSFERASE PRECURSOR (EC 2.4.1.19)
DE (CYCLODEXTRIN-GLYCOSYLTRANSFERASE) (CGTASE).
GN CGT.
OS Bacillus ohbensis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 92000599.
RA Sin K.A., Nakamura A., Kobayashi K., Masaki H., Uozumi T.;
RT "Cloning and sequencing of a cyclodextrin glucanotransferase gene
RT from Bacillus ohbensis and its expression in Escherichia coli.";
RL Appl. Microbiol. Biotechnol. 35:600-605(1991).
CC -|- CATALYTIC ACTIVITY: DEGRADE STARCH TO CYCLODEXTRINS BY FORMATION
CC OF A 1,4-ALPHA-D-GLUCOSIDIC BOND.
CC -|- COFACTOR: BINDS TWO CALCIUM IONS.
CC -|- SUBUNIT: MONOMER.
CC -|- MISCELLANEOUS: CGTASE MAY CONSIST OF TWO PROTEIN DOMAINS: THE ONE
CC IN THE AMINO-TERMINAL SIDE CLEAVES THE ALPHA-1,4-GLUCOSIDIC BOND
CC IN STARCH, AND THE OTHER IN THE C-TERMINAL SIDE CATALYZES OTHER
CC ACTIVITIES, INCLUDING THE RECONSTITUTION OF AN
CC ALPHA-1,4-GLUCOSIDIC LINKAGE FOR CYCLIZING THE
CC MALTOOLIGOSACCHARIDE PRODUCED.
CC -|- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D90243; BAAL4289.1; -.
DR HSPB; P31797; LCYG.
DR PFAM; PF00128; alpha-amylase; 1.
DR PFAM; PF00686; CBD_4; 1.
KW Transferase; Glycosyltransferase; Calcium; Signal.
FT SIGNAL 1 29
FT CHAIN 30 704 CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
FT DISULFID 68 75 BY SIMILARITY.
FT ACT_SITE 251 251 BY SIMILARITY.
FT ACT_SITE 279 279 BY SIMILARITY.
FT ACT_SITE 330 330 BY SIMILARITY.
SQ SEQUENCE 704 AA; 78621 MW; 04FA14951D5ACECB CRC64;

Query Match 65.4%; Score 34; DB 1; Length 704;
Best Local Similarity 70.0%; Pred. No. 30;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
DB 202 GTDFFSYEDS 211

RESULT 15
HV3D_HUMAN
ID HV3D_HUMAN STANDARD; PRT; 115 AA.
AC P01765;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION TIL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RN SEQUENCE.
RX MEDLINE; 78005528.
RA Wang A.-C., Wang I.Y., Fudenberg H.H.;

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RT "Immunoglobulin structure and genetics. Identity between variable
RT regions of a mu and a gamma2 chain.";
RL J. Biol. Chem. 252:7192-7199(1977).
CC -|- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
CC OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
CC GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
CC IDENTICAL.
DR PIR; A02048; H3HUTL.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;

Query Match 63.5%; Score 33; DB 1; Length 115;
Best Local Similarity 70.0%; Pred. No. 6.5;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
DB 26 GTDFFSYEDS 35

```

Search completed: May 27, 2000, 20:07:07
Job time: 979 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 18:59:07 ; Search time 199.56 Seconds
(without alignments)
3.474 Million cell updates/sec

Title: US-09-016-061-48
Perfect score: 52
Sequence: 1 GTTFSSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 segs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SPTREMBL_12.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	38	73.1	370	2 Q52474	Q52474 pseudomonas
2	35	67.3	147	4 Q9Y509	Q9Y509 homo sapien
3	35	67.3	892	5 P91644	P91644 drosophila
4	34	65.4	153	1 Q59587	Q59587 methanobact
5	34	65.4	153	1 Q26237	Q26237 methanobact
6	34	65.4	191	2 Q92EB4	Q92EB4 rickettsia
7	34	65.4	314	5 Q97279	Q97279 plasmodium
8	34	65.4	481	2 Q9X4U5	Q9X4U5 streptococc
9	34	65.4	692	2 Q30565	Q30565 bacillus br
10	34	65.4	704	2 Q82984	Q82984 bacillus sp
11	34	65.4	725	2 Q59239	Q59239 bacillus sp
12	34	65.4	855	5 O15797	O15797 p strain dd
13	34	65.4	2325	10 Q41743	Q41743 zea mays (m
14	33	63.5	251	11 Q63800	Q63800 rattus norv
15	33	63.5	292	3 Q05533	Q05533 saccharomyc
16	33	63.5	287	2 Q70010	Q70010 salmonella
17	32	61.5	118	1 Q9Y9X2	Q9Y9X2 aeropyrum p
18	32	61.5	130	2 Q25823	Q25823 helicobacte
19	32	61.5	130	2 Q9ZK01	Q9ZK01 helicobacte
20	32	61.5	258	2 Q83768	Q83768 treponema p

21	32	61.5	314	2 Q9Z3Q6	Q9Z3Q6 rhizobium m
22	32	61.5	464	2 Q66863	Q66863 aquifex aeo
23	32	61.5	491	2 P94289	P94289 bacillus ci
24	32	61.5	541	10 Q41174	Q41174 ricinus com
25	32	61.5	820	12 Q89364	Q89364 paramecium
26	32	61.5	1586	5 Q18798	Q18798 caenorhabdi
27	32	61.5	2133	12 Q98203	Q98203 molluscum c
28	32	61.5	4564	5 Q77075	Q77075 drosophila
29	31.5	60.6	569	2 Q9ZLB2	Q9ZLB2 helicobacte
30	31	59.6	82	8 Q32985	Q32985 pinus thunb
31	31	59.6	169	10 Q9ZSP1	Q9ZSP1 oryza sativ
32	31	59.6	223	5 P91245	P91245 caenorhabdi
33	31	59.6	235	2 Q9Z8L9	Q9Z8L9 chlamydia p
34	31	59.6	268	3 Q94665	Q94665 schizosacch
35	31	59.6	285	5 Q22849	Q22849 caenorhabdi
36	31	59.6	302	5 Q61139	Q61139 cryptospori
37	31	59.6	314	10 Q23331	Q23331 arabidopsis
38	31	59.6	325	5 Q21300	Q21300 caenorhabdi
39	31	59.6	340	3 Q13749	Q13749 schizosacch
40	31	59.6	367	5 Q16870	Q16870 caenorhabdi
41	31	59.6	390	2 Q85598	Q85598 bruceella ab
42	31	59.6	401	2 Q9ZDY4	Q9ZDY4 rickettsia
43	31	59.6	405	5 Q18134	Q18134 caenorhabdi
44	31	59.6	452	5 Q45148	Q45148 caenorhabdi
45	31	59.6	475	2 Q9X7G9	Q9X7G9 myxococcus

ALIGNMENTS

RESULT 1
Q52474
ID Q52474 PRELIMINARY; PRT; 370 AA.
AC Q52474;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE (STRAIN DC3000).
GN HRPZ.
OS Pseudomonas syringae.
OC Bacteria; Proteobacteria; gamma subdlvision; Pseudomonas group;
OC Pseudomonas.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DC3000;
RX MEDLINE; 96025089.
RA PRESTON G., HUANG H.C., HE S.Y., COLLIER A.;
RT "The HrpZ proteins of Pseudomonas syringae pvs. syringae, glycinea,
RT and tomato are encoded by an operon containing Versinia ysc homologs
RT and elicit the hypersensitive response in tomato but not soybean.";
RL Mol. Plant Microbe Interact. 8:717-732(1995).
DR EMBL; L41861; AAB00127.1; -.
SQ SEQUENCE 370 AA; 36584 MW; 15D35D07 CRC32;

Query Match 73.1%; Score 38; DB 2; Length 370;
Best Local Similarity 88.9%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 9
Db 159 GTTFSSDDM 167
|||||

RESULT 2
Q9Y509 PRELIMINARY; PRT; 147 AA.
ID Q9Y509
AC Q9Y509;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE VH3 PROTEIN (FRAGMENT).
GN VH3.

```

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 96071149.
RA CAO J., VESCOIO R.A., RETTIG M.B., HONG C.H., KIM A., LEE J.C.,
RA LICHTENSTEIN A.K., BERENSON J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1948-1953(1995).
DR EMBL: S80860; AAD14339.1; -.
FT NON_TER 1
SQ SEQUENCE 147 AA; 15768 MW; BDD8F70 CRC32;

Query Match 67.3%; Score 35; DB 4; Length 147;
Best Local Similarity 70.0%; Pred. No. 10;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
Db | |||:| ||
26 GTTFSTYGMS 35

RESULT 3
P91644 PRELIMINARY; PRT; 892 AA.
AC P91644;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DE KEK2 PRECURSOR (FRAGMENT).
GN KEK2.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
[1]
RN SEQUENCE FROM N.A.
RX STRAIN-OREGON R;
RX MEDLINE: 97223506.
RA MUSACCHIO M., PERRIMON N.;
RT "The Drosophila kekkan genes: novel members of both the leucine-rich
RT repeat and immunoglobulin superfamilies expressed in the CNS.";
RL Dev. Biol. 178:63-76(1996).
DR EMBL: U42768; AAC47405.1; -.
DR FLYBASE: FBgn0015400; kek2.
DR PFAM: PF00047; ig; 1.
DR PFAM: PF00560; LRR; 5.
DR PFAM: PF01463; LRRCT; 1.
KW Signal.
FT NON_TER 1
FT SIGNAL <1 17
FT CHAIN 18 892
FT CHAIN KEK2
SQ SEQUENCE 892 AA; 97294 MW; 93DCE450 CRC32;

Query Match 67.3%; Score 35; DB 5; Length 892;
Best Local Similarity 66.7%; Pred. No. 75;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 9
Db | |||:| |
349 GTTFSTYNTL 357

RESULT 4
Q59587 PRELIMINARY; PRT; 153 AA.
ID Q59587
AC Q59587;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)

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DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE RIBOFLAVIN SYNTHASE (EC 2.5.1.9).
GN RIBC.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanobacterium.
[1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 1-42 AND 129-151.
RA EBERHARDT S., KORN S., LOTSPEICH F., BACHER A.;
RL J. Bacteriol. 179:2938-2943(1997).
CC -1- FUNCTION: THE RELATIVELY LOW ACTIVITY OF THIS ENZYME SUGGESTED
CC THAT 6,7-DIMETHYL-8-RIBITYLLUMAZINE MIGHT NOT BE ITS NATURAL
CC SUBSTRATE.
CC -1- CATALYTIC ACTIVITY: 2 6,7-DIMETHYL-8-(1-D-RIBITYL)LUMAZINE -
CC RIBOFLAVIN + 4-(1-D-RIBITYLAMINO)-5-AMINO-2,6-DIHYDROXYPYRIMIDINE.
CC -1- COFACTOR: FLAVOPROTEIN AND MAGNESIUM.
CC -1- ENZYME REGULATION: INHIBITED BY EDTA.
CC -1- PATHWAY: FINAL STEP OF RIBOFLAVIN SYNTHESIS.
CC -1- SUBUNIT: HOMOOLOGOMER.
DR EMBL: X94292; CAA63959.1; -.
KW Riboflavin biosynthesis; Transferase; Flavoprotein; Magnesium.
SQ SEQUENCE 153 AA; 16969 MW; 84FA7E52 CRC32;

Query Match 65.4%; Score 34; DB 1; Length 153;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTFSYDMS 9
Db | ||:| |
9 TTFARYDM 16

RESULT 5
O26237 PRELIMINARY; PRT; 153 AA.
ID O26237;
AC O26237;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE RIBOFLAVIN SYNTHASE (EC 2.5.1.9).
GN RIBC.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanobacterium.
[1]
RN SEQUENCE FROM N.A.
RX STRAIN-DELTA H;
RX MEDLINE: 98037514.
RA SMITH D.R., DOUCETTE-STAMM L.A., DELOUGHERY C., LEE H.-M., DUBOIS J.,
RA ALDREDGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K.,
RA HARRISON D., HOANG L., KEAGLE P., LUMM W., POTHIER B., QIU D.,
RA SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.,
RA JIWANI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S.,
RA MCDUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
RA DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT J. Bacteriol. 179:7135-7155(1997).
CC -1- CATALYTIC ACTIVITY: 2 6,7-DIMETHYL-8-(1-D-RIBITYL)LUMAZINE -
CC RIBOFLAVIN + 4-(1-D-RIBITYLAMINO)-5-AMINO-2,6-DIHYDROXYPYRIMIDINE.
CC -1- COFACTOR: FLAVOPROTEIN AND MAGNESIUM (BY SIMILARITY).
CC -1- ENZYME REGULATION: INHIBITED BY EDTA (BY SIMILARITY).
CC -1- PATHWAY: FINAL STEP OF RIBOFLAVIN SYNTHESIS.
CC -1- SUBUNIT: HOMOOLOGOMER (BY SIMILARITY).
DR EMBL: AE000802; AAB84640.1; -.
KW Riboflavin biosynthesis; Transferase; Flavoprotein; Magnesium.
SQ SEQUENCE 153 AA; 16908 MW; 04664F0F CRC32;

Query Match 65.4%; Score 34; DB 1; Length 153;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY 2 TTFSSYDM 9
 |||: |||
 Db 9 TTFARYDM 16

RESULT 6
 Q9ZEB4 PRELIMINARY; PRT; 191 AA.
 ID Q9ZEB4;
 AC Q9ZEB4;

DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE SC02 PROTEIN PRECURSOR (SC02).
 GN RP031.

OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-MADRID E;

RX MEDLINE; 99039499.

RA ANDERSSON S.G.E., ZOMORODIPOUR A., ANDERSSON J.O.,
 RA SICHERTZ-PONTEN T., ALSMARK U.C.M., PODOMSKI R.M., NAESLUND A.K.,
 RA ERIKSSON A.S., WINKLER H.H., KURLAND C.G.;

RT "The genome sequence of Rickettsia prowazekii and the origin of
 RT mitochondria."
 RL Nature 396:133-140(1998).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-MADRID E;

RA ANDERSSON S.G.E.;

RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ235270; CAA14502.1; -

SQ SEQUENCE 191 AA; 22254 MW; 22A2166E CRC32;

Query Match 65.4%; Score 34; DB 2; Length 191;
 Best Local Similarity 75.0%; Pred. No. 21;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYD 8
 |||: |||
 Db 77 GTTYSLYD 84

RESULT 7
 O97279 PRELIMINARY; PRT; 314 AA.
 ID O97279;
 AC O97279;

DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE PFC0885C PROTEIN.
 GN PFC0885C.

OS Plasmodium falciparum.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=3D7;

RA OLIVER K., BORMAN S., HARRIS D., LAWSON D., QUAIL M., BARRELL B.;

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL034559; CAB39025.1; -

SQ SEQUENCE 314 AA; 36143 MW; 78B99889 CRC32;

Query Match 65.4%; Score 34; DB 5; Length 314;
 Best Local Similarity 66.7%; Pred. No. 37;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTFSSYDMS 10
 |||: |||
 Db 70 TTFSSYDMS 78

RESULT 8
 Q9X4U5 PRELIMINARY; PRT; 481 AA.
 ID Q9X4U5;
 AC Q9X4U5;

DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE CPS2A.
 GN CPS2A.

OS Streptococcus suis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Streptococcus.
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=10;

RX MEDLINE; 99184998.

RA SMITH H.E., DAMMAN M., VAN DER VELDE J., WAGENAAR F., WISSELINK H.J.,
 RA STOCKHOFF-ZURWIENEN N., SMITS M.A.;

RT "Identification and characterization of the cps locus of Streptococcus
 RT suis serotype 2: the capsule protects against phagocytosis and is an
 RT important virulence factor."
 RL Infect. Immun. 67:1750-1756(1999).
 DR EMBL: AF118389; AAD24447.1; -

SQ SEQUENCE 481 AA; 53291 MW; 1E3F1205 CRC32;

Query Match 65.4%; Score 34; DB 2; Length 481;
 Best Local Similarity 66.7%; Pred. No. 60;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TTFSSYDMS 10
 |||: |||
 Db 106 STFSEYEMS 114

RESULT 9
 O30565 PRELIMINARY; PRT; 692 AA.
 ID O30565;
 AC O30565;

DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE CYCLODEXTRIN GLYCOSYLTRANSFERASE (EC 2.4.1.19)
 DE (CYCLODEXTRIN GLYCOSYLTRANSFERASE)
 DE (CYCLODEXTRIN-GLYCOSYLTRANSFERASE) (BACILLUS MACERANS AMYLASE)
 DE (CYCLODEXTRIN GLUCANOTRANSFERASE).
 OS Bacillus brevis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Brevibacillus.
 RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CD162;

RA KIM M.H., SOHN C.B., OH T.K.;

RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: DEGRADATES STARCH TO CYCLODEXTRINS BY FORMATION
 CC OF A 1,4-ALPHA-D- GLUCOSIDIC BOND.
 DR EMBL: AF011388; AAB65420.1; -

DR HSSP; P31797; 1CYG.

DR PFAM; PF00128; alpha-amylase; 1.

DR PFAM; PF00686; CBD_4; 1.

KW Transferase; Glycosyltransferase.

SQ SEQUENCE 692 AA; 77404 MW; 556D245B CRC32;

Query Match 65.4%; Score 34; DB 2; Length 692;
 Best Local Similarity 70.0%; Pred. No. 89;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 |||: |||
 Db 193 GTDFSSYEDS 202

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RESULT 10
ID O82984 PRELIMINARY; PRT; 704 AA.
AC O82984;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE CYCLOMALTODEXTRIN GLUCANOTRANSFERASE.
GN CGT.
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE FROM N.A.
RA OHKAN K., KURIKI T.;
RT "Alkalophilic Bacillus DNA fragment involving MBP, CGTase, CDBase
gene.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB015670; BAA31539.1; -.
DR HSSP; P31797; 1CYG.
DR PFAM; PF00128; alpha-amylase; 1.
DR PFAM; PF00686; CBD_4; 1.
KW Transferase.
SQ SEQUENCE 704 AA; 78528 MW; 7FD9BBBC CRC32;

Query Match 65.4%; Score 34; DB 2; Length 704;
Best Local Similarity 70.0%; Pred. No. 91;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
||| ||||: |
Db 202 GTDFSSYEDS 211

RESULT 11
ID Q59239 PRELIMINARY; PRT; 725 AA.
AC Q59239;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE CYCLODEXTRIN GLUCANOTRANSFERASE PRECURSOR (EC 2.4.1.19)
DE (CYCLOMALTODEXTRIN GLUCANOTRANSFERASE)
DE (CYCLODEXTRIN-GLYCOSYLTRANSFERASE) (BACILLUS MACERANS AMYLASE).
OS Bacillus sp.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE FROM N.A.
RA SCHMID G., HUBER O., SEZITIL J.;
RT "Cloning and nucleotide sequence of a cyclodextrin glycosyltransferase
gene from the alkalophilic Bacillus 1-1.";
RL Proc. Fourth Int. Symp. Cyclods 1:71-76(1988).
RN [2]
RP SEQUENCE FROM N.A.
RA KITAMOTO N., KIMURA T., KITO Y., OHMIYA K.;
RT "Cloning and sequencing of the gene encoding cyclodextrin
glucanotransferase from Bacillus sp. KC201.";
RL J. Ferment. Bioeng. 74:345-351(1992).
CC -1- CATALYTIC ACTIVITY: DEGRADATES STARCH TO CYCLODEXTRINS BY FORMATION
OF A 1,4-ALPHA-D- GLUCOSIDIC BOND.
DR EMBL; D13068; BAA02380.1; -.
DR HSSP; P31797; 1CYG.
DR PFAM; PF00128; alpha-amylase; 1.
DR PFAM; PF00686; CBD_4; 1.
KW Signal; Transferase; Glycosyltransferase.
FT SIGNAL 1 51
FT CHAIN 52 725

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SQ SEQUENCE 725 AA; 80841 MW; E8A2DD1B CRC32;

Query Match 65.4%; Score 34; DB 2; Length 725;
Best Local Similarity 70.0%; Pred. No. 94;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
||| ||||: |
Db 224 GTDFSSYEDS 233

RESULT 12
ID O15797 PRELIMINARY; PRT; 855 AA.
AC O15797;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE STRAIN DD2 HEAT SHOCK PROTEIN 86 (HSP86), O1 (O1), O3 (O3), O2
(O2), C88 (CG8), CG4 (CG4), CG3 (CG3), CG9 (CG9), CG1 (CG1), CG6
(CG6), CHLOROQUINE RESISTANCE CANDIDATE PROTEIN (CG2), AND CG7
(CG7) GENES, COMPLETE CDS (O1) (O2) (CG4) (CG9) (CG6) (CG7).
GN CG4.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DD2;
RX MEDLINE; 98054002.
RA SU X.-Z., KIRKMAN L.A., FUJIOKA H., WELLEMS T.E.;
RT "Complex polymorphisms in an approximately kDa protein are linked to
RT chloroquine-resistant P. falciparum in Southeast Asia and Africa.";
RL Cell 91:593-603(1997).
DR EMBL; AF030694; AAC47838.1; -.
DR HSSP; P19120; 1ATS.
DR PFAM; PF00012; HSP70; 1.
SQ SEQUENCE 855 AA; 97932 MW; 3F30847C CRC32;

Query Match 65.4%; Score 34; DB 5; Length 855;
Best Local Similarity 85.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTFSSYD 8
||| ||||: ||
Db 512 TTFSSYD 518

RESULT 13
ID Q41743 PRELIMINARY; PRT; 2325 AA.
AC Q41743;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE ACETYL-COENZYME A CARBOXYLASE.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
OC Poaceae; Zea.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A188; TISSUE=LEAF;
RX MEDLINE; 95357420.
RA EGLI M.A., LUTZ S.M., SOMERS D.A., GENGENBACH B.G.;
RT "A maize acetyl-coenzyme A carboxylase cDNA sequence.";
RL Plant Physiol. 108:1299-1300(1995).
DR EMBL; U19183; AAA80214.1; -.
DR HSSP; P24182; 1BNC.
DR MENDEL; 11125; Zeama;1004;11125.
DR PFAM; PF00364; biotin_lipoyl; 1.
DR PFAM; PF01039; Carboxyl_trans; 1.

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DR PFAM; PF00289; CPsase_L_chain; 2. 6B27059F CRC32;
SQ SEQUENCE 2325 AA; 257151 MW; 6B27059F CRC32;

Query Match 65.4%; Score 34; DB 10; Length 2325;
Best Local Similarity 70.0%; Pred. No. 3.5e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
Db 26 GTTFSSSSLS 35
|||||:|

RESULT 14
Q63800 PRELIMINARY; PRT; 251 AA.
AC Q63800;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-JAN-1999 (Tremblrel. 09, Last annotation update)
DE RB109.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA NISHIYAMA M.;
RT "RB109 is defined as a rat analogy of HH109."
RL Submitted (DEC-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; D26154; BAA05141.1; -.
SQ SEQUENCE 251 AA; 28608 MW; 34EC34D1 CRC32;

Query Match 63.5%; Score 33; DB 11; Length 251;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 9
Db 206 GTTVSGYDI 214
|||:|:|

RESULT 15
Q05533 PRELIMINARY; PRT; 292 AA.
AC Q05533;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE SIMILAR TO INOSITOL MONOPHOSPHATASE.
GN D9819.7.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C (AB972);
RA FULTON L.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C (AB972);
RA JOHNSTON M., ANDREWS S., BRINKMAN R., COOPER J., DING H., DU Z.,
RA FAVELLO A., FULTON L., GATTUNG S., GRECO T., KIRSTEN J., KUCABA T.,
RA HALLSWORTH K., HAWKINS J., HILLIER L., JIER M., JOHNSON D.,
RA JOHNSTON L., LANGSTON Y., LATREILLE P., LE T., MARDIS E., MENEZES S.,
RA MILLER N., NHAN M., PAULEY A., PELUSO D., RIFKEN L., RILES L.,
RA TAICH A., TREVASKIS E., VIGNATI D., WILCOX L., WOHLDMAN P., VAUDIN M.,
RA WILSON R., WATERSTON R.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
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RC STRAIN-S288C (AB972);
RA WATERSTON R.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C (AB972);
RA JIA Y., CHERRY J.M.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U51031; AAB64472.1; -.
DR HSP; P29218; 2HHM.
DR PFAM; PF00459; Inositol_P; 1.
DR PRINTS; PR00378; INOSPHPTASE.
SQ SEQUENCE 292 AA; 32092 MW; 5CBC9176 CRC32;

Query Match 63.5%; Score 33; DB 3; Length 292;
Best Local Similarity 75.0%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYD 8
Db 32 GTNFCSYD 39
|||:|:|

Search completed: May 27, 2000, 19:38:29
Job time: 2362 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 18:55:06 ; Search time 148.45 Seconds
(without alignments)
1.596 Million cell updates/sec

Title: US-09-016-061-48
Perfect score: 52
Sequence: 1 GTTFSSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23696106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	10	W76014	LM609 grafted anti
2	45	86.5	10	W76007	LM609 grafted anti
3	45	86.5	117	W76001	Vitaxin antibody h
4	42	80.8	117	W86137	Protein sequence o
5	42	80.8	123	W15536	Anti-TGF beta-1 sc
6	42	80.8	128	W54000	Anti-CD4 antibody
7	42	80.8	134	R24713	Sequence encoded b
8	42	80.8	466	R24812	Sequence encoded b
9	41	78.8	139	W21652	Humanised reshaped
10	40	76.9	10	W76015	LM609 grafted anti
11	40	76.9	117	W76003	LM609 antibody hea
12	40	76.9	239	R34511	Fv(TU25). Polypept
13	40	76.9	247	W11917	Murine MAb SK48-E2
14	39	75.0	10	W76016	LM609 grafted anti
15	39	75.0	117	W86141	Protein sequence o
16	39	75.0	119	W11919	Humanised MAb SK48
17	39	75.0	123	W53998	Anti-CD4 antibody
18	38	73.1	98	W59614	Anti-RSV F protein
19	38	73.1	116	R66307	Human immunoglobul
20	38	73.1	116	W13529	Anti-melanoma anti
21	38	73.1	118	W57591	Chimeric antibody
22	38	73.1	118	W57576	Chimeric H chain S
23	38	73.1	118	W89636	Human antibody hea
24	38	73.1	118	W89627	Mouse humanised an
25	38	73.1	119	R79876	Anti-EGFR antibody
26	38	73.1	119	R79887	Anti-EGFR antibody
27	38	73.1	119	R79888	Anti-EGFR antibody
28	38	73.1	121	W86122	Protein sequence o
29	38	73.1	122	R54301	Anti-HIV gp120 imm
30	38	73.1	122	W01259	VH region of HIV n
31	38	73.1	122	W78432	Antibody heavy cha
32	38	73.1	123	W08582	Human antibody C4.
33	38	73.1	128	R69085	Anti-HIV Fab rev16
34	38	73.1	128	R69086	Anti-HIV Fab rev20

35 38 73.1 128 1 W08734 Human anti-HIV Fab
36 38 73.1 128 1 W08735 Human anti-HIV Fab
37 38 73.1 137 1 W57603 Chimeric antibody
38 38 73.1 137 1 W57592 Chimeric antibody
39 38 73.1 137 1 W89635 Human antibody hea
40 38 73.1 137 1 W89625 Mouse humanised an
41 38 73.1 138 1 R20064 MRK16-H chain. Chl
42 38 73.1 239 1 R79866 Anti-EGFR single c
43 37 71.2 98 1 R54816 SpA-reactive VII re
44 37 71.2 102 1 R80088 Human derived heav
45 37 71.2 102 1 W95486 Human-derived RT3

ALIGNMENTS

RESULT 1

W76014
ID W76014 standard; Protein; 10 AA.
AC W76014;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDRL protein fragment #2.
KW Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
FN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49851.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PS Claim 60; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis of also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 100.0%; Score 52; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00035;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTTFSSYDMS 10
|||||
Db 1 GTTFSSYDMS 10

RESULT 2

W76007
ID W76007 standard; Protein; 10 AA.
AC W76007;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDRL protein fragment #1.
KW Vitaxin; antibody; variable region; heavy chain; Integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49844.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Disclosure; Page 40; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region; LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 86.5%; Score 45; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0072;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 | | | | | | | |
 DB 1 GTTFSSYDMS 10

RESULT 3
 W76001 ID W76001 standard; Protein; 117 AA.
 AC W76001;
 DT 02-NOV-1998 (first entry)
 DE Vitaxin antibody heavy chain variable region protein fragment.
 KW vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49820.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 1; Fig 1a; 129pp; English.

CC This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated

CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 SQ Sequence 117 AA;

Query Match 86.5%; Score 45; DB 1; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.1;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 | | | | | | | |
 DB 26 GTTFSSYDMS 35

RESULT 4
 W86137 ID W86137 standard; Protein; 117 AA.
 AC W86137;
 DT 03-MAR-1999 (first entry)
 DE Protein sequence of de-immunised humanised A33 Vh.
 KW Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK;
 KW Immunogl bulin; therapeutic; streptokinase; humanised; de-immunised.
 OS Homo sapiens.
 PN W09852976-AL.
 PD 26-NOV-1998.
 PF 21-MAY-1998; G01473.
 PR 14-APR-1998; GB-007751.
 PR 21-MAY-1997; GB-010480.
 PR 31-JUL-1997; GB-016197.
 PR 28-NOV-1997; GB-025270.
 PR 02-DEC-1997; US-067235.
 PA (BIOV-) BIOVATION LTD.
 PI Carr FJ;
 DR WPI; 99-045301/04.

PT Reducing immunogenicity of proteins - by modifying the amino acid
 PT sequence of the protein to eliminate potential epitopes for T-cells
 PT of a given species
 PS Example 5; Fig 25; 77pp; English.
 CC The invention relates to a method for the production of non-immunogenic
 CC proteins. The method comprises determining at least part of the amino
 CC acid sequence of the protein; (b) identifying in the amino acid sequence
 CC one or more potential epitopes for T-cells (T-cell epitopes) of the given
 CC species; and (c) modifying the amino acid sequence to eliminate at least
 CC one of the T-cell epitopes identified in step (b) thereby to eliminate or
 CC reduce the immunogenicity of the protein when exposed to the immune
 CC system of the given species. A method of analysing a pre-existing protein
 CC to predict the basis for immunogenic responses is also provided. The
 CC methods can be used particularly for reducing the immunogenicity of
 CC immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The
 CC products can be used for diagnosis and therapy. The present sequence
 CC represents the protein sequence of de-immunised humanised A33 Vh.
 SQ Sequence 117 AA;

Query Match 80.8%; Score 42; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 0.37;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 | | | | | | | |
 DB 26 GTTFSTYDMS 35

RESULT 5
 W15536 ID W15536 standard; Protein; 123 AA.
 AC W15536;
 DT 27-NOV-1997 (first entry)
 DE Anti-TGF beta-1 scFv antibody 27C1 VH domain.

KW Transforming growth factor beta-1; TGF-beta-1; human;
KW antibody engineering; scfv; phage display; lung fibrosis;
KW arterial injury; proliferative retinopathy; retinal detachment;
KW adult respiratory distress syndrome; liver cirrhosis;
KW post myocardial infarction; post-angioplasty restenosis;
KW scleroderma; vascular disease; cataract; glaucoma; scarring;
KW glomerulonephritis; osteoporosis; immune disease; inflammation;
KW rheumatoid arthritis; macrophage deficiency disease;
KW macrophage pathogen infection; therapy.
OS Homo sapiens.
PN GB2305921-A.
PD 23-APR-1997; 020920.
PF 07-OCT-1996; GB-001081.
PR 19-JAN-1996; GB-020486.
PR 06-OCT-1995; GB-020486.
PA (CAMEB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI Bacon L, Green JA, Jackson RH, Johnson KS, Pope AR;
PI Tempest PR, Thompson JE, Vaughan TJ, Williams AJ;
PI Wilton AJ;
DR WPI; 97-215360/20.
DR N-PSDB; T60382.
DR Agent contg. antigen-binding domain of human antibody to
PT transforming growth factor beta 1 or 2 - and nucleic acid encoding
PT it, used to neutralise effects of TGF, e.g. for control of fibrosis,
PT immune and inflammatory disease
PS Claim 16; Fig 1c(i); 184pp; English.
CC This polypeptide sequence comprises the VH domain of human scfv
CC antibody 31G9, which is specific for transforming growth factor
CC (TGF) beta-1. It is encoded by a gene (T60382) obtained from a
CC CDR3 spiking experiment. The antigen-binding domains of human
CC antibodies (see W15522-40) to TGF beta-1 and/or beta-2 can be
CC used to counter the adverse effects of TGF beta, such as (i)
CC promotion of fibrosis (in dermal, ocular or keloid scarring, lung
CC fibrosis, arterial injury, proliferative retinopathy, retinal
CC detachment, adult respiratory distress syndrome, liver cirrhosis,
CC post myocardial infarction, post-angioplasty restenosis,
CC scleroderma, vascular disorders, cataract, glaucoma, or esp. neural
CC scarring and glomerulonephritis, also (not claimed) osteoporosis),
CC or (ii) immune and inflammatory diseases (e.g. rheumatoid
CC arthritis, macrophage deficiency diseases or macrophage pathogen
CC infection). Nucleic acids encoding human antibody VH and VL can be
CC used for prodn. of recombinant antigen-binding domains. These are
CC highly specific, have low dissociation constants (pref. less than 5
CC nM) and low IC50s for neutralisation.
SQ Sequence 123 AA;

Query Match 80.8%; Score 42; DB 1; Length 123;
Best Local Similarity 88.9%; Pred. No. 0.39;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDM 9
| | | | | | | |
Db 26 GLTFSSYDM 34

RESULT 6
W54000 ID W54000 standard; Protein; 128 AA.
AC W54000;
DT 29-JUL-1998 (first entry)
DE Anti-CD4 antibody VH3 monkey clone 3-40.
KW Anti-CD4 antibody; monkey; human; therapy; variable heavy domain;
KW Old World monkey; constant domain; eczema; immuno-modulated disease;
KW rheumatoid arthritis.
OS Primate sp.
FH Key Location/Qualifiers
FT Misc_difference 1..128 /note= "Xaa= unspecified amino acid"

US5750105-A.
PN 12-MAY-1998.
PF 07-JUN-1995; 476349.
PR 10-JUL-1992; US-912292.

PR 25-JUL-1991; US-735064.
PR 23-MAR-1992; US-856281.
PR 05-DEC-1995; US-379072.
PR 07-JUN-1995; US-476349.
PA (IDEC-) IDEC PHARM CORP.
PI Hanna N, Newman RA, Raab RW;
DR WPI; 98-296690/26.
PT Improved method for antibody treatment - uses an antibody comprising
PT an Old World monkey variable region and a human constant domain
PS Example 1; Fig 9c; 84pp; English.
CC This sequence represents the VH3 domain of an anti-CD4 antibody
CC (AB). This sequence can be used in the method of the invention for
CC treating a subject, where the treatment comprises administration of an
CC Ab. The method comprises the administration of an antibody which binds to
CC Old World monkey (e.g. baboon or macaque) variable region which binds to
CC an antigen (Ag) (or Ag binding portion), and a human constant domain. The
CC method is useful for the treatment of eczema and immuno-modulated
CC diseases and especially rheumatoid arthritis. The recombinant antibodies
CC used are sufficiently different from native monkey antibodies to allow
CC human antigens to raise these antibodies, but similar enough to human
CC antibody so there is no immune response to the antibodies in humans.
CC Compared to antibodies used in therapy in prior art, these antibodies do
CC not induce human anti-antibodies on repeated administration. They also
CC have longer half-lives and do not have a lack of effector function with
CC human cells.
SQ Sequence 128 AA;

Query Match 80.8%; Score 42; DB 1; Length 128;
Best Local Similarity 80.0%; Pred. No. 0.41;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
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Db 26 GFTFSSYDMN 35

RESULT 7
R24713 ID R24713 standard; Protein; 134 AA.
AC R24713;
DT 28-DEC-1992 (first entry)
DE Sequence encoded by the genomic chimeric heavy chain variable region
DE (VH) gene
KW Chimeric monoclonal antibody; anti-fibrin antibody; PCR;
KW antithrombotic agent; myocardial infarction therapy.
OS Mus musculus.
FH Key Location/Qualifiers
FT peptide 1..19 /label= leader
FT region 23..49 /label= Framework Region (FR) 1
FT region 50..54 /label= Complementarity determining region(CDR)1
FT region 55..68 /label= FR-2
FT region 69..84 /label= CDR-2
FT region 85..114 /label= FR-3
FT region 115..123 /label= CDR-3
FT region 124..134 /label= FR-4
PN EP-491351-A.
PD 24-JUN-1992.
PF 17-DEC-1991; 121591.
PR 18-DEC-1990; JP-413829.
PR 11-NOV-1991; JP-294464.
PA (TAKE) TAKEDA CHEM IND LTD.
PI Iwasa S, Taka H, Watanabe T, Tada H;
DR WPI; 92-209528/26.
DR N-PSDP; Q25666.

PT Chimeric monoclonal antibodies - contain anti-human fibrin
PT antibody light and heavy chain variable and constant for treating
PT thrombotic conditions e.g. myocardial infarction
PS Example; Figure 4; 87pp; English.
CC PCR primers 5'MVH and 3'MVH were used to produce a VH gene-contg.
CC fragment of about 330bp. The fragment was isolated and subcloned in
CC pUC119. The fragment was found to be a functional VH structural
CC gene, referred to as VFH, comprising a VH gene belonging to the
CC subgroup III (WHIII) and the DSP2 and JH4 genes. Northern blot
CC analysis using the whole RNA of FIB1-11 cells confirmed that VFH
CC was the gene expressed in FIB1-11 cells. The sequence is given in
CC Q25666.
SQ Sequence 134 AA;

Query Match 80.8%; Score 42; DB 1; Length 134;
Best Local Similarity 80.0%; Pred. No. 0.43;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | |
Db 45 GTTFSSYDMS 54

RESULT 8
R24812
ID R24812 standard; Protein; 466 AA.
AC R24812;
DE 28-DEC-1992 (first entry)
DE Sequence encoded by the chimeric H chain cDNA contained in pTB1373
KW Chimeric monoclonal antibody; anti-fibrin antibody; primer;
KW antithrombotic agent; myocardial infarction therapy.
OS Synthetic.
FH Key Location/Qualifiers
FT peptide 13..19
FT region 20..134
FT region 135..232
FT region 233..247
FT region 248..357
FT region 358..464
FT misc_difference 465
FT /note= "translated stop codon"
PN EP-491351-A.
PD 24-JUN-1992.
PF 17-DEC-1991; 121591.
PR 18-DEC-1990; JP-413829.
PR 11-NOV-1991; JP-294464.
PA (TAKE) TAKEDA CHEM IND LTD.
PI Iwasa S, Taka H, Watanabe T, Tada H;
DR WPI: 92-209528/26.
DR N-PSDB; Q25692.
PT Chimeric monoclonal antibodies - contain anti-human fibrin
PT antibody light and heavy chain variable and constant for treating
PT thrombotic conditions e.g. myocardial infarction
PS Example; Figure 11; 87pp; English.
CC Plasmid pTB1373 contains the whole length of a mouse-human
CC chimeric anti-human fibrin heavy chain cDNA open reading
CC frame. It was prep'd. using Poly(A)+ RNA from the anti-fibrin
CC chimeric Ab-producing transfectant FIB1-H01/X63 as a template
CC to clone human C-kappa cDNA, using the oligo-dT (Pharmacia) primer as
CC a primer for first strand cDNA synthesis and the 5'C2H and 3'EH
CC primers for the PCR. A human gamma-1 chain CH2-CH3 domain encoding
CC cDNA was amplified. Similarly a human gamma-1 chain CH1 domain
CC encoding cDNA and an anti-fibrin antibody VH cDNA and a leader
CC peptide cDNA were amplified using the primers 3'EH, 3'C2H and 3'C1H
CC respectively as a primer for first strand cDNA synthesis and the
CC primer combination of 5'C1H and 3'C2H, of 5'1H and 3'C1H and of

CC 5'SH and 3'1H respectively as primers for PCR. The amplified gene
CC products were isolated and used to produce plasmids. After
CC confirmation of the cDNA sequence of each plasmid, the cDNA
CC encoding LH, VH, CH1 and CH2CH3 were joined together to give
CC plasmid pTB1373 contg. the whole length chimeric H chain
CC (LH, VH, CH1, CH2CH3), also abbreviated as IgH-FIB,
SQ Sequence 466 AA;

Query Match 80.8%; Score 42; DB 1; Length 466;
Best Local Similarity 80.0%; Pred. No. 1.6;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
| | | | |
Db 45 GTTFSSYDMS 54

RESULT 9
W21652
ID W21652 standard; Protein; 139 AA.
AC W21652;
DT 03-JAN-1998 (first entry)
DE Humanised reshaped MAB 15 heavy chain variable region.
DE Humanised antibody; monoclonal antibody; MAB 15; tumour;
KW lung cancer; therapy.
KW Chimeric Mus musculus.
OS Chimeric Homo sapiens.
OS Chimeric synthetic.
FH Key Location/Qualifiers
FT peptide 1..19
FT Protein 20..139
FT region 20..49
FT region 50..54
FT region 55..68
FT region 69..85
FT region 86..117
FT region 118..128
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FT region 6880..6889
FT region 6890..6899
FT region 6900..6909
FT region 6910..6919
FT region 6920..6929
FT region 6930..6939
FT region 6940..6949
FT region 6950..6959
FT region 6960..6969
FT region 6970..6979
FT region 6980..6989
FT region 6990..6999
FT region 7000..7009
FT region 7010..7019
FT region 7020..7029
FT region 7030..7039
FT region 7040..7049
FT region 7050..7059
FT region 7060..7069
FT region 7070..7079
FT region 7080..7089
FT region 7090..7099
FT region 7100..7109
FT region 7110..7119
FT region 7120..7129
FT region 7130..7139
FT region 7140..7149
FT region 7150..7159
FT region 7160..7169
FT region 7170..7179
FT region 7180..7189
FT region 7190..7199
FT region 7200..7209
FT region 7210..7219
FT region 7220..7229
FT region 7230..7239
FT region 7240..7249
FT region 7250..7259
FT region 7260..7269
FT region 7270..7279
FT region 7280..7289
FT region 72

CC for the constant regions of the light and heavy chain of a human
 CC immunoglobulin; and constructing, expressing and analysing the
 CC complete reshaped human MAB 15. The humanised MAB can be used for
 CC treating tumours, especially lung cancer, and for the manufacture
 CC of a drug related to tumours, especially lung cancer.
 SQ Sequence 139 AA;

Query Match 78.8%; Score 41; DB 1; Length 139;
 Best Local Similarity 80.0%; Pred. No. 0.68;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 | | | | |
 Db 45 GFTFSYDMS 54

RESULT 10
 ID W76015 standard; Protein; 10 AA.
 AC W76015;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR1 protein fragment #3.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49852.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 60; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 76.9%; Score 40; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.063;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 | | | | |
 Db 1 GFTWSSYDMS 10

RESULT 11
 ID W76003 standard; Protein; 117 AA.
 AC W76003;
 DT 02-NOV-1998 (first entry)
 DE LM609 antibody heavy chain variable region protein fragment.

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49822.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 43; Fig 2a; 129pp; English.
 CC This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphaVbeta3
 CC and can be used to inhibit binding of alphaVbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphaVbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 SQ Sequence 117 AA;

Query Match 76.9%; Score 40; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 0.88;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 | | | | |
 Db 26 GFAFSSYDMS 35

RESULT 12
 ID R34511 standard; Protein; 239 AA.
 AC R34511;
 DT 20-AUG-1993 (first entry)
 DE Fv(TU25).
 KW pFv(TU27)-DE; pFv(TU25)-DE; V region; antibody; binding;
 KW heavy; beta; chain; interleukin; IL-2; receptor; inhibition;
 KW immunomodulator; immunosuppressant; graft rejection; allergy;
 KW autoimmune disease; leukemia; cyclosporin.
 OS Homo sapiens.
 PN EP-539748-A.
 PD 05-MAY-1993.
 PF 30-SEP-1992; 116746.
 PR 03-OCT-1991; JP-256335.
 PA (AJIN) AJINOMOTO KK.
 PI Hamuro J, Shimamura T, Taki S;
 DR WPI; 93-145163/18.
 DR N-PSDB; Q40483.
 PT Polypeptide(s) which bind H chain of human IL-2 receptors - for
 PT treating inflammatory, allergic and auto-immune disorders,
 PT leukaemias etc.
 PS Claim 4; Page 19; 27pp; English.
 CC The constructed plasmids pFv(TU27)-DE and pFv(TU25)-DE which express
 CC polypeptides consisting only of the V regions were purified and
 CC sequenced. The polypeptides are capable of binding to the beta
 CC chain of IL-2 receptor and of inhibiting the binding of IL-2 to the
 CC receptor. They are useful as immunomodulators and
 CC immunosuppressants, e.g. to prevent graft rejection or to treat
 CC inflammatory allergic and autoimmune diseases, or leukemia. Unlike
 CC cyclosporin etc. they are both effective and safe.

SQ Sequence 239 AA;

Query Match 76.9%; Score 40; DB 1; Length 239;
 Best Local Similarity 80.0%; Pred. No. 1.9;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 I | | | | | | |
 Db 148 GFAFSSYDMS 157

RESULT 13

W11917
 ID W11917 standard; Protein; 247 AA.

AC W11917;

DT 24-JUN-1997 (first entry)

DE Murine MAb SK48-E26 heavy chain.

KW Interleukin-1 beta; IL-1 beta; recombinant antibody;

KW humanised antibody; chimeric antibody; antibody engineering;

KW monoclonal antibody; MAb; SK48-E26; inflammation; therapy.

OS Homo sapiens.

FH Key Location/Qualifiers

FT peptide 1..19

FT /label= Sig_peptide

FT region 20..49

FT /label= FR1

FT /note= "framework region 1"

FT region 50..54

FT /label= CDR1

FT /note= "complementarity determining region 1

FT (Claim 10, page 48)"

FT region 55..68

FT /label= FR2

FT /note= "framework region 2"

FT region 69..85

FT /label= CDR2

FT /note= "complementarity determining region 2

FT (Claim 10, page 48)"

FT region 86..117

FT /label= FR3

FT /note= "framework region 3"

FT region 118..127

FT /label= FR4

FT /note= "framework region 4"

FT region 139..247

FT /label= Constant_region

FT W09501997-A1.

PN 19-JAN-1995.

PD 07-JUL-1994; U07659.

PF 09-JUL-1993; US-090534.

PR 04-MAR-1994; US-206190.

PA (SMK) SMITHKLINE BEECHAM CORP.

PI Gross MS, Hurle MR, Jackson JR, Jonak ZL, Theisen TW;

PI Young PR;

PI WPI: 95-066868/09.

DR N-PSDB: T51436.

DR Recombinant and humanised chimeric antibodies against human

PT interleukin-1-beta - for preventing and treating

PT interleukin-mediated inflammatory disorders

PS Claim 5; Page 36-37; 62pp; English.

CC Amino acid sequences of the heavy chain (W11917) and light chain

CC (W11918) of anti-human interleukin-1 beta (IL-1 beta) murine

CC monoclonal antibody (MAb) SK48-E26 were deduced from nucleic acids

CC (T51436-37) derived from hybridoma SK48-E26. The heavy and light

CC chains, esp. the complementarity determining region sequences,

CC can be utilised in novel recombinant chimeric and humanised

CC antibodies (see also W11919-20) useful for the treatment and

CC prevention of IL-1 mediated inflammatory disorders.

SQ Sequence 247 AA;

Query Match 76.9%; Score 40; DB 1; Length 247;
 Best Local Similarity 80.0%; Pred. No. 1.9;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 I | | | | | | |
 Db 45 GFAFSSYDMS 54

RESULT 14

W76016
 ID W76016 standard; Protein; 10 AA.

AC W76016;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR1 protein fragment #4.

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis; primer; V-H region; CDR;

KW complementarity determining region.

OS Mus sp.

PN W09833919-A2.

PD 06-AUG-1998.

PF 30-JAN-1998; U01826.

PR 30-JAN-1997; US-791391.

PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

DR WPI: 98-437472/37.

DR N-PSDB: V49853.

PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

PS Claim 60; Page 41; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody

CC vitaxin bind selectively to integrin alphavbeta3 and can be used to

CC inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies

CC contain non-murine framework regions so are suitable for use in humans.

CC Enhanced types of LM609 have affinity more than 90 times greater than

CC that of parent the parent antibody.

CC Sequence 10 AA;

SQ

Query Match 75.0%; Score 39; DB 1; Length 10;

Best Local Similarity 80.0%; Pred. No. 0.098;

Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10

I | | | | | | |

Db 1 GFTFLSYDMS 10

RESULT 15

W86141

ID W86141 standard; Protein; 117 AA.

AC W86141;

DT 03-MAR-1999 (first entry)

DE Protein sequence of de-immunised murine A33 Vh.

KW Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK;

KW Immunogl bulin; therapeutic; streptokinase; murine; de-immunised.

OS Mus sp.

PN W09852976-A1.

PD 26-NOV-1998.

PF 21-MAY-1998; G01473.
 PR 14-APR-1998; GB-007751.
 PR 21-MAY-1997; GB-010480.
 PR 31-JUL-1997; GB-016197.
 PR 28-NOV-1997; GB-025270.
 PR 02-DEC-1997; US-067235.
 PA (BIOV-) BIOVATION LTD.
 PI Carr FJ;
 DR WPI; 99-045301/04.
 PT Reducing immunogenicity of proteins.- by modifying the amino acid
 PT sequence of the protein to eliminate potential epitopes for T-cells
 PT of a given species
 PS Example 6; Fig 27; 77pp; English.
 CC The invention relates to a method for the production of non-immunogenic
 CC proteins. The method comprises determining at least part of the amino
 CC acid sequence of the protein; (b) identifying in the amino acid sequence
 CC one or more potential epitopes for T-cells (T-cell epitopes) of the given
 CC species; and (c) modifying the amino acid sequence to eliminate at least
 CC one of the T-cell epitopes identified in step (b) thereby to eliminate or
 CC reduce the immunogenicity of the protein when exposed to the immune
 CC system of the given species. A method of analysing a pre-existing protein
 CC to predict the basis for immunogenic responses is also provided. The
 CC methods can be used particularly for reducing the immunogenicity of
 CC immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The
 CC products can be used for diagnosis and therapy. The present sequence
 CC represents the protein sequence of de-immunised murine A33 Vh.
 SQ Sequence 117 AA;

Query Match 75.0%; Score 39; DB 1; Length 117;
 Best Local Similarity 70.0%; Pred. No. 1.4;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GTTFSSYDMS 10
 Db | | | | | | | |
 26 GTTFITYDMS 35

Search completed: May 27, 2000, 19:21:30
 Job time: 1584 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2000, 19:26:37 ; Search time 163.56 Seconds
(without alignments)
3.585 Million cell updates/sec

Title: US-09-016-061-50
Perfect score: 58
Sequence: 1 GFTWSSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR_63:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	48	82.8	94	2 S14580	Ig heavy chain V r
2	44	75.9	97	2 S26890	Ig heavy chain V r
3	43	74.1	113	2 S26468	Ig heavy chain V r
4	43	74.1	117	1 HVMS34	Ig heavy chain pre
5	43	74.1	121	2 D27888	Ig heavy chain V r
6	43	74.1	124	2 C27888	Ig heavy chain V r
7	41	70.7	40	2 S33406	Ig heavy chain V r
8	41	70.7	83	2 C25913	Ig heavy chain V r
9	41	70.7	98	2 S26891	Ig heavy chain V r
10	41	70.7	108	2 PL0248	Ig heavy chain V r
11	41	70.7	108	2 PH1006	Ig heavy chain V r
12	41	70.7	117	1 HVMS84	Ig heavy chain pre
13	41	70.7	117	2 PL0249	Ig heavy chain V r
14	41	70.7	117	2 PL0252	Ig heavy chain V r
15	41	70.7	118	2 S38491	Ig heavy chain - h
16	41	70.7	119	2 F27888	Ig heavy chain V r
17	41	70.7	122	2 E27888	Ig heavy chain V r
18	41	70.7	138	2 S09258	Ig heavy chain V r
19	41	70.7	325	2 T25122	hypothetical prote
20	40	69.0	92	2 S56009	Ig heavy chain var
21	40	69.0	92	2 S56008	Ig heavy chain var
22	40	69.0	97	1 HVMS91	Ig heavy chain V r
23	40	69.0	97	2 PH0872	Ig heavy chain V r
24	40	69.0	98	2 S26889	Ig heavy chain V r
25	40	69.0	100	2 D48223	Ig heavy chain V r
26	40	69.0	102	2 S14581	Ig heavy chain V r
27	40	69.0	108	2 PH1648	Ig heavy chain V r
28	40	69.0	108	2 PH1011	Ig heavy chain V r
29	40	69.0	109	2 PH1649	Ig heavy chain V r
30	40	69.0	111	2 PH1659	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S14580
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S14580
R:Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A:Description: Natural polyreactive antibodies differ from Ag-induced antibodies in V
A:Reference number: S14484
A:Accession: S14580
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-94 <CHE>
A:Cross-references: EMBL:X58652; NID:g51293; PIDN:CAA41509.1; PID:g51294
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 82.8%; Score 48; DB 2; Length 94;
Best Local Similarity 90.0%; Pred. No. 0.1;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10

Db 18 GFTFSSYDMS 27

RESULT 2

S26890
Ig heavy chain V region (DP-48) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26890
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups o
A:Reference number: S26885; MUID:93021117
A:Accession: S26890
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <TOM>
A:Cross-references: EMBL:Z12348; NID:g32916; PIDN:CAA78218.1; PID:g32917
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 75.9%; Score 44; DB 2; Length 97;
Best Local Similarity 88.9%; Pred. No. 0.53;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDM 9
|||:|||||
Db 26 GFTFSYDM 34

RESULT 3

S26468

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S26468

R:Kavaler, J.

submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26468

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <NAV>

A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA1833.1; PID:g51945

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:11-94/Domain: immunoglobulin homology <IMM>

Query Match

74.1%; Score 43; DB 2; Length 113;

Best Local Similarity 80.0%; Pred. No. 0.93;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10

|||:|||||

Db 22 GFASFSSYDMS 31

RESULT 4

HVM534

Ig heavy chain precursor V region (345) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C:Accession: JT0502

R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A:Reference number: JT0501; MUID:89279149

A:Accession: JT0502

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A:Note: this sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:41-115/Disulfide bonds: #status predicted

Query Match

74.1%; Score 43; DB 1; Length 117;

Best Local Similarity 80.0%; Pred. No. 0.96;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10

|||:|||||

Db 45 GFASFSSYDMS 54

RESULT 5

D27888

Ig heavy chain V region (H37-60) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C:Accession: D27888

R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to
A:Reference number: A91043; MUID:86300658

A:Accession: D27888

A:Molecule type: DNA

A:Residues: 1-121 <CAT>

A:Experimental source: strain Balb/c

A:Note: this sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match

74.1%; Score 43; DB 2; Length 121;

Best Local Similarity 80.0%; Pred. No. 1;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10

|||:|||||

Db 26 GFASFSSYDMS 35

RESULT 6

C27888

Ig heavy chain V region (H37-62) - mouse

C:Species: Mus musculus (house mouse)

C>Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996

C:Accession: C27888

R:Caton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.

EMBO J. 5, 1577-1587, 1986

A:Title: Structural and functional implications of a restricted antibody response to

A:Reference number: A91043; MUID:86300658

A:Accession: C27888

A:Molecule type: DNA

A:Residues: 1-124 <CAT>

A:Experimental source: strain Balb/c

A:Note: this sequence was determined from the germline gene

C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match

74.1%; Score 43; DB 2; Length 124;

Best Local Similarity 80.0%; Pred. No. 1;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10

|||:|||||

Db 26 GFASFSSYDMS 35

RESULT 7

S33406

Ig heavy chain V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 19-Mar-1997 #sequence_revision 24-Jul-1997 #text_change 17-Jul-1998

C:Accession: S33406

R:Kettleborough, C.A.; Saldanha, J.; Ansell, K.H.; Bendig, M.M.

Eur. J. Immunol. 23, 206-211, 1993

A:Title: Optimization of primers for cloning libraries of mouse immunoglobulin genes

A:Reference number: S33391; MUID:93122092

A:Accession: S33406

A:Molecule type: mRNA

A:Residues: 1-40 <KET>

A:Cross-references: EMBL:X73009

A:Experimental source: strain BALB/c

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-40/Domain: immunoglobulin homology (fragment) <IMM>

Query Match 70.7%; Score 41; DB 2; Length 40;
 Best Local Similarity 80.0%; Pred. No. 0.69;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 |||:|||| ||

Db 26 GFTFSSYDMS 35

RESULT 8

Ig heavy chain V region (BFL14) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 16-Aug-1996
 C:Accession: C25913
 R:Lawler, A.M.; Lin, P.S.; Gearhart, P.J.
 A:Title: Adult B-cell repertoire is biased toward two heavy-chain variable-region genes
 A:Reference number: A94148; MUID:87175692
 A:Accession: C25913
 A:Molecule type: DNA
 A:Residues: 1-83 <LAW>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 70.7%; Score 41; DB 2; Length 83;
 Best Local Similarity 80.0%; Pred. No. 1.5;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 |||:|||| ||

Db 11 GFTFSSYDMS 20

RESULT 9

Ig heavy chain V region (DP-58) - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S26891
 R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewellyn, M.B.; Winter, G.
 J. Mol. Biol. 227, 776-798, 1992
 A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
 A:Reference number: S26885; MUID:93021117
 A:Accession: S26891
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-98 <TOW>
 A:Cross-references: EMBL:Z12358; NID:g32935; PIDN:CAA78228.1; PID:g32936
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.7%; Score 41; DB 2; Length 98;
 Best Local Similarity 70.0%; Pred. No. 1.8;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 |||:||||: |

Db 26 GFTFSSYDMS 35

RESULT 10

Ig heavy chain V region (anti-DNA, DP12VH) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C:Accession: PL0248
 R:Shlomchik, M.; Mascello, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
 J. Exp. Med. 171, 263-297, 1990
 A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A:Reference number: PL0231; MUID:90111618
 A:Accession: PL0248
 A:Molecule type: mRNA
 A:Residues: 1-108 <SHL>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-24/Region: framework 1
 F:9-92/Domain: immunoglobulin homology <IMM>
 F:25-29/Region: complementarity-determining 1
 F:30-43/Region: framework 2
 F:44-60/Region: complementarity-determining 2
 F:61-92/Region: framework 3
 F:93-99/Region: complementarity-determining 3
 F:100-108/Region: framework 4

Query Match 70.7%; Score 41; DB 2; Length 108;
 Best Local Similarity 80.0%; Pred. No. 2;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 |||:|||| ||

Db 20 GFTFSSYDMS 29

RESULT 11

PH1006

Ig heavy chain V region (clone 202.33) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PH1006
 R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
 J. Exp. Med. 176, 761-779, 1992
 A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
 A:Reference number: PH0971; MUID:92381444
 A:Accession: PH1006
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-108 <TIL>
 A:Experimental source: B cell, strain (NZB x NZW)F1
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:10-93/Domain: immunoglobulin homology <IMM>

Query Match 70.7%; Score 41; DB 2; Length 108;
 Best Local Similarity 80.0%; Pred. No. 2;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 |||:|||| ||

Db 21 GFTFSSYDMS 30

RESULT 12

HVMS84

Ig heavy chain precursor V region (5-84) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
 C:Accession: JT0505
 R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
 J. Exp. Med. 169, 2007-2019, 1989
 A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primar
 A:Reference number: JT0501; MUID:89279149
 A:Accession: JT0505
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-117 <LEV>
 A:Experimental source: strain BALB/cJ
 A:Note: This sequence belongs to the VH7183 subfamily
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>
 F:34-117/Domain: immunoglobulin homology <IMM>
 F:41-115/Disulfide bonds: #status predicted

Query Match 70.7%; Score 41; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 2.1;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 |||:||||||
 Db 45 GFTFSSYTMS 54

RESULT 13

PL0249
 Ig heavy chain V region (anti-DNA, 3E12VH) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C;Accession: PL0249
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
 J. Exp. Med. 171, 265-297, 1990
 A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A;Reference number: PL0231; MUID:90111618
 A;Accession: PL0249
 A;Molecule type: mRNA
 A;Residues: 1-117 <SHL>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-49/Region: framework 2
 F:50-66/Region: complementarity-determining 2
 F:67-98/Region: framework 3
 F:99-108/Region: complementarity-determining 3
 F:109-117/Region: framework 4

Query Match 70.7%; Score 41; DB 2; Length 117;
 Best Local Similarity 80.0%; Pred. No. 2.1;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 |||:||||||
 Db 26 GFTFSSYTMS 35

RESULT 14

PL0252
 Ig heavy chain V region (anti-DNA, clones 2E3VH, 6B8VH, and 3G9VH) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
 C;Accession: PL0252; PL0251
 R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A
 J. Exp. Med. 171, 265-297, 1990
 A;Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic
 A;Reference number: PL0231; MUID:90111618
 A;Accession: PL0252
 A;Molecule type: mRNA
 A;Residues: 1-117 <SHL>
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin
 F:1-30/Region: framework 1
 F:15-98/Domain: immunoglobulin homology <IMM>
 F:31-35/Region: complementarity-determining 1
 F:36-49/Region: framework 2
 F:50-66/Region: complementarity-determining 2
 F:67-98/Region: framework 3
 F:99-108/Region: complementarity-determining 3
 F:109-117/Region: framework 4

Query Match 70.7%; Score 41; DB 2; Length 117;
 Best Local Similarity 80.0%; Pred. No. 2.1;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 |||:||||||
 Db 26 GFTFSSYTMS 35

RESULT 15

S38491
 Ig heavy chain - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C;Accession: S38491
 R:Marks, J.D.; Ouweland, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe
 submitted to the EMBL Data Library, June 1993
 A;Description: Human antibody fragments specific for human blood group antigens from
 A;Reference number: S38488
 A;Accession: S38491
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-118 <MAR>
 A;Cross-references: EMBL:Z23032; NID:g414029; PIDN:CAA80567.1; PID:g414030
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotrimer; immunoglobulin
 F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 70.7%; Score 41; DB 2; Length 118;
 Best Local Similarity 88.9%; Pred. No. 2.2;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 9
 |||:||||||
 Db 26 GFTLSSYDMS 34

Search completed: May 27, 2000, 19:26:37
 Job time: 1760 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 20:07:07 ; Search time 69.28 Seconds
(without alignments)
4.396 Million cell updates/sec

Title: US-09-016-061-50
Perfect score: 58
Sequence: 1 GFTWSSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	74.1	117	1 HV55_MOUSE	P18526 mus musculus
2	41	70.7	117	1 HV54_MOUSE	P18525 mus musculus
3	40	69.0	97	1 HV56_MOUSE	P18527 mus musculus
4	40	69.0	117	1 HV3C_HUMAN	P01764 homo sapien
5	39	67.2	117	1 HV53_MOUSE	P18524 mus musculus
6	38	65.5	117	1 HV59_MOUSE	P18530 mus musculus
7	38	65.5	304	1 NKR7_HUMAN	Q14952 homo sapien
8	38	65.5	450	1 NMT_CRYNE	P46548 caenorhabdi
9	37	63.8	116	1 HV1A_RABIT	P01826 oryctolagus
10	37	63.8	117	1 HV2B_RABIT	P01828 oryctolagus
11	37	63.8	311	1 PLC_STAAT	P45723 staphylococ
12	36	62.1	115	1 HV3D_HUMAN	P01765 homo sapien
13	36	62.1	367	1 DIAC_RAT	Q01460 rattus norv
14	36	62.1	385	1 DIAC_HUMAN	Q01459 homo sapien
15	36	62.1	416	1 NMT1_HUMAN	P30419 homo sapien
16	36	62.1	423	1 IDH_BACSU	P39126 bacillus su
17	36	62.1	496	1 NMT1_MOUSE	O70310 mus musculus
18	36	62.1	503	1 AMP_RAT	P00689 rattus norv
19	36	62.1	508	1 AMP_MOUSE	P00688 mus musculus
20	36	62.1	511	1 AMYS_MOUSE	P00687 mus musculus
21	36	62.1	517	1 YB3C_SCHPO	O14342 schizosacch
22	36	62.1	565	1 SYG_METTH	O27874 methanobact
23	36	62.1	707	1 TRFL_MOUSE	P08071 mus musculus
24	36	62.1	781	1 GCS1_CAEEL	Q19426 caenorhabdi
25	35	60.3	117	1 HV52_MOUSE	P06327 mus musculus
26	35	60.3	396	1 CBG_RAT	P31211 rattus norv
27	35	60.3	434	1 SLS4_BRAOL	P17841 brassica ol
28	35	60.3	435	1 SLS2_BRAOA	P22553 brassica ol
29	35	60.3	558	1 AWAL_PLACH	P18445 plasmodium
30	34	58.6	105	1 YQCJ_BACSU	P45949 bacillus su
31	34	58.6	114	1 HV00_MOUSE	P01741 mus musculus
32	34	58.6	114	1 HV01_CANFA	P01784 canis famul
33	34	58.6	118	1 ABBB_TRUAB	P81116 trimeresuru
34	34	58.6	120	1 HV3E_HUMAN	P01766 homo sapien

35	34	58.6	121	1 HV3J_HUMAN	P01771 homo sapien
36	34	58.6	127	1 P044_RAT	P38718 rattus norv
37	34	58.6	213	1 COBQ_PSEDE	P29930 pseudomonas
38	34	58.6	264	1 STE4_SCHPO	P36622 schizosacch
39	34	58.6	304	1 XOOB_CAEEL	O09300 caenorhabdi
40	34	58.6	455	1 NKR4_HUMAN	P43630 homo sapien
41	34	58.6	491	1 NMT_CRYNE	P34809 cryptococcu
42	34	58.6	498	1 NMT2_HUMAN	O60531 homo sapien
43	34	58.6	529	1 NMT2_MOUSE	O70311 mus musculu
44	34	58.6	632	1 YA28_SCHPO	O09699 schizosacch
45	34	58.6	692	1 PHLN_PSEAE	P15713 pseudomonas

ALIGNMENTS

```
RESULT 1
HV55_MOUSE
ID HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 345 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0502; HVMS34.
DR PFAM; PF00047; ig; 1;
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;
```

```
Query Match 74.1%; Score 43; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.73;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
Db 45 GFAFSSYDMS 54
||:|||||
```

```
RESULT 2
HV54_MOUSE
ID HV54_MOUSE STANDARD; PRT; 117 AA.
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 5-84 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
```

RC STRAIN=BALB/CJ;
 RX MEDLINE; 89279149.
 RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR; JT0505; HVMS84.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 70.7%; Score 41; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 1.6;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 |||:||||
 Db 45 GFTFSSYAMS 54

RESULT 3
 HV56_MOUSE
 ID HV56_MOUSE STANDARD; PRT; 97 AA.
 AC P18527;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION 914.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/CJ;
 RX MEDLINE; 89279149.
 RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR; JT0504; HVMS91.
 KW Immunoglobulin V region.
 FT NON_TER 97 97
 SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 69.0%; Score 40; DB 1; Length 97;
 Best Local Similarity 80.0%; Pred. No. 1.9;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 |||:||||
 Db 26 GFTFSSYAMS 35

RESULT 4
 HV3C_HUMAN
 ID HV3C_HUMAN STANDARD; PRT; 117 AA.
 AC P01764;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-III REGION VH26 PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 81101090.
 RA Matthyssens G., Rabbitts T.H.;
 RT "Structure and multiplicity of genes for the human immunoglobulin
 heavy chain variable region.";
 RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
 CC -----
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 CC EMBL; J00236; AAA53516.1; -;
 DR EMBL; M35415; AAA58735.1; -;
 DR PIR; A02047; H3HU26.
 DR PFAM; PF00047; ig; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 69.0%; Score 40; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 2.3;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 |||:||||
 Db 45 GFTFSSYAMS 54

RESULT 5
 HV53_MOUSE
 ID HV53_MOUSE STANDARD; PRT; 117 AA.
 AC P18524;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION RF PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/CJ;
 RX MEDLINE; 89279149.
 RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR; JT0503; HVMSRF.
 DR PFAM; PF00047; ig; 1.
 KW Immunoglobulin V region; Hybridoma; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION RF.
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117

SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;
 Query Match 67.2%; Score 39; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 3.4;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GFTWSSYDMS 10
 III:III II
 Db 45 GFTFSYMS 54
 RESULT 6
 HV59_MOUSE
 ID HV59_MOUSE STANDARD; PRT; 117 AA.
 AC P18530;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION 7-39 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/CJ;
 RX MEDLINE: 89279149.
 RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2019-2019(1989).
 CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR: J0507; HVMS39.
 DR PFAM: PF00047; Ig; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19 IG HEAVY CHAIN V REGION 7-39.
 FT CHAIN 20 117 FRAMEWORK 1.
 FT DOMAIN 20 49 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 50 54 FRAMEWORK 2.
 FT DOMAIN 55 68 FRAMEWORK 3.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;
 Query Match 65.5%; Score 38; DB 1; Length 117;
 Best Local Similarity 70.0%; Pred. No. 5.1;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GFTWSSYDMS 10
 III:III II
 Db 45 GFTFSYMS 54
 RESULT 7
 NK77_HUMAN
 ID NK77_HUMAN STANDARD; PRT; 304 AA.
 AC Q14952; Q00644;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE MHC CLASS I NK CELL RECEPTOR PRECURSOR (NATURAL KILLER ASSOCIATED
 DE TRANSCRIPT 7) (NKAT7).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE: 96270004.
 RX Dohring C., Samaridis J., Colonna M.;
 RA "Alternatively spliced forms of human killer inhibitory receptors.";
 RT

Immunogenetics 44:227-230(1996).
 [2]
 RN SEQUENCE FROM N.A.
 RP TISSUE-LYMPHOID;
 RA Biasoni R.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR HLA-C
 ALLELES. INHIBITS THE ACTIVITY OF NK CELLS THUS PREVENTING
 CELL LYSIS.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL: L76670; AAB36598.1; -;
 DR EMBL: X97231; CAA65870.1; -;
 DR PFAM: PF00047; Ig; 1.
 KW Receptor; Immunoglobulin domain; Glycoprotein; Signal; Transmembrane;
 MW Multigene family.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT CHAIN 22 304 MHC CLASS I NK CELL RECEPTOR.
 FT DOMAIN 22 245 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 246 264 POTENTIAL.
 FT DOMAIN 265 304 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 42 107 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 142 205 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 49 100 BY SIMILARITY.
 FT DISULFID 149 198 BY SIMILARITY.
 FT CARBOHYD 67 67 POTENTIAL.
 FT CARBOHYD 84 84 POTENTIAL.
 FT CARBOHYD 178 178 POTENTIAL.
 SQ SEQUENCE 304 AA; 33717 MW; 80693F79844F9E7E CRC64;
 Query Match 65.5%; Score 38; DB 1; Length 304;
 Best Local Similarity 85.7%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 TWSSYDM 9
 :IIIIII
 Db 151 SWSSYDM 157
 RESULT 8
 NMT_CAEEL
 ID NMT_CAEEL STANDARD; PRT; 450 AA.
 AC P46548;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE PROBABLE GLYCYLPEPTIDE N-TETRADECANOYLTRANSFERASE (EC 2.3.1.97)
 DE (PEPTIDE N-MYRISTOYLTRANSFERASE) (MYRISTOYL-COA:PROTEIN N-
 DE MYRISTOYLTRANSFERASE) (NMT).
 GN T17E9.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
 OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Du Z.;
 RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: ADDS MYRISTOYL GROUP TO N-TERMINAL GLYCINE RESIDUE
 OF CERTAIN CELLULAR AND VIRAL PROTEINS (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: TETRADECANOYL-COA + GLYCYL-PEPTIDE -> COA +
 N-TETRADECANOYLGLYCYL-PEPTIDE.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).

CC -1- SIMILARITY: BELONGS TO THE NMT FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U11280; AAA19436.1; -;
 CC WORMPEP: T17E9.2; CE01406.
 CC PROSITE: PS00975; NMT_1; 1.
 CC PROSITE: PS00976; NMT_2; 1.
 CC PFAM: PF01233; NMT; 1.
 CC KW Hypothetical protein; Transferase; Acyltransferase.
 CC SEQUENCE 450 AA; 50889 MW; 5A639808F7DDA38E CRC64;

Query Match 65.5%; Score 38; DB 1; Length 450;
 Best Local Similarity 60.0%; Pred. No. 19;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GFTWSSYDMS 10
 II III I I I
 Db 108 GFRWSNVDS 117

RESULT 9
 HV1A_RABIT
 ID HV1A_RABIT STANDARD; PRT; 116 AA.
 AC P01826;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-A1 REGION BS-5.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]
 RX SEQUENCE OF 1-69.
 RX MEDLINE; 73220191.
 RA Jaton J.-C.; Braun D.G.;
 RT "Amino acid sequence of the N-terminal sixty-nine residues of heavy
 RT chain derived from a homogeneous rabbit antibody."
 RL Biochem. J. 130:539-546(1972).
 RN [2]
 RP SEQUENCE OF 64-116.
 RX MEDLINE; 75183340.
 RA Jaton J.-C.;
 RT "Completion of the analysis of the primary structure of the variable
 RT domain of a homogeneous rabbit antibody to type III pneumococcal
 RT polysaccharide."
 RL Biochem. J. 143:723-732(1974).
 CC -1- MISCELLANEOUS: THIS GAMMA CHAIN WAS OBTAINED FROM ANTIBODY TO TYPE
 CC III PNEUMOCOCCI AND WAS ISOLATED FROM THE SERUM OF A SINGLE
 CC RABBIT.
 CC PIR; A02102; GARB15.
 CC PFAM; PF00047; ig; 1.
 CC KW Immunoglobulin V region.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT NON_TER 116 116
 SQ SEQUENCE 116 AA; 12349 MW; 95C6FAC93C788C42 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 116;
 Best Local Similarity 77.8%; Pred. No. 7.4;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GFTWSSYDM 9
 II: IIIII
 Db 25 GFSLSYDM 33

RESULT 10
 HV2B_RABIT
 ID HV2B_RABIT STANDARD; PRT; 117 AA.
 AC P01828;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-A2 REGION K-25.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]
 RX MEDLINE; 76039436.
 RA Jaton J.-C.;
 RT "Comparison of the amino acid sequences of the variable domains of
 RT two homogeneous rabbit antibodies to type III pneumococcal
 RT polysaccharide."
 RL Biochem. J. 147:235-247(1975).
 CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO TYPE III
 CC PNEUMOCOCCI AND WAS ISOLATED FROM THE SERUM OF A SINGLE RABBIT.
 CC PIR; A02104; GARB2K.
 CC PFAM; PF00047; ig; 1.
 CC KW Immunoglobulin V region.
 FT MOD_RES 1 1
 FT DISULFID 21 91
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12580 MW; 28DD87FDB9ABE9B8 CRC64;

Query Match 63.8%; Score 37; DB 1; Length 117;
 Best Local Similarity 70.0%; Pred. No. 7.5;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GFTWSSYDMS 10
 II: IIIII
 Db 25 GFSLSGYDMS 34

RESULT 11
 PLC_STAAU
 ID PLC_STAAU STANDARD; PRT; 311 AA.
 AC P45723;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE 1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.10)
 DE (PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (PI-PLC).
 GN PLC.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Staphylococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NEWMAN;
 RX MEDLINE; 94041628.
 RA Daugherty S.; Low M.G.;
 RT "Cloning, expression, and mutagenesis of
 RT phosphatidylinositol-specific phospholipase C from Staphylococcus
 RT aureus: a potential staphylococcal virulence factor."
 RL Infect. Immun. 61:5078-5089(1993).
 CC -1- FUNCTION: CLEAVES GLYCOPHOSPHATIDYLINOSITOL (GPI) AND
 CC PHOSPHATIDYLINOSITOL (PI) ANCHORS NOT PI PHOSPHATES. POTENTIAL
 CC VIRULENCE FACTOR.
 CC -1- CATALYTIC ACTIVITY: 1-PHOSPHATIDYL-D-MYO-INOSITOL - D-MYO-INOSITOL
 CC 1,2-CYCLOC PHOSPHATE + DIACYLGLYCEROL.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: TO OTHER BACTERIAL PI-PLC.
 CC -1- SIMILARITY: DOMAIN X IS CONSERVED IN DIFFERENT FORMS OF PLC AND IS
 CC ESSENTIAL FOR CATALYTIC ACTIVITY.
 CC -----
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RL J. Biol. Chem. 267:19607-19616(1992).
RN [2]
RP SEQUENCE FROM N.A.
RA Liu B., Aronson N.N. Jr.;
RT "Structure of the human gene for lysosomal di-N-acetylchitobiase";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: INVOLVED IN THE DEGRADATION OF ASPARAGINE-LINKED
CC GLYCOPROTEINS. HYDROLYZE OF N-ACETYL-BETA-D-GLUCOSAMINE
CC (1-4)-N-ACETYLGLUCOSAMINE CHITOBIOSE CORE FROM THE REDUCING END
CC OF THE BOND, IT REQUIRES PRIOR CLEAVAGE BY GLYCOSYLASPARAGINASE.
CC -1- SUBCELLULAR LOCATION: LYSOSOMAL.
CC -1- SIMILARITY: BELONGS TO FAMILY 18 OF GLYCOSYL HYDROLASES.
CC
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CC
CC EMBL; M95767; AAA35684.1; -
CC EMBL; AF085706; AAC35852.1; -
CC EMBL; AF085700; AAC35852.1; JOINED.
CC EMBL; AF085701; AAC35852.1; JOINED.
CC EMBL; AF085702; AAC35852.1; JOINED.
CC EMBL; AF085703; AAC35852.1; JOINED.
CC EMBL; AF085704; AAC35852.1; JOINED.
CC EMBL; AF085705; AAC35852.1; JOINED.
CC PIR; A44102; A44102.
CC PIR; S27959; S27959.
CC MIM; 600873; -
CC PROSITE; PS01095; CHITINASE_18; 1.
KW Hydrolase; Glycosidase; Signal; Lysosome; Glycoprotein.
FT SIGNAL 1 38 BY SIMILARITY.
FT CHAIN 39 385 DI-N-ACETYLCHITOBIOSE.
FT ACT_SITE 143 143 PROTON DONOR (BY SIMILARITY).
FT CARBOHYD 193 193 POTENTIAL.
FT CARBOHYD 228 228 POTENTIAL.
FT CARBOHYD 262 262 POTENTIAL.
FT CARBOHYD 299 299 POTENTIAL.
SQ SEQUENCE 385 AA; 43759 MW; 0A9D14C8B26B52EE CRC64;

Query Match 62.1%; Score 36; DB 1; Length 385;
Best Local Similarity 75.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 TWSSYDMS 10
||| |
DB 69 TWKSYDWS 76

RESULT 15
NMT1_HUMAN STANDARD; PRT; 416 AA.
AC P30419;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE GLYCYLPEPTIDE N-TETRADECANOLTRANSFERASE 1 (EC 2.3.1.97) (PEPTIDE N-
DE MYRISTOYLTRANSFERASE 1) (MYRISTOYL-COA:PROTEIN N-MYRISTOYLTRANSFERASE
DE 1) (NMT 1).
GN NMT1 OR NMT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF GLY-412.
RA MEDLINE; 92237320.
RA Duronio R.J., Reed S.I., Gordon J.I.;
RT "Mutations of human myristoyl-CoA:protein N-myristoyltransferase
RT cause temperature-sensitive myristic acid auxotrophy in Saccharomyces

RT cerevisiae.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:4129-4133(1992).
CC -1- FUNCTION: ADDS MYRISTOYL GROUP TO N-TERMINAL GLYCINE RESIDUE
CC OF CERTAIN CELLULAR AND VIRAL PROTEINS.
CC -1- CATALYTIC ACTIVITY: TETRADECANOYL-COA + GLYCYL-PEPTIDE -> COA +
CC N-TETRADECANOYLGLYCYL-PEPTIDE.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: HEART, GUT, KIDNEY, LIVER, AND PLACENTA.
CC -1- SIMILARITY: BELONGS TO THE NMT FAMILY.
CC
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CC
CC EMBL; M86707; -; NOT_ANNOTATED_CDS.
CC PIR; JCI343; JCI343.
CC MIM; 160993; -
CC PROSITE; PS00975; NMT_1; 1.
CC PROSITE; PS00976; NMT_2; 1.
CC PFAM; PF01233; NMT; 1.
KW Transferase; Acyltransferase.
FT MUTAGEN 412 412 G->D,K: REDUCED ACTIVITY.
SQ SEQUENCE 416 AA; 48140 MW; CF08D233B6DD9383 CRC64;

Query Match 62.1%; Score 36; DB 1; Length 416;
Best Local Similarity 55.6%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 9
||||| |
DB 75 GFTWDALDL 83

Search completed: May 27, 2000, 20:07:09
Job time: 981 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:38:29 ; Search time 199.56 Seconds
(without alignments)
3.474 Million cell updates/sec

Title: US-09-016-061-50
Perfect score: 58
Sequence: 1 GFTWSSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SPTREMBL12.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	70.7	325	5 002322	002322 caenorhabdi
2	38	65.5	147	4 09V509	09V509 homo sapien
3	38	65.5	228	5 002109	002109 caenorhabdi
4	38	65.5	325	5 023244	023244 caenorhabdi
5	38	65.5	335	10 064692	064692 arabidopsis
6	38	65.5	356	10 004710	004710 zea mays (m
7	38	65.5	2408	5 022184	022184 caenorhabdi
8	37	63.8	286	3 060065	060065 schizosacch
9	37	63.8	537	3 042801	042801 aspergillus
10	37	63.8	993	5 P91157	P91157 caenorhabdi
11	37	63.8	1156	5 061137	061137 leishmania
12	36	62.1	232	11 061297	061297 mus musculu
13	36	62.1	323	5 P91823	P91823 caenorhabdi
14	36	62.1	425	2 006893	006893 bacillus is
15	36	62.1	483	1 09YEL8	09YEL8 aeropyrum p
16	36	62.1	673	4 043895	043895 homo sapien
17	36	62.1	876	2 Q53576	Q53576 synchococc
18	36	62.1	1324	2 044103	044103 amycolatops
19	36	62.1	1372	5 P91526	P91526 caenorhabdi
20	35	60.3	101	1 006103	006103 methanococc

ALIGNMENTS

RESULT 1

002322

ID 002322 PRELIMINARY; PRT; 325 AA.

AC 002322;

DT 01-JUL-1997 (Tremblrel. 04, Created)

DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)

DT 01-JAN-1999 (Tremblrel. 09, Last annotation update)

DE T22G5.1 PROTEIN.

GN T22G5.1.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;

OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

RN [1]

RP SEQUENCE FROM N.A.

RA SMYE R.;

RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RA MEDLINE; 94150718.

RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M.,

RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RT elegans.";

RL Nature 368:32-38(1994).

DR EMBL; 281127; CAB03386.1; -.

SQ SEQUENCE 325 AA; 36754 MW; DD2E6BF1 CRC32;

Query Match 70.7%; Score 41; DB 5; Length 325;

Best Local Similarity 60.0%; Pred. No. 7;

Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 GFTWSSYDMS 10

||||| |::|

Db 218 GFTWRSWELS 227

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RESULT 2
ID Q9Y509 PRELIMINARY; PRT; 147 AA.
AC Q9Y509;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE VH3 PROTEIN (FRAGMENT).
GN VH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 96071149.
RA CAO J., VESCO R.A., RETTIG M.B., HONG C.H., KIM A., LEE J.C.,
RA LICHTENSTEIN A.K., BERENSON J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1948-1953(1995).
DR EMBL: S80860; AAD14339.1; -.
FT NON-TER 1
SQ SEQUENCE 147 AA; 15768 MW; BDD8F70 CRC32;

Query Match 65.5%; Score 38; DB 4; Length 147;
Best Local Similarity 70.0%; Pred. No. 10;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
   |||:|:|
DB 26 GFTFSYGMS 35

RESULT 3
ID Q02109 PRELIMINARY; PRT; 228 AA.
AC Q02109;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE CODED FOR BY C. ELEGANS CDNA YK97B2.3.
GN W08F4.3
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RX MEDLINE: 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-BRISTOL N2;
RC MADSEN C., GRAVES T.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;

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RA WATERSTON R.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF000266; AAC71167.1; -.
SQ SEQUENCE 228 AA; 25615 MW; ABFAC986 CRC32;

Query Match 65.5%; Score 38; DB 5; Length 228;
Best Local Similarity 60.0%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
   | | | | |
DB 24 GLRWKSYDIS 33

RESULT 4
Q23244 PRELIMINARY; PRT; 325 AA.
ID Q23244;
AC Q23244;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JAN-1998 (TrEMBLrel. 05, Last annotation update)
DE HYPOTHETICAL 36.5 KD PROTEIN ZC155.4 IN CHROMOSOME III.
GN ZC155.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA MILLER N.;
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP REVISIONS.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
CC -|- SIMILARITY: STRONG, TO C.ELEGANS PROTEIN T22G5.1 AND SOME, TO
CC C.ELEGANS PROTEINS F55C5.2 AND T09B9.3.
DR EMBL: U00064; AAB52706.1; -.
DR WORMPEP; ZC155.4; CE01434.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 4 24 POTENTIAL.
FT TRANSMEM 32 52 POTENTIAL.
FT TRANSMEM 242 262 POTENTIAL.
SQ SEQUENCE 325 AA; 36467 MW; 0AF3D8D3 CRC32;

Query Match 65.5%; Score 38; DB 5; Length 325;
Best Local Similarity 50.0%; Pred. No. 24;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
   ||| | | | |
DB 218 GFTWRNLS 227

RESULT 5
ID O64692 PRELIMINARY; PRT; 335 AA.
AC O64692;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE PUTATIVE GA4 PROTEIN.
GN T31E10.11 OR GA20X3.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]

```

RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA ROUNSLEY S.D., KAUL S., LIN X., KETCHUM K.A., CROSBY M.L.,
 RA BRANDON R.C., SYKES S.M., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
 RA SOMERVILLE C.R., VENTER J.C.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 99218343.
 RA THOMAS S.G., PHILLIPS A.L., HEDDEN P.;
 RT "Molecular cloning and functional expression of gibberellin 2-
 RT oxidases, multifunctional enzymes involved in gibberellin
 RT deactivation";
 RL Proc. Natl. Acad. Sci. U.S.A. 96:4698-4703(1999).
 DR EMBL; AC004077; AAC26696.1; -.
 DR EMBL; AJ132437; CAB41009.1; -.
 DR PFAM; PF00671; Fe_Asc-Oxidoreductase; 1.
 SQ SEQUENCE 335 AA; 38216 MW; 595DC30F CRC32;

Query Match 65.5%; Score 38; DB 10; Length 335;
 Best Local Similarity 66.7%; Pred. No. 24;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 FTWSSYDMS 10
 Db 302 FTWSQYKLS 310
 ||||| | |

RESULT 6
 ID 004710 PRELIMINARY; PRT; 356 AA.

AC 004710;
 DT 01-JUL-1997 (TREMREL. 04, Created)
 DT 01-JUL-1997 (TREMREL. 04, Last sequence update)
 DT 01-NOV-1999 (TREMREL. 12, Last annotation update)
 DE ANIONIC PEROXIDASE.
 GN YPR9 OR APL.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
 OC Poaceae; Zea.
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE; 97433264.
 RA TEICHMANN T., GUAN C., KRISTOFFERSEN P., MUSTER G., TIEFZ O.,
 RA PALME K.;
 RT "Cloning and biochemical characterization of an anionic peroxidase
 RT from Zea mays.";
 RL Eur. J. Biochem. 247:826-832(1997).
 DR EMBL; Y13905; CAA74203.1; -.
 DR HSSP; P00433; 1ATJ.
 DR MENDEL; 14986; Zeama; Ypr9; 14986.
 DR PROSITE; PS00435; PEROXIDASE_1; 1.
 DR PROSITE; PS00436; PEROXIDASE_2; 1.
 DR PFAM; PF00141; peroxidase; 1.
 DR PRINTS; PR00458; PEROXIDASE.
 KW Peroxidase.
 SQ SEQUENCE 356 AA; 37774 MW; CD1782DA CRC32;

Query Match 65.5%; Score 38; DB 10; Length 356;
 Best Local Similarity 60.0%; Pred. No. 26;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 Db 36 GLWSFYDVS 45
 | : || || | |

RESULT 7
 ID 022184 PRELIMINARY; PRT; 2408 AA.

AC Q22184;
 DT 01-NOV-1996 (TREMREL. 01, Created)
 DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
 DT 01-JAN-1999 (TREMREL. 09, Last annotation update)
 DE T05AL.4 PROTEIN.
 GN T05AL.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
 OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA LLOYD C.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., McMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RL Nature 368:32-38(1994).
 DR EMBL; Z68219; CAA92477.1; -.
 SQ SEQUENCE 2408 AA; 269763 MW; 7B41468D CRC32;

Query Match 65.5%; Score 38; DB 5; Length 2408;
 Best Local Similarity 62.5%; Pred. No. 2e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYD 8
 Db 1420 GYTWDSEF 1427
 | : | | | | |

RESULT 8
 ID 060055 PRELIMINARY; PRT; 286 AA.
 AC 060055;
 DT 01-AUG-1998 (TREMREL. 07, Created)
 DT 01-AUG-1998 (TREMREL. 07, Last sequence update)
 DT 01-AUG-1998 (TREMREL. 07, Last annotation update)
 DE HYPOTHETICAL 32.8 KD PROTEIN.
 GN SPBC13G1.03C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Archiascomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-972H;
 RA LYNE M., WOOD V., RAJANDREAM M.A., BARRELL B.G., BADCOCK K.,
 RA CHURCHER C.M.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL022600; CAA18656.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 286 AA; 32813 MW; 46A8E7FC CRC32;

Query Match 63.8%; Score 37; DB 3; Length 286;
 Best Local Similarity 55.6%; Pred. No. 31;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTWSSYDM 9
 Db 81 GFAWSAYSL 89
 | | | | | |

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RESULT 9
O42801 ID O42801 PRELIMINARY; PRT; 537 AA.
AC O42801;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE SUCROSE-SUCROSE 1-FRUCTOSYLTRANSFERASE PRECURSOR (EC 3.2.1.26).
OS Aspergillus foetidus.
OC Eukaryota; Fungi; Ascomycota; Euascomycetes; Plectomycetes;
OC Eutotiales; Trichocomaceae; anamorphic Trichocomaceae; Aspergillus.
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE; 98155160.
RX REHM J., WILLMITZER L., HEYER A.G.;
RT "Production of 1-kestose in transgenic yeast expressing a
RT fructosyltransferase from Aspergillus foetidus.";
RL J. Bacteriol. 180:1305-1310(1998).
CC 1- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
DR EMBL; AJ000493; CAA04131.1; -.
DR PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.
DR PFAM; PF00251; Glyco_hydro_32; 2.
KW Signal; Transferase; Hydrolase; Glycosidase.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 537 SUCROSE-SUCROSE 1-FRUCTOSYLTRANSFERASE.
SQ SEQUENCE 537 AA; 59150 MW; 27713226 CRC32;

Query Match 63.8%; Score 37; DB 3; Length 537;
Best Local Similarity 62.5%; Pred. No. 60;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYD 8
Db 160 GLTWTYYD 167

RESULT 10
P91157 ID P91157 PRELIMINARY; PRT; 993 AA.
AC P91157;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DE COSMID C44C3.
GN C44C3.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
[1]
RN SEQUENCE FROM N.A.
RP STRAIN-BRISTOL N2;
RX MEDLINE; 94150718;
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KRISTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
[2]
RN SEQUENCE FROM N.A.
RP STRAIN-BRISTOL N2;
RA TIN A.;
RI- Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
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RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U80028; AAB37360.1; -.
DR PFAM; PF01604; 7tm_5; 1.
SQ SEQUENCE 993 AA; 115001 MW; A6FCFA5E CRC32;

Query Match 63.8%; Score 37; DB 5; Length 993;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYD 8
Db 166 GFVWSNED 173

RESULT 11
O61137 ID O61137 PRELIMINARY; PRT; 1156 AA.
AC O61137;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
DE AMINOPHOSPHOLIPID TRANSLOCASE.
GN APLT1.
OS Leishmania donovani.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
[1]
RN SEQUENCE FROM N.A.
RC STRAIN-ETHIOPIAN L82;
RA MEADE J.C., XUE L., CASE S.T.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF067496; AAC19127.1; -.
SQ SEQUENCE 1156 AA; 129296 MW; 284D104A CRC32;

Query Match 63.8%; Score 37; DB 5; Length 1156;
Best Local Similarity 70.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
Db 405 GRUWYSYDMS 414

RESULT 12
O61297 ID O61297 PRELIMINARY; PRT; 232 AA.
AC O61297;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE PANCREATIC ALPHA AMYLASE ISOZYME.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RN SEQUENCE FROM N.A.
RC STRAIN-CE/J;
RX MEDLINE; 85126875.
RA TOSI M., BOVEY R., ASTOLFI S., BODARY S., MEISLER M., WELLAUER P.K.;
RT "Multiple non-allelic genes encoding pancreatic alpha-amylase of mouse
RT are expressed in a strain-specific fashion.";
RL EMBO J. 3:2809-2816(1984).
DR EMBL; X02579; CAA26417.1; -.
DR HSP; P00690; 1BVN.
DR PFAM; PF00128; alpha-amylase; 1.
SQ SEQUENCE 232 AA; 26509 MW; 5913ED1A CRC32;
```

Query Match 62.1%; Score 36; DB 11; Length 232;
Best Local Similarity 62.5%; Pred. No. 37;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTWSSYD 8
II : : II
Db 11 GFCWAQYD 18

RESULT 13
P91823
ID P91823 PRELIMINARY; PRT; 323 AA.
AC P91823;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE T22A3.6 PROTEIN.
GN T22A3.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RL MCMURRAY A.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
DR EMBL; Z81125; CAB03383.1; -.
DR HSSP; P00747; SHPG.
SQ SEQUENCE 323 AA; 36900 MW; 52913D93 CRC32;

Query Match 62.1%; Score 36; DB 5; Length 323;
Best Local Similarity 60.0%; Pred. No. 53;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
II : : IIII
Db 56 GFPYTDYDMS 65

RESULT 14
O06893
ID O06893 PRELIMINARY; PRT; 425 AA.
AC O06893;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE ISOCITRATE DEHYDROGENASE.
OS Bacillus israeli.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE FROM N.A.
RA DAJANI R., SCAMEN M., NICHOLIS D., SUNDARAM T.K., GODA S.K.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y13358; CAA73794.1; -.
DR HSSP; P08200; IIKA.
DR PROSITE; PS00470; IDH_IMDH; 1.

DR PFAM; PF00180; isodh; 1.
SQ SEQUENCE 425 AA; 46869 MW; 44B572C6 CRC32;

Query Match 62.1%; Score 36; DB 2; Length 425;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FTWSSYD 8
III : II
Db 251 FTWAEYD 257

RESULT 15
Q9YEL8
ID Q9YEL8 PRELIMINARY; PRT; 483 AA.
AC Q9YEL8;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE 483AA LONG HYPOTHETICAL PROTEIN.
GN APE0560.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Aeropyrum.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-K1.
RX MEDLINE; 99310339.
RA KAWARABAYASI Y., HINO Y., HORIKAWA H., YAMAZAKI S., HAIKAWA Y.,
RA JIN-NO K., TAKAHASHI M., SEKINE M., BABA S., ANKAI A., KOSUGI H.,
RA HOSOGAWA A., FUKUI S., NAGAI Y., NISHIJIMA K., NAKAZAWA H.,
RA TAKAMIYA M., MASUDA S., FUNAHASHI T., TANAKA T., KUDOH Y.,
RA YAMAZAKI J., KUSHIDA N., OGUCHI A., AOKI K., KUBOTA K., NAKAMURA Y.,
RA NOMURA N., SAKO Y., KIKUCHI H.;
RT "Complete genome sequence of an aerobic hyper-thermophilic
RT crenarchaeon, Aeropyrum pernix K1.";
RL DNA Res. 6:83-101(1999).
DR EMBL; AP000060; BAA79528.1; -.
SQ SEQUENCE 483 AA; 52783 MW; 40C8153D CRC32;

Query Match 62.1%; Score 36; DB 1; Length 483;
Best Local Similarity 75.0%; Pred. No. 81;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 TWSSYDMS 10
: IIIII I
Db 46 SWSSYDYS 53

Search completed: May 27, 2000, 19:38:31
Job time: 2364 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:21:30 ; Search time 148.45 Seconds
(without alignments)
1.596 Million cell updates/sec

Title: US-09-016-061-50
Perfect score: 58
Sequence: 1 GFTWSSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	10	W76015	LM609 grafted anti
2	48	82.8	10	W76007	LM609 grafted anti
3	48	82.8	117	W76001	Vitaxin antibody h
4	45	77.6	117	W60137	Protein sequence o
5	45	77.6	128	W54000	Anti-CD4 antibody
6	45	77.6	134	R24713	Sequence encoded b
7	45	77.6	466	R24812	Sequence encoded b
8	44	75.9	139	W21652	Humanised reshaped
9	43	74.1	117	W76003	LM609 antibody hea
10	43	74.1	239	R34511	Fv(TU25). Polypept
11	43	74.1	247	W11917	Murine Mab SK48-E2
12	42	72.4	10	W76016	LM609 grafted anti
13	42	72.4	117	W86141	Protein sequence o
14	42	72.4	119	W11919	Humanised MAB SK48
15	42	72.4	123	W53998	Anti-CD4 antibody
16	41	70.7	98	W59614	Anti-RSV F protein
17	41	70.7	116	R66307	Human immunoglobul
18	41	70.7	116	W13529	Anti-melanoma anti
19	41	70.7	118	W57591	Chimeric antibody
20	41	70.7	118	W57576	Chimeric H chain S
21	41	70.7	118	W89636	Human antibody hea
22	41	70.7	118	W89627	Mouse humanised an
23	41	70.7	119	R79876	Anti-EGFR antibody
24	41	70.7	119	R79887	Anti-EGFR antibody
25	41	70.7	119	R79888	Anti-EGFR antibody
26	41	70.7	121	W86122	Protein sequence o
27	41	70.7	122	R54301	Anti-HIV gp120 imm
28	41	70.7	122	W01259	VH region of HIV n
29	41	70.7	122	W78432	Antibody heavy cha
30	41	70.7	123	W08582	Human antibody C4
31	41	70.7	128	R69085	Anti-HIV Fab rev16
32	41	70.7	128	R69086	Anti-HIV Fab rev20
33	41	70.7	128	W08734	Human anti-HIV Fab
34	41	70.7	128	W08735	Human anti-HIV Fab

35 41 70.7 137 1 W57603 Chimeric antibody
36 41 70.7 137 1 W57592 Chimeric antibody
37 41 70.7 137 1 W89635 Human antibody hea
38 41 70.7 137 1 W89625 Mouse humanised an
39 41 70.7 138 1 R20064 MRK16-H chain. Chl
40 41 70.7 239 1 R79866 Anti-EGFR single c
41 40 69.0 10 1 W76014 LM609 grafted anti
42 40 69.0 98 1 R54816 SpA-reactive VH re
43 40 69.0 102 1 R80088 Human-derived heav
44 40 69.0 102 1 W95486 Human-derived RT3
45 40 69.0 108 1 R95284 Anti-proenkephalin

ALIGNMENTS

RESULT 1

W76015
ID W76015 standard; Protein; 10 AA.
AC W76015;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDRL protein fragment #3.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998: U01826.
PR 30-JAN-1997: US-791391.
PA (IXSY-) IXSY INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49852.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
integrin - and related grafted antibodies based on murine monoclonal
LM609, also related nucleic acid, used to treat, prevent or diagnose
angiogenesis or restenosis
PS Claim 60: Page 41: 129pp: English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
LM609 heavy and light chain variable region. LM609 and the antibody
vitaxin bind selectively to integrin alphavbeta3 and can be used to
inhibit binding of alphavbeta3 to a ligand and thus block
integrin-mediated signal transduction. This is useful in the treatment,
prevention and diagnosis of alphavbeta3-mediated disease, specifically,
angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
arthritis, macular degeneration, osteoporosis etc.). The antibodies
contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 100.0%; Score 58; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00025;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
Db 1 GFTWSSYDMS 10
|||||

RESULT 2

W76007
ID W76007 standard; Protein; 10 AA.
AC W76007;

DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDRL protein fragment #1.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PR 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V4984.
 DR Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT Integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Disclosure; Page 40; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 82.8%; Score 48; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.012;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSSYDMS 10
 |||:|||||
 Db 1 GFTFSSYDMS 10

RESULT 3
 ID W76001 standard; Protein; 117 AA.

AC W76001;
 DE Vitaxin antibody heavy chain variable region protein fragment.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PR 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49820.
 DR Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT Integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 1; Fig 1a; 129pp; English.
 CC This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphaVbeta3 and can be used to inhibit binding of alphaVbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphaVbeta3-mediated

CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 SQ Sequence 117 AA;

Query Match 82.8%; Score 48; DB 1; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.18;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSSYDMS 10
 |||:|||||
 Db 26 GFTFSSYDMS 35

RESULT 4

W86137 standard; Protein; 117 AA.

ID W86137;
 AC W86137;
 DT 03-MAR-1999 (first entry)
 DE Protein sequence of de-immunised humanised A33 Vh.
 KW Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK;
 KW immunogl bulin; therapeutic; streptokinase; humanised; de-immunised.
 OS Homo sapiens.
 PN W09852976-A1.
 PD 26-NOV-1998.
 PR 21-MAY-1998; G01473.
 PR 14-APR-1998; GB-007751.
 PR 21-MAY-1997; GB-010480.
 PR 31-JUL-1997; GB-016197.
 PR 28-NOV-1997; GB-025270.
 PR 02-DEC-1997; US-067235.
 PA (BIOV-) BIOVATION LTD.
 PI Carr FJ;
 DR WPI: 99-045301/04.
 PT Reducing immunogenicity of proteins - by modifying the amino acid
 PT sequence of the protein to eliminate potential epitopes for T-cells
 PT of a given species
 PS Example 5; Fig 25; 77pp; English.
 CC The invention relates to a method for the production of non-immunogenic
 CC proteins. The method comprises determining at least part of the amino
 CC acid sequence of the protein; (b) identifying in the amino acid sequence
 CC one or more potential epitopes for T-cells (T-cell epitopes) of the given
 CC species; and (c) modifying the amino acid sequence to eliminate at least
 CC one of the T-cell epitopes identified in step (b) thereby to eliminate or
 CC reduce the immunogenicity of the protein when exposed to the immune
 CC system of the given species. A method of analysing a pre-existing protein
 CC to predict the basis for immunogenic responses is also provided. The
 CC methods can be used particularly for reducing the immunogenicity of
 CC immunoglobulins or therapeutic proteins, e.g. streptokinase (SK). The
 CC products can be used for diagnosis and therapy. The present sequence
 CC represents the protein sequence of de-immunised humanised A33 Vh.
 SQ Sequence 117 AA;

Query Match 77.6%; Score 45; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 0.58;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSSYDMS 10
 |||:|||||
 Db 26 GFTFSSYDMS 35

RESULT 5

W54000 standard; Protein; 128 AA.

ID W54000
 AC W54000;
 DT 29-JUL-1998 (first entry)
 DE Anti-CD4 antibody Vh3 monkey clone 3-40.

KW Anti-CD4 antibody; monkey; human; therapy; variable heavy domain;
 KW Old World monkey; constant domain; eczema; immuno-modulated disease;
 KW rheumatoid arthritis.
 OS Primate sp.
 FH Key Location/Qualifiers
 FT Misc_difference 1..128 /note= "Xaa= unspecified amino acid"
 FT
 PN US5750105-A.
 PD 12-MAY-1998.
 PF 07-JUN-1995; 476349.
 PR 10-JUL-1992; US-912292.
 PR 23-JUL-1991; US-735064.
 PR 23-MAR-1992; US-856281.
 PR 05-DEC-1995; US-379072.
 PR 07-JUN-1995; US-476349.
 PA (IDEC-) IDEC PHARM CORP.
 PI Hanna N. Newman RA, Raab RW;
 DR WPI; 98-296690/26.
 CC Improved method for antibody treatment - uses an antibody comprising
 FT an Old World monkey variable region and a human constant domain
 PS Example 1; Fig 9c; 84pp; English.
 CC This sequence represents the VH3 domain of an anti-CD4 antibody
 CC (Ab). This sequence can be used in the method of the invention for
 CC treating a subject, where the treatment comprises administration of an
 CC Ab. The method comprises the administration of an antibody which has an
 CC Old World monkey (e.g. baboon or macaque) variable region which binds to
 CC an antigen (Ag) (or Ag binding portion), and a human constant domain. The
 CC method is useful for the treatment of eczema and immuno-modulated
 CC diseases and especially rheumatoid arthritis. The recombinant antibodies
 CC used are sufficiently different from native monkey antibodies to allow
 CC human antigens to raise these antibodies, but similar enough to human
 CC antibody so there is no immune response to the antibodies in humans.
 CC Compared to antibodies used in therapy in prior art, these antibodies do
 CC not induce human anti-antibodies on repeated administration. They also
 CC have longer half-lives and do not have a lack of effector function with
 CC human cells.
 CC Sequence 128 AA;
 SQ

Query Match 77.6%; Score 45; DB 1; Length 128;
 Best Local Similarity 80.0%; Pred. No. 0.65;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
 Db 26 GFTFSSYDMN 35
 |||:|||||

RESULT 6
 R24713
 ID R24713 standard; Protein; 134 AA.
 AC R24713;
 DT 28-DEC-1992 (first entry)
 DE Sequence encoded by the genomic chimeric heavy chain variable region
 DE (VFH) gene
 KW Chimeric monoclonal antibody; anti-fibrin antibody; PCR;
 KW antithrombotic agent; myocardial infarction therapy.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT peptide 1..19 /label= leader
 FT region 23..49 /label= Framework Region (FR) 1
 FT region 50..54 /label= Complementarity determining region(CDR)1
 FT region 55..68 /label= FR-2
 FT region 69..84 /label= FR-2
 FT region 85..114 /label= CDR-2
 FT region 115..123 /label= FR-3
 FT region /label= CDR-3

FT region 124..134 /label= FR-4
 FT EP-491351-A.
 PN 24-JUN-1992.
 PF 17-DEC-1991; 121591.
 PR 18-DEC-1990; JP-413829.
 PR 11-NOV-1991; JP-294464.
 PA (TAKE) TAKEDA CHEM IND LTD.
 PI Iwasa S, Taka H, Watanabe T, Tada H;
 DR WPI; 92-209528/26.
 DR N-PSDB; Q25666.
 CC Chimeric monoclonal antibodies - contain anti-human fibrin
 FT antibody light and heavy chain variable and constant for treating
 FT thrombotic conditions e.g. myocardial infarction
 PS Example; Figure 4; 87pp; English.
 CC PCR primers 5'MVH and 3'MVH were used to produce a VH gene-contg.
 CC fragment of about 330bp. The fragment was isolated and subcloned in
 CC pUC119. The fragment was found to be a functional VH structural
 CC gene, referred to as VFH, comprising a VH gene belonging to the
 CC subgroup III (VHIII) and the DSP2 and JH4 genes. Northern blot
 CC analysis using the whole RNA of FTB1-11 cells confirmed that VFH
 CC was the gene expressed in FTB1-11 cells. The sequence is given in
 CC Q25666.
 SQ Sequence 134 AA;
 Query Match 77.6%; Score 45; DB 1; Length 134;
 Best Local Similarity 80.0%; Pred. No. 0.68;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GFTWSSYDMS 10
 Db 45 GFTFSSYDMS 54
 |||:|||||

RESULT 7
 R24812
 ID R24812 standard; Protein; 466 AA.

AC R24812;
 DT 28-DEC-1992 (first entry)
 DE Sequence encoded by the chimeric H chain cDNA contained in pTB1373
 DE Chimeric monoclonal antibody; anti-fibrin antibody; primer;
 KW antithrombotic agent; myocardial infarction therapy.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT peptide 13..19 /label= Leader
 FT region 20..134 /label= VH
 FT region 135..232 /label= CH1
 FT region 233..247 /label= hinge
 FT region 248..357 /label= CH2
 FT region 358..464 /label= CH3
 FT misc_difference 465 /note= "translated stop codon"
 FT EP-491351-A.
 PN 24-JUN-1992.
 PF 17-DEC-1991; 121591.
 PR 18-DEC-1990; JP-413829.
 PR 11-NOV-1991; JP-294464.
 PA (TAKE) TAKEDA CHEM IND LTD.
 PI Iwasa S, Taka H, Watanabe T, Tada H;
 DR WPI; 92-209528/26.
 DR N-PSDB; Q25692.
 CC Chimeric monoclonal antibodies - contain anti-human fibrin
 FT antibody light and heavy chain variable and constant for treating
 FT thrombotic conditions e.g. myocardial infarction
 PS Example; Figure 11; 87pp; English.
 CC Plasmid pTB1373 contains the whole length of a mouse-human

CC chimeric anti-human fibrin heavy chain cDNA open reading
 CC frame. It was prepd. using Poly(A)+ RNA from the anti-fibrin
 CC chimeric Ab-producing transfectant FIB1-H01/X63 as a template
 CC to clone human C-kappa cDNA, using the oligo-dT (Pharmacia) primer as
 CC a primer for first strand cDNA synthesis and the 5'C2H and 3'EH
 CC primers for the PCR. A human gamma-1 chain CH2-CH3 domain encoding
 CC cDNA was amplified. Similarly a human gamma-1 chain CH1 domain
 CC encoding cDNA and an anti-fibrin antibody VH cDNA and a leader
 CC peptide cDNA were amplified using the primers 3'EH, 3'C2H and 3'CIH
 CC respectively as a primer for first strand cDNA synthesis and the
 CC primer combination of 5'CIH and 3'C2H, of 5'EH and 3'CIH and of
 CC 5'SH and 3'EH respectively as primers for PCR. The amplified gene
 CC products were isolated and used to produce plasmids. After
 CC confirmation of the cDNA sequence of each plasmid, the cDNA
 CC encoding LH, VH, CH1 and CH2CH3 were joined together to give
 CC plasmid pTB1373 contg. the whole length chimeric H chain
 CC (LH, VH, CH1, CH2CH3), also abbreviated as IgH-FIB,
 SQ Sequence 466 AA;

Query Match 77.6%; Score 45; DB 1; Length 466;
 Best Local Similarity 80.0%; Pred. No. 2.7; Mismatches 0; Indels 0; Gaps 0;
 Matches 8; Conservative 2;

QY 1 GFTWSSYDMS 10
 |||:|||||
 Db 45 GFTFSYDMS 54

RESULT 8
 ID W21652 standard; Protein; 139 AA.
 AC W21652;
 DT 03-JAN-1998 (first entry)
 DE Humanised reshaped MAB 15 heavy chain variable region.
 KW Humanised antibody; monoclonal antibody; MAB 15; tumour;
 KW lung cancer; therapy.
 OS Chimeric Mus musculus.
 OS Chimeric Homo sapiens.
 OS Chimeric synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= Sig_peptide
 FT Protein 20..139
 FT /label= Mat_protein
 FT Region 20..49
 FT /label= Framework-1
 FT Region 50..54
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT Region 55..68
 FT /label= Framework-2
 FT Region 69..85
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT Region 86..117
 FT /label= Framework-3
 FT Region 118..128
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 FT Region 129..138
 FT /label= Framework-4
 FT EP-781847-A1.
 PN 02-JUL-1997.
 PD 25-OCT-1996; 117154.
 PR 06-NOV-1995; EP-117407.
 PA (MERE) MERCK PATENT GMBH.
 PI Bendig M, Jones T, Saldana J;
 DR WPI; 97-334904/31.
 DR N-PSDB; T72237.
 PT Humanised form of murine monoclonal antibody MAB 15 - useful for
 PT treating lung cancer
 PS Claim 2; Fig 12; 71pp; English.

CC This polypeptide comprises the heavy chain variable region VH
 CC of humanised reshaped monoclonal antibody (MAB) 15 comprising
 CC complementarity determining regions of murine MAB 15 (DSM ACC2117),
 CC and reshaped human 30P1 framework regions. It is expressed by a
 CC cDNA clone (see T72237) prepared using PCR mutagenesis methods. A
 CC claimed process for preparation of humanised reshaped MAB 15
 CC involves: cloning and sequencing murine MAB 15 VL and VH regions
 CC (see W21653 and W21654); constructing, expressing and analysing
 CC chimeric MAB 15 antibody (see W21655-56); modelling the structure
 CC of murine MAB 15 variable regions; designing reshaped human MAB 15
 CC variable regions; preparing an oligonucleotide sequence which codes
 CC for the constant regions of the light and heavy chain of a human
 CC immunoglobulin; and constructing, expressing and analysing the
 CC complete reshaped human MAB 15. The humanised MAB can be used for
 CC treating tumours, especially lung cancer, and for the manufacture
 CC of a drug related to tumours, especially lung cancer.
 SQ Sequence 139 AA;

Query Match 75.9%; Score 44; DB 1; Length 139;
 Best Local Similarity 80.0%; Pred. No. 1;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GFTWSSYDMS 10
 |||:|||||
 Db 45 GFTFSYDMS 54

RESULT 9
 W76003
 ID W76003 standard; Protein; 117 AA.
 AC W76003;
 DT 02-NOV-1998 (first entry)
 DE LM609 antibody heavy chain variable region protein fragment.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IASY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49822.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 43; Fig 2a; 129pp; English.
 CC This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 SQ Sequence 117 AA;

Query Match 74.1%; Score 43; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 1.3;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GFTWSSYDMS 10
 |||:|||||

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Db      26 GFAPSSYDMS 35

RESULT 10
R34511
ID      R34511 standard; Protein; 239 AA.
AC      R34511;
DT      20-AUG-1993 (first entry)
DE      Fv(TU25).
KW      pFv(TU27)-DE; pFv(TU25)-DE; V region; antibody; binding;
KW      heavy; beta; chain; interleukin; IL-2; receptor; inhibition;
KW      immunomodulator; immunosuppressant; graft rejection; allergy;
KW      autoimmune disease; leukemia; cyclosporin.
OS      Homo sapiens.
PN      EP-539748-A.
PD      05-MAY-1993.
PF      30-SEP-1992; 116746.
PR      03-OCT-1991; JP-256335.
PA      (AJIN ) AJINOMOTO KK.
PI      Hamuro J, Shimamura T, Taki S;
DR      WPI: 93-145163/18.
DR      N-PSDB: Q40463.
PT      Polypeptides(s) which bind H chain of human IL-2 receptors - for
PT      treating inflammatory, allergic and auto-immune disorders,
PT      leukemias etc.
PS      Claim 4; Page 19; 27pp; English.
CC      The constructed plasmids pFv(TU27)-DE and pFv(TU25)-DE which express
CC      polypeptides consisting only of the V regions were purified and
CC      sequenced. The polypeptides are capable of binding to the beta
CC      chain of IL-2 receptor and of inhibiting the binding of IL-2 to the
CC      receptor. They are useful as immunomodulators and
CC      immunosuppressants, e.g. to prevent graft rejection or to treat
CC      inflammatory allergic and autoimmune diseases, or leukemia. Unlike
CC      cyclosporin etc. they are both effective and safe.
SQ      Sequence 239 AA;

Query Match      74.1%; Score 43; DB 1; Length 239;
Best Local Similarity 80.0%; Pred. No. 2.8;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GFTWSSYDMS 10
        II :IIIIII
DB      148 GFAPSSYDMS 157

RESULT 11
W11917
ID      W11917 standard; Protein; 247 AA.
AC      W11917;
DT      24-JUN-1997 (first entry)
DE      Murine MAb SK48-E26 heavy chain.
KW      Interleukin-1 beta; IL-1 beta; recombinant antibody;
KW      humanised antibody; chimeric antibody; antibody engineering;
KW      monoclonal antibody; MAb; SK48-E26; inflammation; therapy.
OS      Homo sapiens.
FH      Key Location/Qualifiers
FT      peptide 1..19
FT      /label= Sig_peptide
FT      region 20..49
FT      /label= FR1
FT      /note= "framework region 1"
FT      region 50..54
FT      /label= CDR1
FT      /note= "complementarity determining region 1
FT      (Claim 10, page 48)"
FT      region 55..68
FT      /label= FR2
FT      /note= "framework region 2"
FT      region 69..85
FT      /label= CDR2
FT      /note= "complementarity determining region 2
FT      (Claim 10, page 48)"

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FT      region 86..117
FT      /label= FR3
FT      /note= "framework region 3"
FT      region 118..127
FT      /label= CDR3
FT      /note= "complementarity determining region 3
FT      (Claim 10, page 48)"
FT      region 128..138
FT      /label= FR4
FT      /note= "framework region 4"
FT      region 139..247
FT      /label= Constant_region
PN      W09501997-A1.
PD      19-JAN-1995.
PF      07-JUL-1994; U07659.
PR      09-JUL-1993; US-090534.
PR      04-MAR-1994; US-206190.
PA      (SMIK ) SMITHKLINE BEECHAM CORP.
PI      Gross MS, Hurler MR, Jackson JR, Jonak ZL, Theisen TW;
PI      Young PR;
DR      WPI: 95-066868/09.
DR      N-PSDB; T51436.
PT      Recombinant and humanised chimeric antibodies against human
PT      interleukin-1-beta - for preventing and treating
PT      interleukin-mediated inflammatory disorders
PS      Claim 5; Page 36-37; 62pp; English.
CC      Amino acid sequences of the heavy chain (W11917) and light chain
CC      (W11918) of anti-human interleukin-1 beta (IL-1 beta) murine
CC      monoclonal antibody (MAb) SK48-E26 were deduced from nucleic acids
CC      (T51436-37) derived from hybridoma SK48-E26. The heavy and light
CC      chains, esp. the complementarity determining region sequences,
CC      can be utilised in novel recombinant chimeric and humanised
CC      antibodies (see also W11919-20) useful for the treatment and
CC      prevention of IL-1 mediated inflammatory disorders.
SQ      Sequence 247 AA;

Query Match      74.1%; Score 43; DB 1; Length 247;
Best Local Similarity 80.0%; Pred. No. 2.9;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 GFTWSSYDMS 10
        II :IIIIII
DB      45 GFAPSSYDMS 54

RESULT 12
W76016
ID      W76016 standard; Protein; 10 AA.
AC      W76016;
DT      02-NOV-1998 (first entry)
DE      LM609 grafted antibody V-H region CDR1 protein fragment #4.
KW      Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW      LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW      diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW      neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW      macular degeneration; osteoporosis; primer; V-H region; CDR;
KW      complementarity determining region.
OS      Mus sp.
PN      W09833919-A2.
PD      06-AUG-1998.
PF      30-JAN-1998; U01826.
PR      30-JAN-1997; US-791391.
PA      (IXSY-) IXSYS INC.
PI      Glaser SM, Huse WD;
DR      WPI: 98-437472/37.
DR      N-PSDB; V49853.
PT      Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT      integrin - and related grafted antibodies based on murine monoclonal
PT      LM609, also related nucleic acid, used to treat, prevent or diagnose
PT      angiogenesis or restenosis
PS      Claim 60; Page 41; 129pp; English.
CC      W76007-W76040 are protein fragments of the grafted monoclonal antibody

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CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 72.4%; Score 42; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.12;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 |||:|||||
 Db 1 GFTFLSYDMS 10

RESULT 13

W86141 ID W86141 standard; Protein; 117 AA.

AC W86141;
 DT 03-MAR-1999 (first entry)
 DE Protein sequence of de-immunised murine A33 Vh.
 KW Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK;
 KW Immunogl bulin; therapeutic; streptokinase; murine; de-immunised.
 OS Mus sp.

PN W09852976-A1.

PD 26-NOV-1998.

PF 21-MAY-1998; G01473.

PR 14-APR-1998; GB-007751.

PR 21-MAY-1997; GB-010480.

PR 31-JUL-1997; GB-016197.

PR 28-NOV-1997; GB-025270.

PR 02-DEC-1997; US-067235.

PA (BIOV-) BIOVATION LTD.

PI Carr FJ;

DR WPI; 99-045301/04.

PT Reducing immunogenicity of proteins - by modifying the amino acid
 PT sequence of the protein to eliminate potential epitopes for T-cells

PT of a given species

PS Example 6; Fig 27; 77pp; English.

CC The invention relates to a method for the production of non-immunogenic
 CC proteins. The method comprises determining at least part of the amino
 CC acid sequence of the protein; (b) identifying in the amino acid sequence
 CC one or more potential epitopes for T-cells (T-cell epitopes) of the given
 CC species; and (c) modifying the amino acid sequence to eliminate at least
 CC one of the T-cell epitopes identified in step (b) thereby to eliminate or
 CC reduce the immunogenicity of the protein when exposed to the immune
 CC system of the given species. A method of analysing a pre-existing protein
 CC to predict the basis for immunogenic responses is also provided. The
 CC methods can be used particularly for reducing the immunogenicity of
 CC immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The
 CC products can be used for diagnosis and therapy. The present sequence
 CC represents the protein sequence of de-immunised murine A33 Vh.
 SQ Sequence 117 AA;

Query Match 72.4%; Score 42; DB 1; Length 117;
 Best Local Similarity 70.0%; Pred. No. 1.9;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 |||:|||||
 Db 26 GFTFTYDMS 35

RESULT 14

W53998 ID W53998 standard; Protein; 123 AA.

DE Humanised Mab SK48-E26 heavy chain.
 DE Interleukin-1 beta; IL-1 beta; recombinant antibody;
 KW humanised antibody; chimeric antibody; antibody engineering;
 KW monoclonal antibody; MAb; SK48-E26; inflammation; therapy.
 OS Chimeric Homo sapiens;
 OS Chimeric Mus sp.

PN W09852976-A1.

PD 26-NOV-1998.

PF 21-MAY-1998; G01473.

PR 14-APR-1998; GB-007751.

PR 21-MAY-1997; GB-010480.

PR 31-JUL-1997; GB-016197.

PR 28-NOV-1997; GB-025270.

PR 02-DEC-1997; US-067235.

PA (BIOV-) BIOVATION LTD.

PI Carr FJ;

DR WPI; 99-045301/04.

PT Reducing immunogenicity of proteins - by modifying the amino acid
 PT sequence of the protein to eliminate potential epitopes for T-cells

PT of a given species

PS Example 6; Fig 27; 77pp; English.

CC The invention relates to a method for the production of non-immunogenic
 CC proteins. The method comprises determining at least part of the amino
 CC acid sequence of the protein; (b) identifying in the amino acid sequence
 CC one or more potential epitopes for T-cells (T-cell epitopes) of the given
 CC species; and (c) modifying the amino acid sequence to eliminate at least
 CC one of the T-cell epitopes identified in step (b) thereby to eliminate or
 CC reduce the immunogenicity of the protein when exposed to the immune
 CC system of the given species. A method of analysing a pre-existing protein
 CC to predict the basis for immunogenic responses is also provided. The
 CC methods can be used particularly for reducing the immunogenicity of
 CC immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The
 CC products can be used for diagnosis and therapy. The present sequence
 CC represents the protein sequence of de-immunised murine A33 Vh.
 SQ Sequence 117 AA;

W11919 ID W11919 standard; Protein; 119 AA.
 AC W11919;
 DT 24-JUN-1997 (first entry)
 DE Humanised Mab SK48-E26 heavy chain.
 DE Interleukin-1 beta; IL-1 beta; recombinant antibody;
 KW humanised antibody; chimeric antibody; antibody engineering;
 KW monoclonal antibody; MAb; SK48-E26; inflammation; therapy.
 OS Chimeric Homo sapiens;
 OS Chimeric Mus sp.

PN W09501997-A1.

PD 19-JAN-1995.

PF 07-JUL-1994; U07659.

PR 09-JUL-1993; US-090534.

PR 04-MAR-1994; US-206190.

PA (SMIK) SMITHKLINE BEECHAM CORP.

PI Gross MS, Hurler MR, Jackson JR, Jonak ZL, Theisen TW;

DR WPI; 95-066868/09.

DR N-PSDB: T51438.

PT Recombinant and humanised chimeric antibodies against human

PT interleukin-1-beta - for preventing and treating

PT interleukin-mediated inflammatory disorders

PS Claim 39; Page 40-41; 62pp; English.

CC The heavy chain variable region (W11919) and light chain variable

CC region (W11920) of humanised anti-human interleukin-1 beta (IL-1

CC beta) murine monoclonal antibody (MAb) SK48-E26 comprise the

CC complementarity determining regions from MAb SK48-E26 (see also

CC W11917-18) grafted into human frameworks. The humanised antibody

CC can be produced in e.g. COS cells transfected with vectors carrying

CC humanised heavy and light chain nucleic acids (T51437-39) for use

CC in the treatment and prevention of IL-1 mediated inflammatory

CC disorders.

SQ Sequence 119 AA;

Query Match 72.4%; Score 42; DB 1; Length 119;
 Best Local Similarity 80.0%; Pred. No. 1.9;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 ||:|||||
 Db 26 GFTFSSYDMS 35

RESULT 15
 W53998

AC W53998;
DT 29-JUL-1998 (first entry)
DE Anti-CD4 antibody VH3 monkey clone 3-34.
KW Anti-CD4 antibody; monkey; human; therapy; variable heavy domain;
KW Old World monkey; constant domain; eczema; immuno-modulated disease;
KW rheumatoid arthritis.
OS Primate sp.
FH Key Location/Qualifiers
FT Misc_difference 1. .123 /note= "Xaa= unspecified amino acid"
FT US5750105-A.
PN 12-MAY-1998. 476349.
PF 07-JUN-1995; US-912292.
PR 10-JUL-1992; US-735064.
PR 25-JUL-1991; US-735064.
PR 23-MAR-1992; US-856281.
PR 05-DEC-1995; US-379072.
PR 07-JUN-1995; US-476349.
PA (IDEC-) IDEC PHARM CORP.
PI Hanna N, Newman RA, Raab RW;
DT WPI; 98-296690/26.
PT Improved method for antibody treatment - uses an antibody comprising
PT an Old World monkey variable region and a human constant domain
PS Example 1; Fig 9c; 84pp; English.
CC This sequence represents the VH3 domain of an anti-CD4 antibody
CC (Ab). This sequence can be used in the method of the invention for
CC treating a subject, where the treatment comprises administration of an
CC Ab. The method comprises the administration of an antibody which binds to
CC Old World monkey (e.g. baboon or macaque) variable region which binds to
CC an antigen (Ag) (or Ag binding portion), and a human constant domain. The
CC method is useful for the treatment of eczema and immuno-modulated
CC diseases and especially rheumatoid arthritis. The recombinant antibodies
CC used are sufficiently different from native monkey antibodies to allow
CC human antigens to raise these antibodies, but similar enough to human
CC antibody so there is no immune response to the antibodies in humans.
CC Compared to antibodies used in therapy in prior art, these antibodies do
CC not induce human anti-antibodies on repeated administration. They also
CC have longer half-lives and do not have a lack of effector function with
CC human cells.
SQ Sequence 123 AA;

Query Match 72.4%; Score 42; DB 1; Length 123;
Best Local Similarity 70.0%; Pred. No. 2;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTWSSYDMS 10
 |||:|:|:
Db 26 GFTFSTYDMT 35

Search completed: May 27, 2000, 19:21:30
Job time: 1584 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 20:07:09 ; Search time 69.28 Seconds
(without alignments)
4.396 Million cell updates/sec

Title: US-09-016-061-52
Perfect score: 53
Sequence: 1 GFTFLSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	42	79.2	117	1 HV55_MOUSE	P18526 mus musculus
2	40	75.5	117	1 HV54_MOUSE	P18525 mus musculus
3	39	73.6	97	1 HV56_MOUSE	P18527 mus musculus
4	39	73.6	117	1 HV3C_HUMAN	P06327 homo sapien
5	38	71.7	117	1 HV52_MOUSE	P06327 mus musculus
6	37	71.7	117	1 HV53_MOUSE	P18524 mus musculus
7	37	69.8	117	1 HV59_MOUSE	P18530 mus musculus
8	36	67.9	3106	1 LMA2_MOUSE	Q60675 mus musculus
9	35	66.0	115	1 HV3D_HUMAN	P01786 homo sapien
10	35	66.0	117	1 HV17_MOUSE	P01786 mus musculus
11	34	64.2	117	1 HV58_MOUSE	P18529 mus musculus
12	34	64.2	326	1 YE08_SCHPO	O13805 schizosacch
13	34	64.2	451	1 ARP2_PLAFA	P13824 plasmodium
14	33	62.3	114	1 HV00_MOUSE	P01741 mus musculus
15	33	62.3	114	1 HV01_CANFA	P01784 canis faml
16	33	62.3	116	1 HV1A_RABIT	P01826 oryctolagus
17	33	62.3	117	1 HV2B_RABIT	P01828 oryctolagus
18	33	62.3	120	1 HV3E_HUMAN	P01766 homo sapien
19	33	62.3	121	1 HV3J_HUMAN	P01771 homo sapien
20	33	62.3	396	1 EFTU_STIAU	P42479 stigmatella
21	33	62.3	706	1 VGLH_EBV	P03231 epstein-bar
22	32	60.4	114	1 HV3B_HUMAN	P01763 homo sapien
23	32	60.4	117	1 HV14_MOUSE	P01758 mus musculus
24	32	60.4	122	1 HV3G_HUMAN	P01768 homo sapien
25	32	60.4	136	1 HV16_MOUSE	P01783 mus musculus
26	32	60.4	247	1 ATP6_ACACA	Q37385 acanthamoeb
27	32	60.4	281	1 Y373_MYCCE	P47613 mycoplasma
28	32	60.4	281	1 Y373_MYCPN	P75227 mycoplasma
29	32	60.4	550	1 INV1_HANAN	P40912 hescherichia
30	32	60.4	747	1 FHUA_ECOLI	P06971 escherichia
31	31	58.5	111	1 HV35_MOUSE	P01804 mus musculus
32	31	58.5	113	1 HV27_MOUSE	P01796 mus musculus
33	31	58.5	113	1 HV28_MOUSE	P01797 mus musculus
34	31	58.5	113	1 HV29_MOUSE	P01798 mus musculus

ALIGNMENTS

RESULT 1

HV55_MOUSE
ID HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 345 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -|- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR: J70502; HWS34.
DR PFAM: PF00047; ig:1.
KW Immunoglobulin V region; Signal.

FT CHAIN 1 19
FT DOMAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;

Query Match 79.2%; Score 42; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
Db 45 GFAFSSYDMS 54

RESULT 2

HV54_MOUSE
ID HV54_MOUSE STANDARD; PRT; 117 AA.
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 5-84 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=BALB/CJ;
 RX MEDLINE; 89279149.
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR; JT0505; HVMS84.
 DR PFAM; PF00047; ig; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 75.5%; Score 40; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 0.37;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 |||||
 Db 45 GFTFSSYTMS 54

RESULT 3
 HV56_MOUSE
 ID HV56_MOUSE STANDARD; PRT; 97 AA.
 AC P18527;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION 914.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/CJ;
 RX MEDLINE; 89279149.
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR; JT0504; HVMS91.
 DR PFAM; PF00047; ig; 1.
 KW Immunoglobulin V region.
 FT NON_TER 97 97
 SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

Query Match 73.6%; Score 39; DB 1; Length 97;
 Best Local Similarity 80.0%; Pred. No. 0.48;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 |||||
 Db 26 GFTFSSYAMS 35

RESULT 4
 HV3C_HUMAN
 ID HV3C_HUMAN STANDARD; PRT; 117 AA.
 AC P01764;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-III REGION VH26 PRECURSOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 81101090.
 RA Matthyssens G., Rabbitts T.H.;
 RT "Structure and multiplicity of genes for the human immunoglobulin
 heavy chain variable region.";
 RT Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; J00236; AAA53516.1; -;
 DR EMBL; M35415; AAA58735.1; -;
 DR PIR; A02047; H3HU26.
 DR PFAM; PF00047; ig; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12582 MW; E826733FIA3CB0F1 CRC64;

Query Match 73.6%; Score 39; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 0.58;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 |||||
 Db 45 GFTFSSYAMS 54

RESULT 5
 HV52_MOUSE
 ID HV52_MOUSE STANDARD; PRT; 117 AA.
 AC P06327;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION VH558 A1/A4 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 85099340.
 RA Yancopoulos G.D., Alt F.W.;
 RT "Developmentally controlled and tissue-specific expression of
 unrearranged VH gene segments.";
 RL Cell 40:271-281(1985).
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 or send an email to license@isb-sib.ch).
 CC
 DR EMBL; M13787; AAA38499.1; -;
 DR PIR; A02029; HVMSA1.
 DR PFAM; PF00047; ig; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19

FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 AL/A4.
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 71.7%; Score 38; DB 1; Length 117;
 Best Local Similarity 60.0%; Pred. No. 0.92;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 1 GFTFLSYDMS 10
 Db 45 GYFTSYDIN 54

RESULT 6
 HV53_MOUSE STANDARD; PRT; 117 AA.
 ID HV53_MOUSE STANDARD; PRT; 117 AA.
 AC P18524;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION RF PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/CJ;
 RX MEDLINE; 89279149.

RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response."
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR; JT0503; HVMSRF.
 DR PFAM; PF00047; ig; 1.
 KW Immunoglobulin V region; Hybridoma; Signal.

FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION RF.
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 71.7%; Score 38; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 0.92;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 GFTFLSYDMS 10
 Db 45 GFTFSYMS 54

RESULT 7
 HV59_MOUSE STANDARD; PRT; 117 AA.
 ID HV59_MOUSE STANDARD; PRT; 117 AA.
 AC P18530;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION 7-39 PRECURSOR.
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/CJ;
 RX MEDLINE; 89279149.
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response."
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
 DR PIR; JT0507; HVMS39.
 DR PFAM; PF00047; ig; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 7-39.
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;

Query Match 69.8%; Score 37; DB 1; Length 117;
 Best Local Similarity 70.0%; Pred. No. 1.4;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 GFTFLSYDMS 10
 Db 45 GFTFSNYGMS 54

RESULT 8
 LMA2_MOUSE STANDARD; PRT; 3106 AA.
 ID LMA2_MOUSE STANDARD; PRT; 3106 AA.
 AC Q60675; Q05003; Q64061;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE LAMININ ALPHA-2 CHAIN PRECURSOR (LAMININ M CHAIN) (MEROSIN HEAVY
 CHAIN).
 DE LMA2.
 GN Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=EMBRYO, AND HEART;
 RX MEDLINE; 95316259.
 RA Bernier S.M., Utani A., Sugiyama S., Doi T., Polistina C.,
 RA Yamada Y.;
 RT "Cloning and expression of laminin alpha 2 chain (M-chain) in the
 mouse."
 RL Matrix Biol. 14:447-455(1995).
 RN [2]
 RP SEQUENCE OF 2162-2279 FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=THYMUS;
 RX MEDLINE; 93346725.
 RA Chang A.C., Wadsworth S., Colligan J.E.;
 RT "Expression of merosin in the thymus and its interaction with
 thymocytes."
 RL J. Immunol. 151:1789-1801(1993).
 RN [3]
 RP SEQUENCE OF 64-281 FROM N.A.
 RX MEDLINE; 95179178.
 RA Xu H., Wu X.R., Wewer U.M., Engvall E.;
 RT "Murine muscular dystrophy caused by a mutation in the laminin alpha
 2 (Lama2) gene."
 RL Nat. Genet. 8:297-302(1994).
 CC -!- FUNCTION: BINDING TO CELLS VIA A HIGH AFFINITY RECEPTOR, LAMININ

CC IS THOUGHT TO MEDIATE THE ATTACHMENT, MIGRATION, & ORGANIZATION OF
 CC CELLS INTO TISSUES DURING EMBRYONIC DEVELOPMENT BY INTERACTING
 CC WITH OTHER EXTRACELLULAR MATRIX COMPONENTS.
 CC -!- SUBUNIT: LAMININ IS A COMPLEX GLYCOPROTEIN, CONSISTING OF THREE
 CC DIFFERENT POLYPEPTIDE CHAINS (ALPHA, BETA, GAMMA), WHICH ARE BOUND
 CC TO EACH OTHER BY DISULFIDE BONDS INTO A CROSS-SHAPED MOLECULE
 CC COMPRISING ONE LONG & THREE SHORT ARMS WITH GLOBULES AT EACH END.
 CC THE ALPHA-2 CHAIN IS A SUBUNIT OF LAMININ-2 (MEROSIN) AND LAMININ-
 CC 4 (S-MEROSIN).
 CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -!- TISSUE SPECIFICITY: FOUND IN THE BASEMENT MEMBRANES (MAJOR
 CC COMPONENT).
 CC -!- DOMAIN: THE ALPHA-HELICAL DOMAINS I AND II ARE THOUGHT TO INTERACT
 CC WITH OTHER LAMININ CHAINS TO FORM A COILED COIL STRUCTURE.
 CC -!- DOMAIN: DOMAINS VI, IV AND G ARE GLOBULAR.
 CC -!- DISEASE: DEFECTS IN LAMA2 ARE A CAUSE OF MURINE MUSCULAR DYSTROPHY
 CC (DY2J).
 CC -!- SIMILARITY: CONTAINS 1 LAMININ N-TERMINAL DOMAIN (DOMAIN VI).
 CC -!- SIMILARITY: CONTAINS 17 LAMININ EGF-LIKE DOMAINS.
 CC -!- SIMILARITY: CONTAINS 2 LAMININ DOMAINS IV.
 CC -!- SIMILARITY: CONTAINS 5 LAMININ G-LIKE DOMAINS.
 CC -----
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 CC -----
 CC EMBL; U12147; AAC52165.1; -;
 CC EMBL; X69869; CAA49502.1; -;
 CC EMBL; S75315; AAB33573.1; -;
 CC HSSP; P02468; 1KLO.
 CC MGD; MGI:99912; LAMA2.
 CC PRINTS; PR00011; EGFLAMININ.
 CC PROSITE; PS00022; EGF_1; 11.
 CC PROSITE; PS01186; EGF_2; 3.
 CC PROSITE; PS01248; LAMININ_TYPE_EGF; 14.
 CC PFAM; PF00052; laminin_B_2.
 CC PFAM; PF00053; laminin_EGF; 15.
 CC PFAM; PF00054; laminin_G; 5.
 CC PFAM; PF00055; laminin_Nterm; 1.
 CC Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
 CC Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
 CC SIGNAL 1 22 POTENTIAL.
 CC CHAIN 23 3106 LAMININ ALPHA-2 CHAIN.
 CC DOMAIN 23 282 LAMININ N-TERMINAL (DOMAIN VI).
 CC DOMAIN 283 523 4.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
 CC V).
 CC DOMAIN 283 339 LAMININ EGF-LIKE 1.
 CC DOMAIN 340 409 LAMININ EGF-LIKE 2.
 CC DOMAIN 410 464 LAMININ EGF-LIKE 3.
 CC DOMAIN 465 513 LAMININ EGF-LIKE 4.
 CC DOMAIN 514 523 LAMININ EGF-LIKE 5 (N-TERMINAL).
 CC DOMAIN 524 719 LAMININ DOMAIN IV 1 (DOMAIN IV B).
 CC DOMAIN 720 1171 9 X LAMININ EGF-LIKE REPEATS (DOMAIN
 CC III B).
 CC DOMAIN 720 752 LAMININ EGF-LIKE 5 (C-TERMINAL).
 CC DOMAIN 753 802 LAMININ EGF-LIKE 6.
 CC DOMAIN 803 860 LAMININ EGF-LIKE 7.
 CC DOMAIN 861 913 LAMININ EGF-LIKE 8.
 CC DOMAIN 914 962 LAMININ EGF-LIKE 9.
 CC DOMAIN 963 1009 LAMININ EGF-LIKE 10.
 CC DOMAIN 1010 1055 LAMININ EGF-LIKE 11.
 CC DOMAIN 1056 1101 LAMININ EGF-LIKE 12.
 CC DOMAIN 1102 1161 LAMININ EGF-LIKE 13.
 CC DOMAIN 1162 1171 LAMININ EGF-LIKE 14 (N-TERMINAL).
 CC DOMAIN 1172 1375 LAMININ DOMAIN IV 2 (DOMAIN IV A).
 CC DOMAIN 1376 1568 3.5 X LAMININ EGF-LIKE REPEATS (DOMAIN
 CC III A).
 CC DOMAIN 1376 1415 LAMININ EGF-LIKE 14 (C-TERMINAL).
 CC DOMAIN 1416 1464 LAMININ EGF-LIKE 15.

FT DOMAIN 1465 1522 LAMININ EGF-LIKE 16.
 FT DOMAIN 1523 1569 LAMININ EGF-LIKE 17.
 FT DOMAIN 1570 2149 DOMAIN II AND I.
 FT DOMAIN 2150 3106 5 X LAMININ G-LIKE REPEATS (DOMAIN G).
 FT DOMAIN 2150 2323 LAMININ G-LIKE 1.
 FT DOMAIN 2324 2516 LAMININ G-LIKE 2.
 FT DOMAIN 2517 2746 LAMININ G-LIKE 3.
 FT DOMAIN 2747 2929 LAMININ G-LIKE 4.
 FT DOMAIN 2930 3106 LAMININ G-LIKE 5.
 FT DOMAIN 1662 1863 COILED COIL (POTENTIAL).
 FT DOMAIN 1923 2146 COILED COIL (POTENTIAL).
 FT DISULFID 283 292 BY SIMILARITY.
 FT DISULFID 285 303 BY SIMILARITY.
 FT DISULFID 305 314 BY SIMILARITY.
 FT DISULFID 317 337 BY SIMILARITY.
 FT DISULFID 340 349 BY SIMILARITY.
 FT DISULFID 342 374 BY SIMILARITY.
 FT DISULFID 377 386 BY SIMILARITY.
 FT DISULFID 389 407 BY SIMILARITY.
 FT DISULFID 410 422 BY SIMILARITY.
 FT DISULFID 412 438 BY SIMILARITY.
 FT DISULFID 440 449 BY SIMILARITY.
 FT DISULFID 452 462 BY SIMILARITY.
 FT DISULFID 465 478 BY SIMILARITY.
 FT DISULFID 467 482 BY SIMILARITY.
 FT DISULFID 484 493 BY SIMILARITY.
 FT DISULFID 496 511 BY SIMILARITY.
 FT DISULFID 753 762 BY SIMILARITY.
 FT DISULFID 755 769 BY SIMILARITY.
 FT DISULFID 772 781 BY SIMILARITY.
 FT DISULFID 804 800 BY SIMILARITY.
 FT DISULFID 818 818 BY SIMILARITY.
 FT DISULFID 805 828 BY SIMILARITY.
 FT DISULFID 831 840 BY SIMILARITY.
 FT DISULFID 843 858 BY SIMILARITY.
 FT DISULFID 861 875 BY SIMILARITY.
 FT DISULFID 863 882 BY SIMILARITY.
 FT DISULFID 885 894 BY SIMILARITY.
 FT DISULFID 897 911 BY SIMILARITY.
 FT DISULFID 914 926 BY SIMILARITY.
 FT DISULFID 916 933 BY SIMILARITY.
 FT DISULFID 935 944 BY SIMILARITY.
 FT DISULFID 963 960 BY SIMILARITY.
 FT DISULFID 963 975 BY SIMILARITY.
 FT DISULFID 965 981 BY SIMILARITY.
 FT DISULFID 983 992 BY SIMILARITY.
 FT DISULFID 995 1007 BY SIMILARITY.
 FT DISULFID 1010 1019 BY SIMILARITY.
 FT DISULFID 1012 1026 BY SIMILARITY.
 FT DISULFID 1028 1037 BY SIMILARITY.
 FT DISULFID 1040 1053 BY SIMILARITY.
 FT DISULFID 1056 1068 BY SIMILARITY.
 FT DISULFID 1058 1075 BY SIMILARITY.
 FT DISULFID 1077 1086 BY SIMILARITY.
 FT DISULFID 1089 1099 BY SIMILARITY.
 FT DISULFID 1416 1425 BY SIMILARITY.
 FT DISULFID 1418 1432 BY SIMILARITY.
 FT DISULFID 1435 1444 BY SIMILARITY.
 FT DISULFID 1447 1462 BY SIMILARITY.
 FT DISULFID 1465 1480 BY SIMILARITY.
 FT DISULFID 1467 1490 BY SIMILARITY.
 FT DISULFID 1493 1502 BY SIMILARITY.
 FT DISULFID 1505 1520 BY SIMILARITY.
 FT DISULFID 1523 1535 BY SIMILARITY.
 FT DISULFID 1525 1542 BY SIMILARITY.
 FT DISULFID 1544 1553 BY SIMILARITY.
 FT DISULFID 1556 1567 BY SIMILARITY.
 FT DISULFID 1570 1574 INTERCHAIN (PROBABLE).
 FT DISULFID 1574 1574 INTERCHAIN (PROBABLE).
 FT CARBOHYD 51 51 POTENTIAL.
 FT CARBOHYD 85 85 POTENTIAL.
 FT CARBOHYD 299 299 POTENTIAL.
 FT CARBOHYD 359 359 POTENTIAL.

ET CARBOHYD 376 376 POTENTIAL.
 FT CARBOHYD 466 466 POTENTIAL.
 FT CARBOHYD 742 742 POTENTIAL.
 FT CARBOHYD 919 919 POTENTIAL.
 FT CARBOHYD 1031 1031 POTENTIAL.
 FT CARBOHYD 1057 1057 POTENTIAL.
 FT CARBOHYD 1593 1593 POTENTIAL.
 FT CARBOHYD 1610 1610 POTENTIAL.
 FT CARBOHYD 1696 1696 POTENTIAL.
 FT CARBOHYD 1806 1806 POTENTIAL.
 FT CARBOHYD 1897 1897 POTENTIAL.
 FT CARBOHYD 1912 1912 POTENTIAL.
 FT CARBOHYD 1916 1916 POTENTIAL.
 FT CARBOHYD 2013 2013 POTENTIAL.
 FT CARBOHYD 2024 2024 POTENTIAL.
 FT CARBOHYD 2041 2041 POTENTIAL.
 FT CARBOHYD 2122 2122 POTENTIAL.
 FT CARBOHYD 2236 2236 POTENTIAL.

Query Match 67.9%; Score 36; DB 1; Length 3106;
 Best Local Similarity 66.7%; Pred. No. 62;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDM 9
 ||| |||
 Db 2817 GFTFLSYDL 2825

RESULT 9
 HV3D_HUMAN
 ID HV3D_HUMAN STANDARD; PRT; 115 AA.
 AC P01765;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V-III REGION TIL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 78005528.
 RA Wang A.-C., Wang I.-Y., Fudenberg H.H.;
 RT "Immunoglobulin structure and genetics. Identity between variable
 regions of a mu and a gamma2 chain.";
 RL J. Biol. Chem. 252:7192-7199(1977).
 CC -1- MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS
 OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL
 GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
 IDENTICAL.
 DR PIR; A02048; H3HUTL.
 DR PFAM; PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT NON_TER 115 115
 SQ SEQUENCE 115 AA; 12356 MW; 4DCC67D179F62326 CRC64;

Query Match 66.0%; Score 35; DB 1; Length 115;
 Best Local Similarity 70.0%; Pred. No. 3.5;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 |||| : |||
 Db 26 GFTFLSYDMS 35

RESULT 10
 HV17_MOUSE
 ID HV17_MOUSE STANDARD; PRT; 117 AA.
 AC P01786;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE IG HEAVY CHAIN V REGION MOPC 47A.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 80049769.
 RA Robinson E.A., Appella E.;
 RT "Amino acid sequence of a mouse myeloma immunoglobulin heavy chain
 (MOPC 47 A) with a 100-residue deletion.";
 RL J. Biol. Chem. 254:11418-11430(1979).
 CC -1- MISCELLANEOUS: THIS ALPHA CHAIN WAS ISOLATED FROM A MYELOMA
 PROTEIN THAT CONTAINS ONE LIGHT AND ONE HEAVY CHAIN PER MOLECULE,
 LINKED BY A DISULFIDE BOND. IN CONTRAST, NORMAL MOUSE IGA
 MOLECULES CONTAIN TWO LIGHT AND TWO HEAVY CHAINS AND LACK A
 LIGHT-HEAVY CHAIN DISULFIDE BOND.
 CC PIR; A02069; AIMS47.
 DR HSP; P01789; 2MCP.
 DR PFAM; PF00047; Ig; 1.
 KW Immunoglobulin V region.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12975 MW; 0C74BE8BB154BDF4 CRC64;

Query Match 66.0%; Score 35; DB 1; Length 117;
 Best Local Similarity 70.0%; Pred. No. 3.5;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 |||| | |||
 Db 26 GFTFLSYDMS 35

RESULT 11
 HV58_MOUSE
 ID HV58_MOUSE STANDARD; PRT; 117 AA.
 AC P18529;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG HEAVY CHAIN V REGION 5-76 PRECURSOR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALE/CJ;
 RX MEDLINE; 89279149.
 RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
 RT "Early onset of somatic mutation in immunoglobulin VH genes during
 the primary immune response.";
 RL J. Exp. Med. 169:2007-2019(1989).
 CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH183 SUBFAMILY.

DR PIR; J70506; HVMS57
 DR PFAM; PF00047; Ig; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-76.
 FT DOMAIN 20 49 FRAMEWORK 1.
 FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 55 68 FRAMEWORK 2.
 FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 86 117 FRAMEWORK 3.
 FT DISULFID 41 115 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12991 MW; 93A04782B78B8FA0 CRC64;

Query Match 64.2%; Score 34; DB 1; Length 117;
 Best Local Similarity 70.0%; Pred. No. 5.6;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10

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|||||
45 GFTFNKYAMS 54

Db
RESULT 12
YE08_SCHPO STANDARD; PRT; 326 AA.
AC O13805;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE POTATIVE MITOCHONDRIAL CARRIER C17H9.08.
GN SPAC17H9.08.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
OC Schizosaccharomycetaceae; Schizosaccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA Skelton J., Churcher C.M., Barrell B.G., Rajandream M.A., Wood V.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. MITOCHONDRIAL
CC INNER MEMBRANE (POTENTIAL).
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
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CC -----
DR EMBL; Z98597; CAB1217.1; -
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 2.
DR PFAM; PF00153; mito_carr; 1.
KW Hypothetical protein; Mitochondrion; Inner membrane; Repeat;
KW Transmembrane; Transport.
FT TRANSMEM 16 36 POTENTIAL.
FT TRANSMEM 120 140 POTENTIAL.
FT TRANSMEM 191 211 POTENTIAL.
FT TRANSMEM 240 260 POTENTIAL.
FT TRANSMEM 294 314 POTENTIAL.
SQ SEQUENCE 326 AA; 37059 MW; 12163A73260F35D2 CRC64;

Query Match 64.2%; Score 34; DB 1; Length 326;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
| :|||:
Db 203 GMSFLAYDLA 212

RESULT 13
ARP2_PLAFA STANDARD; PRT; 451 AA.
AC P13824;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE CLUSTERED-ASPARAGINE-RICH PROTEIN (FRAGMENT).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 86206015.
RA Wahlgren M., Aslund L., Franzen L., Sundvall M., Wahlin B.,
RA Berzins K., McNicol L.A., Bjoerkman A., Wigzell H., Perlmann P.,
RA Pettersson U.;

"A Plasmodium falciparum antigen containing clusters of asparagine
residues.";
Proc. Natl. Acad. Sci. U.S.A. 83:2677-2681(1986).
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DR EMBL; M13021; AAA29485.1; -
DR PIR; A23535; A23535.
DR PFAM; PF00076; rrm; 2.
KW Malaria.
FT NON_TER 1 1
SQ SEQUENCE 451 AA; 52204 MW; B686354D85F8C293 CRC64;

Query Match 64.2%; Score 34; DB 1; Length 451;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYD 8
| :|||
Db 407 GFGFVSVD 414

RESULT 14
HV00_MOUSE STANDARD; PRT; 114 AA.
AC P01741;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last annotation update)
DE IG HEAVY CHAIN V REGION (ANTI-ARSONATE ANTIBODY).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE; 79195438.
RA Capra J.D., Nisonoff A.;
RT "Structural studies on induced antibodies with defined idiotypic
RT specificities. VII. The complete amino acid sequence of the heavy
RT chain variable region of anti-p-azophenylarsenate antibodies from A/J
RT mice bearing a cross-reactive idiotype.";
RL J. Immunol. 123:279-284(1979).
CC -1- MISCELLANEOUS: ANTIBODY ISOLATED FROM TEN MICE WAS EXCLUSIVELY OF
CC THE IGGL SUBCLASS. THERE WAS NO HETEROGENEITY IN THE HEAVY CHAIN V
CC REGION SEQUENCE.
DR PIR; A02022; GIMSAA.
DR PFAM; PF00047; ig; 1.
KW Immunoglobulin V region; Antiarsonate antibody.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12555 MW; 99DD8F0B6A69F4BE CRC64;

Query Match 62.3%; Score 33; DB 1; Length 114;
Best Local Similarity 55.6%; Pred. No. 8.5;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDM 9
| :|||
Db 26 GYTFSSYEL 34

RESULT 15
HV01_CANFA STANDARD; PRT; 114 AA.
ID HV01_CANFA
AC P01784;
```

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION GOM.
OS Canis familiaris (Dog)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RP SEQUENCE.
RX MEDLINE; 77242268.
RA Wasserman R.L.; Capra J.D.;
RT "Primary structure of the variable regions of two canine
RL immunoglobulin heavy chains."
RL Biochemistry 16:3160-3168(1977).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR: A02067; AVDGGM.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12430 MW; BID4745D2C4E13C4 CRC64;

Query Match 62.3%; Score 33; DB 1; Length 114;
Best Local Similarity 66.7%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GFTFLSYDM 9
Db 26 GITFSGYDM 34

Search completed: May 27, 2000, 20:07:09
Job time: 981 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:38:31 ; Search time 199.56 Seconds
(without alignments)
3.474 Million cell updates/sec

Title: US-09-016-061-52
Perfect score: 53
Sequence: 1 GFTFLSYDMS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SPTREMBL_12.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	69.8	147	4 Q9Y509	Q9Y509 homo sapien
2	36	67.9	312	12 Q67551	Q67551 garlic late
3	36	67.9	1924	12 Q67654	Q67654 garlic late
4	36	67.9	1967	12 Q65652	Q65652 blueberry s
5	36	67.9	2183	12 Q64962	Q64962 apple stem
6	35	66.0	314	10 Q9ZQR7	Q9ZQR7 arabidopsis
7	35	66.0	323	5 P91823	P91823 caenorhabdi
8	35	66.0	363	10 Q9ZU66	Q9ZU66 arabidopsis
9	34	64.2	289	10 Q9ZU04	Q9ZU04 arabidopsis
10	34	64.2	305	10 Q9ZQD6	Q9ZQD6 arabidopsis
11	34	64.2	347	8 Q34096	Q34096 crithidia f
12	34	64.2	349	12 Q65125	Q65125 african swi
13	34	64.2	475	5 Q3XWR7	Q3XWR7 caenorhabdi
14	34	64.2	868	10 Q38710	Q38710 abies grand
15	34	64.2	1418	5 Q01837	Q01837 caenorhabdi
16	34	64.2	1456	5 Q19127	Q19127 caenorhabdi
17	33	62.3	85	2 Q53774	Q53774 stigmatella
18	33	62.3	128	3 Q94499	Q94499 schizosacch
19	33	62.3	223	12 Q9YF85	Q9YF85 sugarcane s
20	33	62.3	315	5 Q20116	Q20116 caenorhabdi

21 33 62.3 355 8 Q34937 leishmania
22 33 62.3 455 2 Q87953 vibrio algi
23 33 62.3 470 8 Q32371 gracilaria
24 33 62.3 472 8 Q32364 gracilaria
25 33 62.3 491 2 P94289 bacillus ci
26 33 62.3 723 11 Q35193 mus musculu
27 33 62.3 763 3 Q12653 pichia caps
28 33 62.3 852 11 Q35192 mus musculu
29 33 62.3 928 2 Q86164 chlamydia p
30 33 62.3 968 10 Q04623 arabidopsis
31 33 62.3 1378 11 Q07314 rattus norv
32 33 62.3 1395 11 Q07313 rattus norv
33 33 62.3 1399 11 Q07280 rattus norv
34 33 62.3 1438 11 Q07312 rattus norv
35 33 62.3 1471 11 Q07311 rattus norv
36 33 62.3 1578 11 Q07310 rattus norv
37 33 62.3 2023 12 Q91632 sour cherry
38 33 62.3 2342 12 Q65980 cherry capi
39 33 62.3 3623 11 Q70244 rattus norv
40 32 60.4 103 8 Q32718 nicotiana t
41 32 60.4 179 5 Q18409 caenorhabdi
42 32 60.4 272 8 Q33574 trypanosoma
43 32 60.4 288 1 Q27837 methanobact
44 32 60.4 293 4 Q60812 homo sapien
45 32 60.4 311 12 Q84443 paramesium

ALIGNMENTS

RESULT 1
Q9Y509 PRELIMINARY; PRT; 147 AA.
AC Q9Y509; (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE VH3 PROTEIN (FRAGMENT).
GN VH3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96071149.
RA CAO J., VESCOIO R.A., RETTIG M.B., HONG C.H., KIM A., LEE J.C.,
RA LICHTENSTEIN A.K., BERENSON J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1948-1953(1995).
DR EMBL; S80860; AAD14339.1; -.
FT NON_TER 1
SQ SEQUENCE 147 AA; 15768 MW; BDD8F70 CRC32;

Query Match 69.8%; Score 37; DB 4; Length 147;
Best Local Similarity 70.0%; Pred. No. 6;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
DB 26 GFTFLSYDMS 35

RESULT 2
Q67551 PRELIMINARY; PRT; 312 AA.
ID Q67551
AC Q67551;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
DE RNA REPLICASE (FRAGMENT).
OS garlic latent virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
 RP SEQUENCE FROM N.A.
 RA TSUNYOSHI T., SUMI S.;
 RT "Differentiation among garlic viruses in mixed infections based on RT-PCR procedures and direct tissue blotting immunoassays."
 RL Phytopathology 86:253-259(1996).
 DR EMBL; D11161; BAA01931.1; -.
 FT NON_TER 1
 SQ SEQUENCE 312 AA; 36230 MW; 6280CA5B CRC32;

Query Match 67.9%; Score 36; DB 12; Length 312;
 Best Local Similarity 66.7%; Pred. No. 21;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FTFLSYDMS 10
 Db 168 FTFLRYDLN 176

RESULT 3
 Q67654 PRELIMINARY; PRT; 1924 AA.
 ID Q67654
 AC Q67654;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE REPLICASE.
 OS garlic latent virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-WONJU;
 RA JIN NAM C., SANG IK S., JONG TAE S., JONG SEOB L., YANG DO C.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z68502; CAA92815.1; -.
 DR PFAM; PF01443; Viral_helicase1; 1.
 SQ SEQUENCE 1924 AA; 218937 MW; D6CFA107 CRC32;

Query Match 67.9%; Score 36; DB 12; Length 1924;
 Best Local Similarity 66.7%; Pred. No. 1.5e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FTFLSYDMS 10
 Db 1780 FTFLRYDLN 1788

RESULT 4
 Q63652 PRELIMINARY; PRT; 1967 AA.
 ID Q63652
 AC Q63652;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE BLUEBERRY SCORCH CARLAVIRUS MRNA.
 OS Blueberry scorch virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NJ-2;
 RX MEDLINE; 94201746.
 RA CAVILIER T.D., HALPERN B.T., LAWRENCE D.M., PODLECKIS E.V.,
 RA MARTIN R.R., HILLMAN B.I.;
 RT "Nucleotide sequence of the carlavirus associated with blueberry scorch and similar diseases."
 RL J. Gen. Virol. 75:711-720(1994).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NJ-2;
 RX MEDLINE; 95176530.

RA LAWRENCE D.M., ROZANOV M.N., HILLMAN B.I.;
 RT "Autocatalytic processing of the 223-kDa protein of blueberry scorch carlavirus by a papain-like proteinase."
 RL Virology 207:127-135(1995).
 DR EMBL; L25658; AAA68984.1; -.
 SQ SEQUENCE 1967 AA; 223428 MW; 16278090 CRC32;

Query Match 67.9%; Score 36; DB 12; Length 1967;
 Best Local Similarity 75.0%; Pred. No. 1.5e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FTFLSYDM 9
 Db 1823 FTFLQYDL 1830

RESULT 5
 Q64962 PRELIMINARY; PRT; 2183 AA.
 ID Q64962
 AC Q64962;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE VIRAL RNA-DEPENDENT RNA POLYMERASE.
 OS apple stem pitting virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Carlavirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ASPV;
 RX MEDLINE; 94292903.
 RA JELKMANN W.;
 RT "Nucleotide sequences of apple stem pitting virus and of the coat protein gene of a similar virus from pear associated with vein yellows disease and their relationship with potex- and carlaviruses."
 RL J. Gen. Virol. 75:1535-1542(1994).
 DR EMBL; D21829; BAA04853.1; -.
 DR PFAM; PF01443; Viral_helicase1; 1.
 KW RNA-directed RNA polymerase.
 SQ SEQUENCE 2183 AA; 247259 MW; EAB17054 CRC32;

Query Match 67.9%; Score 36; DB 12; Length 2183;
 Best Local Similarity 66.7%; Pred. No. 1.7e+02;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 FTFLSYDMS 10
 Db 2036 FTFLRYDLN 2044

RESULT 6
 Q9ZQR7 PRELIMINARY; PRT; 314 AA.
 ID Q9ZQR7
 AC Q9ZQR7;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE PUTATIVE SPLICEOSOMAL ASSOCIATED PROTEIN.
 GN T13p21.7.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC eudicotyledons; Magnoliophyta; Eudicotyledons;
 OC core.eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 OC Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV. COLUMBIA;
 RA LIN X., KAUL S., SHEA T.P., FUJII C.Y., SHEN M., VANAKEN S.E.,
 RA BARNSTEAD M.E., MASON T.M., BOWMAN C.L., RONNING C.M., BENITO M.,
 RA CARRERA A.J., CREASY T.H., BUELL C.R., TOWN C.D., NIERMAN W.C.,
 RA FRASER C.M., VENTER J.C.;
 RT "Arabidopsis thaliana chromosome II BAC T13p21 genomic sequence.";

RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006067; AADI5475.1; -
DR HSSP; P09651; 1HAI.
SQ SEQUENCE 314 AA; 35267 MW; B9A8C63C CRC32;

Query Match 66.0%; Score 35; DB 10; Length 314;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYD 8
|||:||||
Db 128 GFGFISYD 135

RESULT 7
ID P91823 PRELIMINARY; PRT; 323 AA.
AC P91823;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE T22A3.6 PROTEIN.
GN T22A3.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RA MCMURRAY A.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans*;
RL Nature 368:32-38(1994).
DR EMBL; Z81125; CAB03383.1; -
DR HSSP; P00747; 5HPG.
SQ SEQUENCE 323 AA; 36900 MW; 52913D93 CRC32;

Query Match 66.0%; Score 35; DB 5; Length 323;
Best Local Similarity 60.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
|||:||||
Db 56 GFGPYTDYDMS 65

RESULT 8
ID Q92U66 PRELIMINARY; PRT; 363 AA.
AC Q92U66;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE PUTATIVE SPLICSOMAL PROTEIN (RNA BINDING PROTEIN).
GN F24H14.14.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;

OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA LIN X., KAUL S., SHEA T.P., FUJII C.Y., SHEN M., VANAKEN S.E.,
RA BARNSTEAD M.E., MASON T.M., BOWMAN C.L., RONNING C.M., BENITO M.,
RA CARRERA A.J., CREASY T.H., BUELL C.R., TOWN C.D., NIERMAN W.C.,
RA FRASER C.M., VENTER J.C.;
RT "Arabidopsis thaliana chromosome II BAC F24H14 genomic sequence.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006135; AADI2222.1; -
DR HSSP; P09651; 1HAI.
SQ SEQUENCE 363 AA; 39888 MW; 0A9E91BF CRC32;

Query Match 66.0%; Score 35; DB 10; Length 363;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYD 8
|||:||||
Db 155 GFGFISYD 162

RESULT 9
ID Q9ZU04 PRELIMINARY; PRT; 289 AA.
AC Q9ZU04;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE PUTATIVE RNA BINDING PROTEIN.
GN F365.1.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. COLUMBIA;
RA ROUNSELY S.D., LIN X., KAUL S., SHEA T.P., FUJII C.Y., MASON T.M.,
RA SHEN M., RONNING C.M., FRASER C.M., SOMERVILLE C.R., VENTER J.C.;
RT "Arabidopsis thaliana chromosome II BAC F365 genomic sequence.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC005896; AAC98043.1; -
DR HSSP; P09651; 1UP1.
DR MENDEL; 35355; Arath;2406;35355.
DR PROSITE; PS00030; RNP_1; 2.
KW RNA-binding.
SQ SEQUENCE 289 AA; 30718 MW; 8B9336E3 CRC32;

Query Match 64.2%; Score 34; DB 10; Length 289;
Best Local Similarity 60.0%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
|||:||||
Db 246 GFGFVTDSS 255

RESULT 10
ID Q9ZQD6 PRELIMINARY; PRT; 305 AA.
AC Q9ZQD6;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE PUTATIVE RNA-BINDING PROTEIN.
GN T2N18.2.
OS Arabidopsis thaliana (Mouse-ear cross).

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OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA LIN X., KAUL S., SHEA T.P., FUJII C.Y., SHEN M., VANAKEN S.E.,
RA BARNSTEAD M.E., MASON T.M., BOWMAN C.L., RONNING C.M., BENITO M.,
RA CARRERA A.J., CREASY T.H., BUELL C.R., TOWN C.D., NIERMAN W.C.,
RA FRASER C.M., VENTER J.C.;
RT "Arabidopsis thaliana chromosome II BAC T2N18 genomic sequence.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC006260; AAD18156.1; -.
DR HSSP; P09651; 1HA1.
DR MENDEL; 39684; Arath:2406;39684.
DR PROSITE; PS00030; RNP_1; 2.
KW RNA-binding.
SQ SEQUENCE 305 AA; 32552 MW; 79094AAA CRC32;

Query Match 64.2%; Score 34; DB 10; Length 305;
Best Local Similarity 60.0%; Pred. No. 49;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
Db 246 GGFVYDSS 255

RESULT 11
Q34096
ID Q34096 PRELIMINARY; PRT; 347 AA.
AC Q34096;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE MURF2 PROTEIN
OS Crithidia fasciculata.
OG Mitochondrion.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Crithidia.
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE; 89315227.
RA VAN DER SPEK H., ARTS G.J., VAN DEN BURG J., SLOOF P., BENNE R.;
RT "The nucleotide sequence of mitochondrial maxicircle genes of
RT Crithidia fasciculata.";
RL Nucleic Acids Res. 17:4876-4876(1989).
DR EMBL; X15081; CAA33190.1; -.
KW Mitochondrion.
SQ SEQUENCE 347 AA; 42540 MW; CD0FA053 CRC32;

Query Match 64.2%; Score 34; DB 8; Length 347;
Best Local Similarity 60.0%; Pred. No. 57;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
Db 238 GFILSYGLA 247

RESULT 12
Q65125
ID Q65125 PRELIMINARY; PRT; 349 AA.
AC Q65125;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE MULTIGENE FAMILY 360 PROTEIN.
GN LMW3HL.
OS African swine fever virus (ASFV).
OC Viruses; dsDNA viruses, no RNA stage;

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OC African swine fever-like viruses.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MALAWI LIL-20/1; TISSUE=MYELOID;
RX MEDLINE; 94303219.
RA YOZAWA T., KUTISH G.F., AFONSO C.L., LU Z., ROCK D.L.;
RT "Two novel multigene families, 530 and 300, in the terminal variable
RT regions of African swine fever virus genome.";
RL Virology 202:997-1002(1994).
DR EMBL; U03762; AAA50538.1; -.
DR PFAM; PF00023; ank; 1.
SQ SEQUENCE 349 AA; 41010 MW; 34193446 CRC32;

Query Match 64.2%; Score 34; DB 12; Length 349;
Best Local Similarity 85.7%; Pred. No. 57;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 TFLSYDM 9
Db 342 TFLSYDL 348

RESULT 13
Q9XWR7
ID Q9XWR7 PRELIMINARY; PRT; 475 AA.
AC Q9XWR7;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE Y1LD7A.3 PROTEIN.
GN Y1LD7A.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA STEWARD C.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWKNEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
DR EMBL; AL032632; CAA21581.1; -.
SQ SEQUENCE 475 AA; 52953 MW; 8D74F8E6 CRC32;

Query Match 64.2%; Score 34; DB 5; Length 475;
Best Local Similarity 66.7%; Pred. No. 79;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GFTFLSYDM 9
Db 332 GFNFLSYSV 340

RESULT 14
Q38710

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ID Q38710 PRELIMINARY; PRT; 868 AA.
AC Q38710;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE ABIETADIENE CYCLASE.
GN AC22.
OS Abies grandis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
OC Abies.
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=WOUNDED STEM;
RA STOPFER-VOGEL B., WILDUNG M.R., VOGEL G., CROTEAU R.B.;
RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U50768; AAB05407.1; -.
DR HSSP; Q40577; SEAS.
DR MENDEL; 11447; Abigr; 2507; 11447.
DR PFAM; PF01397; Terpene_synth; 1.
SQ SEQUENCE 868 AA; 99535 MW; 1EE6FEF1 CRC32;

Query Match 64.2%; Score 34; DB 10; Length 868;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYD 8
DB 179 GYFLAYD 186

RESULT 15
001837 PRELIMINARY; PRT; 1418 AA.
ID 001837;
AC 001837;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE SIMILARITY TO THE CATALYTIC DOMAIN OF SER/THR-PROTEIN KINASES.
GN B0414.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU 2., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER J., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SHALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.*
RL Nature 368:32-38(1994).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA SAMMONS L., WOHLDMANN P., ROHLFING T.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA WATERSTON R.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003145; AAB57718.1; -.
PFAM; PF00069; pkinase; 1.

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SQ SEQUENCE 1418 AA; 163391 MW; 6E8DAD9F CRC32;

Query Match 64.2%; Score 34; DB 5; Length 1418;
 Best Local Similarity 85.7%; Pred. No. 2.6e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSY 7
 DB 995 GFTFLQY 1001

Search completed: May 27, 2000, 19:38:33
 Job time: 2366 sec

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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:21:30 ; Search time 148.45 Seconds
(without alignments)
1.596 Million cell updates/sec

Title: US-09-016-061-52

Perfect score: 53

Sequence: 1 GFTFLSYDMS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	53	100.0	10	1 W76016	LM609 grafted anti
2	47	88.7	10	1 W76007	LM609 grafted anti
3	47	88.7	117	1 W76001	Vitaxin antibody h
4	45	84.9	117	1 W86141	Protein sequence o
5	44	83.0	117	1 W86137	Protein sequence o
6	44	83.0	128	1 W54000	Anti-CD4 antibody
7	44	83.0	134	1 R24713	Sequence encoded b
8	44	83.0	225	1 R05710	TRV40. Single poly
9	44	83.0	225	1 R06478	TRV40. Single poly
10	44	83.0	225	1 R43675	Single chain polyp
11	44	83.0	225	1 R99645	Single chain bindi
12	44	83.0	236	1 R06479	TRV61. Single poly
13	44	83.0	236	1 R43676	Single chain polyp
14	44	83.0	236	1 R99646	Single chain bindi
15	44	83.0	236	1 W02188	TRV61 single chain
16	44	83.0	246	1 R06480	TRV59. Single poly
17	44	83.0	246	1 R43677	Single chain polyp
18	44	83.0	246	1 R99647	Single chain bindi
19	44	83.0	246	1 W02189	TRV59 single chain
20	44	83.0	250	1 R06481	TRV104b. Single po
21	44	83.0	250	1 R43678	Single chain polyp
22	44	83.0	250	1 R99648	Single chain bindi
23	44	83.0	250	1 W02190	TRV104b single cha
24	44	83.0	448	1 R06476	Heavy chain of ant
25	44	83.0	448	1 R43673	Mouse anti-bovine
26	44	83.0	448	1 R99643	Anti-BGH monoclon
27	44	83.0	448	1 R97376	Murine anti-BGH MA
28	44	83.0	466	1 R24812	Sequence encoded b
29	43	81.1	139	1 W21652	Humanised reshaped
30	42	79.2	10	1 W76015	LM609 grafted anti
31	42	79.2	117	1 W76003	LM609 antibody hea
32	42	79.2	121	1 W86122	Protein sequence o
33	42	79.2	239	1 R34511	Fv(TU25). Polypept
34	42	79.2	247	1 W11917	Murine MAb SK48-E2

35 41 77.4 119 1 W11919 Humanised MAb SK48
36 41 77.4 123 1 W53998 Anti-CD4 antibody
37 40 75.5 98 1 W59614 Anti-RSV F protein
38 40 75.5 116 1 R66307 Human Immunoglobul
39 40 75.5 116 1 W13529 Anti-melanoma anti
40 40 75.5 118 1 W57591 Chimeric antibody
41 40 75.5 118 1 W57576 Chimeric H chain S
42 40 75.5 118 1 W89636 Human antibody hea
43 40 75.5 118 1 W89627 Mouse humanised an
44 40 75.5 119 1 R79876 Anti-EGFR antibody
45 40 75.5 119 1 R79887 Anti-EGFR antibody

ALIGNMENTS

RESULT 1

W76016
ID W76016 standard; Protein; 10 AA.
AC W76016;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDRI protein fragment #4.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PE 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49853.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PS angiogenesis or restenosis
PS Claim 60; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 100.0%; Score 53; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.9e-05;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
Db 1 GFTFLSYDMS 10
|||||||

RESULT 2

W76007
ID W76007 standard; Protein; 10 AA.
AC W76007;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDRI protein fragment #1.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SW, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49844.
 DR Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Disclosure; Page 40; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 88.7%; Score 47; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.00095;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 |||||
 Db 1 GFTFSSYDMS 10

RESULT 3
 W76001 ID W76001 standard; Protein; 117 AA.

DT 02-NOV-1998 (first entry)
 DE Vitaxin antibody heavy chain variable region protein fragment.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SW, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49820.
 DR Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 1; Fig 1a; 129pp; English.

CC This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated

CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 SQ Sequence 117 AA;

Query Match 88.7%; Score 47; DB 1; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 |||||
 Db 26 GFTFSSYDMS 35

RESULT 4

W86141 ID W86141 standard; Protein; 117 AA.

DT 03-MAR-1999 (first entry)
 DE Protein sequence of de-immunised murine A33 Vh.

KW Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK;
 KW immunogl bulin; therapeutic; streptokinase; murine; de-immunised.

OS Mus sp.
 PN W09852976-A1.

PD 26-NOV-1998.

PF 21-MAY-1998; G01473.

PR 14-APR-1998; GB-007751.

PR 21-MAY-1997; GB-010480.

PR 31-JUL-1997; GB-016197.

PR 28-NOV-1997; GB-025270.

PR 02-DEC-1997; US-067235.

PA (BIOV-) BIOVATION LTD.

PI Carr FJ;

DR WPI; 99-045301/04.

PT Reducing immunogenicity of proteins - by modifying the amino acid
 PT sequence of the protein to eliminate potential epitopes for T-cells
 PT of a given species

PS Example 6; Fig 27; 77pp; English.

CC The invention relates to a method for the production of non-immunogenic
 CC proteins. The method comprises determining at least part of the amino
 CC acid sequence of the protein; (b) identifying in the amino acid sequence
 CC one or more potential epitopes for T-cells (T-cell epitopes) of the given
 CC species; and (c) modifying the amino acid sequence to eliminate at least
 CC one of the T-cell epitopes identified in step (b) thereby to eliminate or
 CC reduce the immunogenicity of the protein when exposed to the immune
 CC system of the given species. A method of analysing a pre-existing protein
 CC to predict the basis for immunogenic responses is also provided. The
 CC methods can be used particularly for reducing the immunogenicity of
 CC immunoglobulins or therapeutic proteins, e.g. streptokinase (SK). The
 CC products can be used for diagnosis and therapy. The present sequence
 CC represents the protein sequence of de-immunised murine A33 Vh.
 SQ Sequence 117 AA;

Query Match 84.9%; Score 45; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 0.034;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 |||||
 Db 26 GFTFSSYDMS 35

RESULT 5

W86137 ID W86137 standard; Protein; 117 AA.

AC W86137

DT 03-MAR-1999 (first entry)
 DE Protein sequence of de-immunised humanised A33 Vh.

KW Non-immunogenic; epitope; T-cell; immunogenicity; immune system; SK;
 KW Homoglu bulin; therapeutic; streptokinase; humanised; de-immunised.
 OS Homo sapiens.
 PN WO9852976-A1.
 PD 26-NOV-1998.
 PF 21-MAY-1998; G01473.
 PR 14-APR-1998; GB-007751.
 PR 21-MAY-1997; GB-010480.
 PR 31-JUL-1997; GB-016197.
 PR 28-NOV-1997; GB-025270.
 PR 02-DEC-1997; US-067235.
 PA (BIOV-) BIOVATION LTD.
 PI Carr FJ;
 DR WPI; 99-045301/04.
 PT Reducing immunogenicity of proteins - by modifying the amino acid
 PT sequence of the protein to eliminate potential epitopes for T-cells
 PT of a given species
 PS Example 5; Fig 25; 77pp; English.
 CC The invention relates to a method for the production of non-immunogenic
 CC proteins. The method comprises determining at least part of the amino
 CC acid sequence of the protein; (b) identifying in the amino acid sequence
 CC one or more potential epitopes for T-cells (T-cell epitopes) of the given
 CC species; and (c) modifying the amino acid sequence to eliminate at least
 CC one of the T-cell epitopes identified in step (b) thereby to eliminate or
 CC reduce the immunogenicity of the protein when exposed to the immune
 CC system of the given species. A method of analysing a pre-existing protein
 CC to predict the basis for immunogenic responses is also provided. The
 CC methods can be used particularly for reducing the immunogenicity of
 CC immunoglobulins or therapeutic proteins, e.g. Streptokinase (SK). The
 CC products can be used for diagnosis and therapy. The present sequence
 CC represents the protein sequence of de-immunised humanised A33 Vh.
 SQ Sequence 117 AA;

Query Match 83.0%; Score 44; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 0.055;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 Db |||||:||||
 Db 26 GFTFSTYDMS 35

RESULT 6
 W54000 ID W54000 standard; Protein; 128 AA.
 AC W54000;
 DT 29-JUL-1998 (first entry)
 DE Anti-CD4 antibody VH3 monkey clone 3-40.
 KW Anti-CD4 antibody; monkey; human; therapy; variable heavy domain;
 KW Old World monkey; constant domain; eczema; immuno-modulated disease;
 KW Rheumatoid arthritis.
 OS Primate sp.
 FH Key Location/Qualifiers
 FT Misc_difference 1..128 /note="Xaa- unspecified amino acid"
 FT Key
 PN US5750105-A.
 PD 12-MAY-1998.
 PF 07-JUN-1995; 476349.
 PR 10-JUL-1992; US-912292.
 PR 25-JUL-1991; US-735064.
 PR 23-MAR-1992; US-856281.
 PR 05-DEC-1995; US-379072.
 PR 07-JUN-1995; US-476349.
 PA (IDEC-) IDEC PHARM CORP.
 PI Hanna N, Newman RA, Raab RW;
 DR WPI; 98-296690/26.
 PT Improved method for antibody treatment - uses an antibody comprising
 PT an Old World monkey variable region and a human constant domain
 PS Example 1; Fig 9c; 84pp; English.
 CC This sequence represents the VH3 domain of an anti-CD4 antibody
 CC (Ab). This sequence can be used in the method of the invention for
 CC treating a subject, where the treatment comprises administration of an

CC Ab. The method comprises the administration of an antibody which has an
 CC Old World monkey (e.g. baboon or macaque) variable region which binds to
 CC an antigen (Ag) (or Ag binding portion), and a human constant domain. The
 CC method is useful for the treatment of eczema and immuno-modulated
 CC diseases and especially rheumatoid arthritis. The recombinant antibodies
 CC used are sufficiently different from native monkey antibodies to allow
 CC human antigens to raise these antibodies, but similar enough to human
 CC antibody so there is no immune response to the antibodies in humans.
 CC Compared to antibodies used in therapy in prior art, these antibodies do
 CC not induce human anti-antibodies on repeated administration. They also
 CC have longer half-lives and do not have a lack of effector function with
 CC human cells.
 SQ Sequence 128 AA;

Query Match 83.0%; Score 44; DB 1; Length 128;
 Best Local Similarity 80.0%; Pred. No. 0.06;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 Db |||||:||||
 Db 26 GFTFSSYDMN 35

RESULT 7
 R24713 ID R24713 standard; Protein; 134 AA.
 AC R24713;
 DT 28-DEC-1992 (first entry)
 DE Sequence encoded by the genomic chimeric heavy chain variable region
 DE (VFH) gene
 KW Chimeric monoclonal antibody; anti-fibrin antibody; PCR;
 KW antithrombotic agent; myocardial infarction therapy.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT peptide 1..19
 FT /label= leader
 FT region 23..49
 FT /label= Framework Region (FR) 1
 FT region 50..54
 FT /label= Complementarity determining region(CDR)1
 FT region 55..68
 FT /label= FR-2
 FT region 69..84
 FT /label= CDR-2
 FT region 85..114
 FT /label= FR-3
 FT region 115..123
 FT /label= CDR-3
 FT region 124..134
 FT /label= FR-4
 PN EP-491351-A.
 PD 24-JUN-1992.
 PF 17-DEC-1991; 121591.
 PR 18-DEC-1990; JP-413829.
 PR 11-NOV-1991; JP-294464.
 PA (TAKE) TAKEDA CHEM IND LTD.
 PI Iwasa S, Taka H, Watanabe T, Tada H;
 DR WPI; 92-209528/26.
 DR N-PSDP; Q25666.
 PT Chimeric monoclonal antibodies - contain anti-human fibrin
 PT antibody light and heavy chain variable and constant for treating
 PT thrombotic conditions e.g. myocardial infarction
 PS Example; Figure 4; 87pp; English.
 CC PCR primers 5'mVH and 3'mVH were used to produce a VH gene-contg.
 CC fragment of about 330bp. The fragment was isolated and subcloned in
 CC pUC119. The fragment was found to be a functional VH structural
 CC gene, referred to as VFH, comprising a VH gene belonging to the
 CC subgroup III (VHIII) and the DSP2 and JH4 genes. Northern blot
 CC analysis using the whole RNA of FIB1-11 cells confirmed that VFH
 CC was the gene expressed in FIB1-11 cells. The sequence is given in
 CC Q25666.
 SQ Sequence 134 AA;

Query Match 83.0%; Score 44; DB 1; Length 134;
 Best Local Similarity 80.0%; Pred. No. 0.063;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 Db 45 GFTFSYDMS 54
 ||||:||||

RESULT 8

R05710
 ID R05710 standard; protein; 225 AA.

AC R05710;
 DT 07-JAN-1991 (first entry)

DE TRY40.
 KW Monoclonal antibody; variable chain anti-bovine growth hormone.

OS Mus musculus.

FH Feature

region Location/Qualifier

4. .126

/label= LCVR(1-41)

Peptide linker 127. .147

/label= linker

148. .471

/label= HCVR(8-115)

Peptide 472. .483

/label= linker

484. .678

/label= LCVR(45-109)

US4946778-A.

PN 07-AUG-1990.

PD 19-JAN-1989; 299617.

PF 02-SEP-1986; US-902971.

PR 02-SEP-1987; US-092110.

PR 19-JAN-1989; US-299617.

PA (GENE-) GENEX CORP.

PI Ladner RC, Bird RE, Hardman K;

DR N-PSDB; Q05710.

PT Single polypeptide chain binding molecules - having light chain
 PT variable region of antibody linked by peptide to heavy chain

PT variable region.

PS Disclosure; Fig 24; 68pp; English.

CC The sequence was constructed from the variable regions of a MAB
 CC produced by the cell line 3C2, an IgG1 with a gamma 1 heavy chain
 CC and kappa light chain. The sequence encodes a single chain binding
 CC molecule comprising the variable regions of heavy and light chains
 CC linked by a peptides. The variable region of each DNA chain was
 CC prep. by introducing a ClaI site and an initiation codon (atcgatg)
 CC prior to the first codon of the mature sequence and a HindIII site
 CC and termination codon (taagctt) after codon 123 (heavy chain) or
 CC 109 (light chain). The plasmids constructed to contain these
 CC portions were pgx3772 and pgx3773 (heavy and light resp.). TRY40
 CC has the following polypeptide structure:
 CC Met-[LCVR(1-41)]-I-A-K-A-F-K-N-[HCVR(8-115)]-P-G-S-[LCVR(45-109)].
 CC See also Q05708-19.

CC Sequence 225 AA;

SQ

Query Match 83.0%; Score 44; DB 1; Length 225;
 Best Local Similarity 80.0%; Pred. No. 0.11;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 Db 68 GFTFSYDMS 77
 ||||:||||

RESULT 9

R06478

ID R06478 standard; protein; 225 AA.

AC R06478;

DT 07-JAN-1991 (first entry)
 DE TRY40.

KW Monoclonal antibody; variable chain anti-bovine growth hormone.

OS Mus musculus.

FH Feature

misc_rna

misc_rna Location/Qualifier

2. .42

/label= LCVR(1-41)

peptide 43. .49

/label= linker

misc_rna 50. .157

/label= HCVR(8-115)

peptide 158. .160

/label= linker

misc_rna 161. .225

/*tag= e

/label= LCVR(45-109)

PN US4946778-A.

PD 07-AUG-1990.

PF 19-JAN-1989; 299617.

PR 02-SEP-1986; US-902971.

PR 02-SEP-1987; US-092110.

PR 19-JAN-1989; US-299617.

PA (GENE-) GENEX CORP.

PI Ladner RC, Bird RE, Hardman K;

DR WPI; 90-260350/34.

DR N-PSDB; Q05710.

PT Single polypeptide chain binding molecules - having light chain

PT variable region of antibody linked by peptide to heavy chain

PT variable region.

PS Disclosure; Fig 24; 68pp; English.

CC The sequence was constructed from the variable regions of a MAB
 CC produced by the cell line 3C2, an IgG1 with a gamma 1 heavy chain
 CC and kappa light chain. The sequence encodes a single chain binding
 CC molecule comprising the variable regions of heavy and light chains
 CC linked by a peptides. The variable region of each DNA chain was
 CC prep. by introducing a ClaI site and an initiation codon (atcgatg)
 CC prior to the first codon of the mature sequence and a HindIII site
 CC and termination codon (taagctt) after codon 123 (heavy chain) or
 CC 109 (light chain). The plasmids constructed to contain these
 CC portions were pgx3772 and pgx3773 (heavy and light resp.). TRY40
 CC was carried on pgx3775. The polypeptide has the following poly-
 CC peptide structure:
 CC Met-[LCVR(1-41)]-I-A-K-A-F-K-N-[HCVR(8-115)]-P-G-S-[LCVR(45-109)].
 CC See also R06476-R06484.

SQ Sequence 225 AA;

Query Match 83.0%; Score 44; DB 1; Length 225;
 Best Local Similarity 80.0%; Pred. No. 0.11;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
 Db 68 GFTFSYDMS 77
 ||||:||||

RESULT 10
 R43675

ID R43675 standard; protein; 225 AA.

AC R43675;

DT 23-MAY-1994 (first entry)

DE Single chain polypeptide with affinity for bovine growth hormone.
 KW Monoclonal antibody; MAB; affinity; binding; antigen; diagnostics;
 KW therapy; imaging; purification; biosensors.

OS Synthetic.

PN US5260203-A.

PD 09-NOV-1993.

PF 02-SEP-1986; 902971.

PR 02-SEP-1986; US-902971.

PR 02-SEP-1987; US-092110.

PR 19-JAN-1989; US-299617.

PR 25-APR-1990; US-512910.

PA (ENZO-) ENZON INC.

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PI Bird RE, Hardman K, Ladner RC;
DR WPI; 93-367875/46.
DR N-PSDB; Q51536.
PT Single chain polypeptide for binding antigen - comprising light
PT and heavy chain antigen binding portions linked by peptide linker
PS Example 1; Figure 24; 78pp; English.
CC The single chain polypeptide is derived from the mature light and
CC heavy chains of a mouse monoclonal antibody (MAB) and has affinity
CC for a given antigen (Bovine growth hormone). It comprises a first
CC polypeptide comprising the antigen binding portion of of the light
CC chain variable region of an antibody and a second polypeptide
CC comprising the antigen binding portion of the heavy chain variable
CC region of an antibody and at least one peptide linker linking the
CC first and second polypeptide chains. The resulting single chain
CC polypeptide can be used in diagnostics, therapy
CC (in vivo and in vitro), imaging, purifications and biosensors.
CC This particular single chain binding molecule was designated TRY40
CC and contains two linker peptides.
SQ Sequence 225 AA;

Query Match 83.0%; Score 44; DB 1; Length 225;
Best Local Similarity 80.0%; Pred. No. 0.11;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFELSYDMS 10
DB 68 GFTFISYGMS 77
||||:|||||

RESULT 11
R99645
ID R99645 standard; Protein; 225 AA.
AC R99645;
DE Single chain binding molecule TRY40.
KW Antibody engineering; single polypeptide chain binding molecule;
KW heavy chain; light chain; monoclonal antibody; MAB;
KW bovine growth hormone; bGH; immunoaffinity purification; TRY40.
OS Chimeric Mus sp.;
OS Chimeric synthetic.
FH Key Location/Qualifiers
FT domain 2..42
FT /label= L-chain
FT /note= "MAB 3C2 VL amino acids 1-41"
FT region 43..49
FT /label= Linker
FT /note= "Linker derived from MCPC-603"
FT domain 50..157
FT /label= H-chain
FT /note= "MAB 3C2 VH amino acids 8-105"
FT region 158..160
FT /label= Linker
FT /note= "Linker derived from MCPC-603 Fv region"
FT domain 161..225
FT /label= L-chain
FT /note= "MAB 3C2 VL amino acids 45-109"
FT US5534621-A.
PN 09-JUL-1996.
PD 02-SEP-1986; 902971.
PF 02-SEP-1986; US-902971.
PR 02-SEP-1987; US-092110.
PR 19-JAN-1989; US-299617.
PR 25-APR-1990; US-512910.
PR 01-APR-1993; US-040440.
PR 06-JUN-1995; US-468992.
PA (ENZO-) ENZON LABS INC.
PI Bird RE, Hardman K, Ladner RC;
DR WPI; 96-333309/33.
DR N-PSDB; T13735.
PT Immuno-purificn. using single binding chain molecule including
PT antigen-binding parts of antibody light and heavy chain variable
PT regions connected by a linker - is smaller, stabler and less

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PT expensive than complete antibodies
PS Example 1; Fig 24; 78pp; English.
CC A novel single chain binding molecule (R99645), designated TRY40,
CC is a 2-linker construction incorporating VL and VH regions from
CC IgG1 anti-bovine growth hormone mouse IgG1 monoclonal antibody 3C2,
CC and peptide linkers from the Fv region of the IgA anti-phosphoryl
CC choline myeloma antibody MCPC-603. The single chain binding
CC molecule was expressed in E.coli transformants carrying pGX3776,
CC which incorporates encoding DNA (T13735), at a level of 7.2% of total
CC cell protein. Single chain binding molecules (see also R99646-51)
CC retain the binding specificity and affinity of the light and heavy
CC chain aggregate variable region of the native antibody but have the
CC advantages of smaller size, greater stability and reduced cost.
SQ Sequence 225 AA;

Query Match 83.0%; Score 44; DB 1; Length 225;
Best Local Similarity 80.0%; Pred. No. 0.11;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFELSYDMS 10
DB 68 GFTFISYGMS 77
||||:|||||

RESULT 12
R06479
ID R06479 standard; protein; 236 AA.
AC R06479;
DE 07-JAN-1991 (first entry)
DE TRY61.
KW Monoclonal antibody; variable chain anti-bovine growth hormone; ss.
OS Mus musculus.
FH Feature Location/Qualifier
FT region 2..105
FT /label= LCVR(1-104) 106..119
FT Peptide
FT /label= linker
FT region 120..235
FT /label= HCVR(7-123)
PN US4946778-A.
PD 07-AUG-1990.
PF 19-JAN-1989; 299617.
PR 02-SEP-1986; US-902971.
PR 02-SEP-1987; US-092110.
PR 19-JAN-1989; US-299617.
PA (GENE-) GENEX CORP.
PI Ladner RC, Bird RE, Hardman K;
DR WPI; 90-260350/34.
DR N-PSDB; Q05711.
PT Single polypeptide chain binding molecules - having light chain
PT variable region of antibody linked by peptide to heavy chain
PT variable region.
PS Disclosure; Fig 26; 68pp; English.
CC The sequence was constructed from the variable regions of a MAB
CC produced by the cell line 3C2, an IgG1 with a gamma 1 heavy chain
CC and kappa light chain. The sequence encodes a single chain binding
CC molecule comprising the variable regions of heavy and light chains
CC linked by a peptides. The variable region of each DNA chain was
CC prepd. by introducing a ClaI site and an initiation codon (atcgatg)
CC prior to the first codon of the mature sequence and a HindIII site
CC and termination codon (taagctt) after codon 123 (heavy chain) or
CC 109 (light chain). The plasmids constructed to contain these
CC portions were pGX3772 and pGX3773 (heavy and light resp.). TRY61
CC was carried on plasmid pGX4904. The polypeptide has the following
CC polypeptide structure:
CC Met-[LCVR(1-104)]-V-R-G-S-P-A-I-N-V-A-V-H-V-F-[HCVR(7-123)]
CC See also R06476-84.
CC Sequence 236 AA;

Query Match 83.0%; Score 44; DB 1; Length 236;
Best Local Similarity 80.0%; Pred. No. 0.12;

```

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
||||:||||
Db 139 GFTFISYGMS 148

RESULT 13

R43676 ID R43676 standard; Protein; 236 AA.
AC R43676;
DT 23-MAY-1994 (first entry)
DE Single chain polypeptide with affinity for bovine growth hormone.
KW Monoclonal antibody; MAb; affinity; binding; antigen; diagnostics;
KW therapy; imaging; purification; biosensors.
OS Synthetic.
PN US5260203-A.
PD 09-NOV-1993.
PF 02-SEP-1986; 902971.
PR 02-SEP-1986; US-902971.
PR 02-SEP-1987; US-092110.
PR 19-JAN-1989; US-299617.
PR 25-APR-1990; US-512910.
PA (ENZO-) ENZON LABS INC.
PI Bird RE, Hardman K, Ladner RC;
DR WPI; 93-367875/46.
DR N-PSDB; Q51537.
PT Single chain polypeptide for binding antigen - comprising light and heavy chain antigen binding portions linked by peptide linker
PS Example 2; Figure 26; 78pp; English.
CC The single chain polypeptide is derived from the mature light and heavy chains of a mouse monoclonal antibody (MAb) and has affinity for a given antigen (Bovine growth hormone). It comprises a first polypeptide comprising the antigen binding portion of the light chain variable region of an antibody and a second polypeptide comprising the antigen binding portion of the heavy chain variable region of an antibody and at least one peptide linker linking the first and second polypeptide chains. The resulting single chain polypeptide can be used in diagnostics, therapy and biosensors. (in vivo and in vitro), imaging, purifications and biosensors.
CC This particular single chain binding molecule was designated TRY61 and contains one linker peptide.
SQ Sequence 236 AA;

Query Match 83.0%; Score 44; DB 1; Length 236;
Best Local Similarity 80.0%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
||||:||||
Db 139 GFTFISYGMS 148

RESULT 14

R99646 ID R99646 standard; Protein; 236 AA.
AC R99646;
DT 11-OCT-1996 (first entry)
DE Single chain binding molecule TRY61.
KW Antibody engineering; single polypeptide chain binding molecule; heavy chain; light chain; monoclonal antibody; MAb;
KW bovine growth hormone; bGH; immunoaffinity purification; TRY61.
OS Chimeric Mus sp.
OS Chimeric synthetic.
FH Key Location/Qualifiers
FT domain 2..105
FT /label= L-chain
FT /note= "Mab 3C2 VL amino acids 1-104"
FT region 106..119
FT /label= Linker
FT domain 120..236
FT /label= H-chain
FT /note= "linker derived from MCPC-603"

FT /label= H-chain
PN /note= "Mab 3C2 VH amino acids 7-123"

US5534621-A.
09-JUL-1996.
PD 02-SEP-1986; 902971.
PF 02-SEP-1986; US-902971.
PR 02-SEP-1987; US-092110.
PR 19-JAN-1989; US-299617.
PR 25-APR-1990; US-512910.
PR 01-APR-1993; US-040440.
PR 06-JUN-1995; US-468992.
PA (ENZO-) ENZON LABS INC.
PI Bird RE, Hardman K, Ladner RC;
DR WPI; 96-333309/33.
DR N-PSDB; T13736.
PT Immuno-purificn. using single binding chain molecule including antigen-binding parts of antibody light and heavy chain variable regions connected by a linker - is smaller, stabler and less expensive than complete antibodies
PS Example 2; Fig 26; 78pp; English.
CC A novel single chain binding molecule (R99646), designated TRY61, incorporates VL and VH regions from IgG1 anti-bovine growth hormone mouse IgG1 monoclonal antibody 3C2, and a peptide linker from the Fv region of the IgA anti-phosphorylcholine myeloma antibody MCPC-603. The single chain binding molecule was expressed in E.coli transformants carrying pGX4904, which incorporates encoding DNA (T13736), at a level of below 2.0% of total cell protein. Single chain binding molecules (see also R99645 and R99647-51) retain the binding specificity and affinity of the aggregate of the original light and heavy chains of the variable region of the antibody but have the advantages of smaller size, greater stability and reduced cost.
SQ Sequence 236 AA;

Query Match 83.0%; Score 44; DB 1; Length 236;
Best Local Similarity 80.0%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GFTFLSYDMS 10
||||:||||
Db 139 GFTFISYGMS 148

RESULT 15

W02188 ID W02188 standard; Protein; 236 AA.
AC W02188;
DT 13-NOV-1996 (first entry)
DE TRY61 single chain binding protein.
KW Antibody engineering; monoclonal antibody; MAB;
KW single chain antibody; immunoassay; bovine growth hormone; bGH;
KW TRY61; single chain binding protein.
OS Chimeric Mus musculus;
OS Chimeric synthetic.
FH Key Location/Qualifiers
FT domain 2..105
FT /label= L-chain
FT /note= "Mab light chain aal-104"
FT region 106..119
FT /label= Linker
FT domain 120..236
FT /label= H-chain
FT /note= "Mab heavy chain aa7-123"

US5518889-A.
21-MAY-1996.
PD 02-SEP-1986; 902971.
PF 02-SEP-1986; US-902971.
PR 02-SEP-1987; US-092110.
PR 19-JAN-1989; US-299617.
PR 25-APR-1990; US-512910.
PR 01-APR-1993; US-040440.
PR 06-JUN-1995; US-468988.
PA (ENZO-) ENZON LABS INC.

PI Bird RE, Hardman K, Ladner RC;
DR WPI; 96-259060/26.
DR N-PSDB; T36460.
PT Immunoassay using single chain antigen binding mol. - as replacement
PT for labelled or immobilised antibody, are less immunogenic, easier
PT to engineer, more stable and less expensive
PS Example 2; Fig 26; 78pp
CC Computer-designed single chain antigen binding molecule TRY61
CC (W02188), encoded by the DNA sequence given in T36460, has the
CC formula Met-(L-chain 1-104)-linker-(H-chain 7-123). The L (light)
CC and H (heavy) chains are from a murine monoclonal antibody (see also
CC R97377 and R97376) specific for bovine growth hormone (BGH). Plasmid
CC pGX3772' (contg. the heavy chain variable region) was cloned into
CC pGX3773 (contg. the light chain sequence) with 2 synthetic
CC oligonucleotides that encoded the linker. The resulting plasmid was
CC inserted into vector pGX3703 and introduced into E. coli. TRY61 was
CC expressed at over 2% of total cellular protein. It was able to
CC bind BGH as effectively as the original monoclonal antibody.
SQ Sequence 236 AA;

Query Match 83.0%; Score 44; DB 1; Length 236;
Best Local Similarity 80.0%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GFTFLSYDMS 10
 ||||:|
Db 139 GFTFISYGMS 148

Search completed: May 27, 2000, 19:21:30
Job time: 1584 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:26:37 ; Search time 163.56 seconds
(without alignments)
3.585 Million cell updates/sec

Title: US-09-016-061-54
Perfect score: 55
Sequence: 1 WYAKVSGGG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR_63.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	80.0	118	2 S20641	Ig heavy chain V r
2	43	78.2	108	2 PL0248	Ig heavy chain V r
3	43	78.2	138	2 S09258	Ig heavy chain V r
4	42	76.4	111	2 S40090	Ig heavy chain - m
5	42	76.4	111	2 PH1007	Ig heavy chain V r
6	42	76.4	113	2 S26468	Ig heavy chain V r
7	42	76.4	117	1 HVMS34	Ig heavy chain pre
8	40	72.7	254	2 B31790	Ig heavy chain V r
9	39	70.9	108	2 PH1006	Ig heavy chain V r
10	39	70.9	117	1 HVMS84	Ig heavy chain pre
11	39	70.9	121	2 H27888	Ig heavy chain V r
12	39	70.9	123	2 D27888	Ig heavy chain V r
13	39	70.9	408	2 D70549	hypothetical prote
14	38	69.1	92	2 S56009	Ig heavy chain var
15	38	69.1	92	2 S56008	Ig heavy chain var
16	38	69.1	97	1 HVMS91	Ig heavy chain V r
17	38	69.1	112	2 S26327	Ig heavy chain V r
18	38	69.1	121	2 H27887	Ig heavy chain V r
19	38	69.1	128	2 PH0094	Ig heavy chain V r
20	38	69.1	128	2 PH0095	Ig kappa chain V r
21	38	69.1	509	2 A49094	methylnalonyl-CoA
22	37	67.3	83	2 C25913	Ig heavy chain V r
23	37	67.3	108	2 PH1010	Ig heavy chain V r
24	37	67.3	108	2 PH1011	Ig heavy chain V r
25	37	67.3	114	2 PH1009	Ig heavy chain V r
26	37	67.3	117	1 HVMS57	Ig heavy chain pre
27	37	67.3	118	2 PH0096	Ig heavy chain V r
28	37	67.3	118	2 PH0097	Ig heavy chain V r
29	37	67.3	119	2 F27888	Ig heavy chain V r
30	37	67.3	120	2 S55336	Ig heavy chain V r

31	37	67.3	120	2 S55337	Ig heavy chain V r
32	37	67.3	121	2 B27888	Ig heavy chain V r
33	37	67.3	121	2 I27887	Ig heavy chain V r
34	37	67.3	121	2 D27888	Ig heavy chain V r
35	37	67.3	121	2 A27888	Ig heavy chain V r
36	37	67.3	122	2 E27888	Ig heavy chain V r
37	37	67.3	123	2 S63597	Ig heavy chain, V
38	37	67.3	124	2 C27888	Ig heavy chain V r
39	37	67.3	124	2 I27888	Ig heavy chain V r
40	37	67.3	137	2 S78054	Ig heavy chain pre
41	37	67.3	186	2 T29117	hypothetical prote
42	37	67.3	138	2 T04166	thumatin-like prote
43	37	67.3	459	2 S11878	chlorophyll a/b-bi
44	37	67.3	469	2 S69229	probable polyketid
45	37	67.3	548	2 S38864	Ig epsilon chain C

ALIGNMENTS

RESULT 1

S20641
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S20641
R:Losman, M.; Easzy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A:Description: Relationships among antinuclear antibodies from autoimmune MRL mice re
A:Reference number: S20639
A:Accession: S20641
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-118 <LOS>
A:Cross-references: EMBL:X65003; NID:g52602; PIDN:CAA46136.1; PID:g52603
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 80.0%; Score 44; DB 2; Length 118;
Best Local Similarity 70.0%; Pred. No. 0.65;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WYAKVSGGG 10
Db 47 WYANISSGGG 56
||| : ||||

RESULT 2

PL0248
Ig heavy chain V region (anti-DNA, DPL2VH) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C:Accession: PL0248
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat
A:Reference number: PL0231; MUID:90111618
A:Accession: PL0248
A:Molecule type: mRNA
A:Residues: 1-108 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-24/Region: framework 1
F:9-92/Domain: immunoglobulin homology <IMM>
F:25-29/Region: complementarity-determining 1
F:30-43/Region: framework 2
F:44-60/Region: complementarity-determining 2
F:61-92/Region: framework 3
F:93-99/Region: complementarity-determining 3
F:100-108/Region: framework 4

Query Match 78.2%; Score 43; DB 2; Length 108;
 Best Local Similarity 70.0%; Pred. No. 0.91;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAVKVSGGG 10
 ||| : ||||
 Db 41 WVAITSSGGG 50

RESULT 3

S09258
 Ig heavy chain V region precursor - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 23-Jul-1999
 C:Accession: S09258

R:Hamada, H.; Maezawa, K.; Tsuruo, T.
 Nucleic Acids Res. 18, 1900, 1990
 A:Title: Nucleotide sequences of the variable regions of a mouse monoclonal antibody MRK
 A:Reference number: S09258; MUID:90245594

A:Accession: S09258
 A:Molecule type: DNA
 A:Residues: 1-138 <HAM>
 A:Cross-references: EMBL:X51719; NID:g53207; PIDN:CAA36012.1; PID:g297545
 C:Genetics:

A:Introns: 16/1
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 78.2%; Score 43; DB 2; Length 138;
 Best Local Similarity 70.0%; Pred. No. 1.1;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAVKVSGGG 10
 ||| : ||||
 Db 66 WVAITSSGGG 75

RESULT 4

S40090
 Ig heavy chain - mouse

C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S40090

R:Maier, C.C.; Galin, F.S.; Jarpe, M.A.; Jackson, P.; Krishna, N.R.; Gautam, A.M.; Zhou,
 submitted to the EMBL Data Library, December 1993
 A:Description: A V-lambda x-bearing monoclonal antibody with similar specificity and seq
 A:Reference number: S40090

A:Accession: S40090
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-111 <MAI>
 A:Cross-references: EMBL:X76751; NID:g435680; PIDN:CAA54154.1; PID:gl334154
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 42; DB 2; Length 111;
 Best Local Similarity 70.0%; Pred. No. 1.4;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAVKVSGGG 10
 ||| : ||||
 Db 39 WVAIKSNGG 48

RESULT 5

PHI007

Ig heavy chain V region (clone 163-cl) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C:Accession: PHI007

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444

A:Accession: PHI007

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-111 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 42; DB 2; Length 111;
 Best Local Similarity 70.0%; Pred. No. 1.4;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAVKVSGGG 10
 ||| : ||||
 Db 47 WVAISSGGG 56

RESULT 6

S26468

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S26468

R:Kavaler, J.

submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26468

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <KAV>

A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 76.4%; Score 42; DB 2; Length 113;
 Best Local Similarity 70.0%; Pred. No. 1.4;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAVKVSGGG 10
 ||| : ||||
 Db 43 WVAISSGGG 52

RESULT 7

HVM334

Ig heavy chain precursor V region (345) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C:Accession: JT0502

R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primar

A:Reference number: JT0501; MUID:89279149

A:Accession: JT0502

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A:Note: this sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>
F:41-115/Disulfide bonds: #status predicted

Query Match 76.4%; Score 42; DB 1; Length 117;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAVKVSGGG 10
||| : ||||
Db 66 WVAIISGGG 75

RESULT 8

Ig heavy chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 23-May-1997
C:Accession: B31790
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1988
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an antibody
A:Reference number: A92686; MUID:89034213
A:Accession: B31790
A:Molecule type: mRNA
A:Residues: 1-254 <SCH>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 72.7%; Score 40; DB 2; Length 254;
Best Local Similarity 60.0%; Pred. No. 6.9;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAVKVSGGG 10
||| : ||||
Db 47 WVAIISGGG 56

RESULT 9

Ig heavy chain V region (clone 202.33) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PH1006
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell
A:Reference number: PH0971; MUID:92381444
A:Accession: PH1006
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-108 <TIL>
A:Experimental source: B cell, strain [N2B x N2W]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:10-93/Domain: immunoglobulin homology <IMM>

Query Match 70.9%; Score 39; DB 2; Length 108;
Best Local Similarity 60.0%; Pred. No. 4.8;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WVAVKVSGGG 10
||| : ||||
Db 42 WVAIISGGG 51

RESULT 10

HVMS84
Ig heavy chain precursor V region (5-84) - mouse
C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
C:Accession: JT0505
R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989
A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
A:Reference number: JT0501; MUID:89279149
A:Accession: JT0505
A:Status: translation not shown
A:Molecule type: mRNA
A:Residues: 1-117 <LEV>
A:Experimental source: strain BALB/cJ
A:Note: This sequence belongs to the VH7183 subfamily
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:41-115/Disulfide bonds: #status predicted

Query Match 70.9%; Score 39; DB 1; Length 117;
Best Local Similarity 60.0%; Pred. No. 5.1;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAVKVSGGG 10
||| : ||||
Db 66 WVAIISGGG 75

RESULT 11

Ig heavy chain V region (H37-40) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C:Accession: H27888
R:Catton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to
A:Reference number: A91043; MUID:86300658
A:Accession: H27888
A:Molecule type: DNA
A:Residues: 1-121 <CAT>
A:Experimental source: strain Balb/c
A:Note: This sequence was determined from the germline gene
C:Comment: This chain was isolated from a hybridoma protein that binds influenza viru
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.9%; Score 39; DB 2; Length 121;
Best Local Similarity 66.7%; Pred. No. 5.3;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 WVAVKVSGGG 9
||| : ||||
Db 47 WVAIISGGG 55

RESULT 12

Ig heavy chain V region (H28-A2) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 15-Dec-1988 #text_change 16-Aug-1996
C:Accession: G27888
R:Catton, A.J.; Brownlee, G.G.; Staudt, L.M.; Gerhard, W.
EMBO J. 5, 1577-1587, 1986
A:Title: Structural and functional implications of a restricted antibody response to
A:Reference number: A91043; MUID:86300658
A:Accession: G27888
A:Molecule type: DNA
A:Residues: 1-123 <CAT>
A:Experimental source: strain Balb/c

A:Note: this sequence was determined from the germline gene
 C:Comment: This chain was isolated from a hybridoma protein that binds influenza virus H
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 70.9%; Score 39; DB 2; Length 123;
 Best Local Similarity 66.7%; Pred. No. 5.4;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVAKVSGG 9
 |||: |||
 Db 47 WVAEISGG 55

RESULT 13
 D70549
 hypothetical protein Rv0561c - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
 C:Accession: D70549
 R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
 ; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
 Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Scares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98295987
 A:Accession: D70549
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-408 <COL>
 A:Cross-references: GB:295558; GB:AL123456; NID:g3261781; PIDN:CAB08972.1; PID:e316806;
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: Rv0561c

Query Match 70.9%; Score 39; DB 2; Length 408;
 Best Local Similarity 70.0%; Pred. No. 16;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGG 10
 |||: |||
 Db 386 WVARVRGG 395

RESULT 14
 S56009
 Ig heavy chain variable region against dystrophin - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
 C:Accession: S56009
 R;Morris, G.E.; Nguyen, C.; Man, N.T.
 Biochem. J. 309, 353-359, 1995
 A:Title: Specificity and V(H) sequence of two monoclonal antibodies against the N-termin
 A:Reference number: S56008; MUID:95344393
 A:Accession: S56009
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-92 <MOR>
 A:Cross-references: EMBL:246661
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F;6-86/Domain: immunoglobulin homology <IMM>

Query Match 69.1%; Score 38; DB 2; Length 92;
 Best Local Similarity 66.7%; Pred. No. 6.3;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGG 9

Db 38 WVASISGG 46
 |||: |||

RESULT 15
 S56008

Ig heavy chain variable region MANEX1B against dystrophin - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
 C:Accession: S56008
 R;Morris, G.E.; Nguyen, C.; Man, N.T.
 Biochem. J. 309, 353-359, 1995
 A:Title: Specificity and V(H) sequence of two monoclonal antibodies against the N-ter
 A:Reference number: S56008; MUID:95344393
 A:Accession: S56008
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-92 <MOR>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F;6-86/Domain: immunoglobulin homology <IMM>

Query Match 69.1%; Score 38; DB 2; Length 92;
 Best Local Similarity 66.7%; Pred. No. 6.3;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGG 9
 |||: |||
 Db 38 WVASISGG 46

Search completed: May 27, 2000, 19:26:38
 Job time: 1761 sec

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OM protein - protein search, using sw model

Run on: May 27, 2000, 20:07:09 ; Search time 69.28 Seconds
(without alignments)
4.396 Million cell updates/sec

Title: US-09-016-061-54
Perfect score: 55
Sequence: 1 WYAKVSGGG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	76.4	117	1 HV55_MOUSE	P18526 mus musculus
2	39	70.9	117	1 HV54_MOUSE	P18525 mus musculus
3	39	70.9	188	1 YLAI_LACAC	P29470 lactobacilli
4	38	69.1	97	1 HV56_MOUSE	P18527 mus musculus
5	37	67.3	117	1 HV58_MOUSE	P18529 mus musculus
6	37	67.3	256	1 CB4B_LYCES	P27525 lycopersico
7	36	65.5	37	1 THHS_HORVU	P33045 hordeum vul
8	36	65.5	247	1 HS77_HUMAN	P48741 homo sapien
9	35.5	64.5	196	1 SODF_TETPY	P19666 tetrahymena
10	35	63.6	593	1 CSG_METPE	P27373 methanother
11	35	63.6	593	1 CSG_METSC	P27374 methanother
12	35	63.6	3432	1 POLG_JAEV1	P27395 j genome po
13	35	63.6	3432	1 POLG_JAEV5	P19110 j genome po
14	35	63.6	3432	1 POLG_JAEVJ	P32886 j genome po
15	34	61.8	121	1 NLTP_BOVIN	P07857 bos taurus
16	34	61.8	135	1 RM16_PROWI	P46751 prototheca
17	34	61.8	202	1 P21_SOYBN	P25096 glycine max
18	34	61.8	206	1 TAAT_MAIZE	P13867 zea mays (m
19	34	61.8	227	1 ZEAM_MAIZE	P33679 zea mays (m
20	34	61.8	301	1 YFE4_YEAST	P43558 saccharomyc
21	34	61.8	311	1 BLAC_STRAU	P10509 streptomyc
22	34	61.8	311	1 BLAC_STRCE	O05650 streptomyc
23	34	61.8	547	1 NLTP_CHICK	Q07598 gallus gall
24	34	61.8	547	1 NLTP_MOUSE	P32020 mus musculus
25	34	61.8	547	1 NLTP_HUMAN	P11915 rattus norv
26	34	61.8	547	1 NLTP_RAT	P32069 arabidopsis
27	34	61.8	621	1 TPX_ARATH	P36858 aspergillus
28	34	61.8	867	1 NIA_ASPNG	P36842 leptosphaer
29	34	61.8	893	1 NIA_LEPMC	P39863 fusarium ox
30	34	61.8	905	1 NIA_FUSOX	P03314 y genome po
31	34	61.8	3411	1 POLG_YEFV1	P19901 y genome po
32	34	61.8	3411	1 POLG_YEFV2	P06935 w genome po
33	34	61.8	3430	1 POLG_WNV	P14335 k genome po
34	34	61.8	3433	1 POLG_KUNUM	

35	33	60.0	98	1 HV57_MOUSE	P18528 mus musculus
36	33	60.0	122	1 MPP2_PHLPR	P43214 phleum prat
37	33	60.0	137	1 RL16_SPICI	O31162 spiroplasma
38	33	60.0	138	1 RL16_MYCBO	O06049 mycobacteri
39	33	60.0	138	1 RL16_MYCTU	P95056 mycobacteri
40	33	60.0	194	1 PTH_ECOLI	P23332 escherichia
41	33	60.0	194	1 PTH_HAEIN	P44682 haemophilus
42	33	60.0	194	1 PTH_SALTI	O60001 salmonella
43	33	60.0	234	1 RL6_MESCR	P34091 mesembryant
44	33	60.0	261	1 CB4_SPIOL	P36494 spinacia ol
45	33	60.0	329	1 CC06_CAEEL	P18831 caenorhabdi

ALIGNMENTS

RESULT 1
HV55_MOUSE
ID HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 345 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALE/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -|- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; J0502; HWS34.
DR PFAM; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;

Query Match 76.4%; Score 42; DB 1; Length 117;
Best Local Similarity 70.0%; Pred. No. 0.37;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYAKVSGGG 10
||| : |||
Db 66 WYAYISSGGG 75

RESULT 2
HV54_MOUSE
ID HV54_MOUSE STANDARD; PRT; 117 AA.
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 5-84 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.

```

RC STRAIN-BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
   the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PFAM; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 70.9%; Score 39; DB 1; Length 117;
Best Local Similarity 60.0%; Pred. No. 1.4;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVKSGG 10
   ||| : |||
Db 66 WVAVISNGG 75

RESULT 3
YLAL_LACAC STANDARD; PRT; 188 AA.
AC F29470;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE HYPOTHETICAL PROTEIN IN LAF 5'REGION (ORF1) (FRAGMENT).
OS Lactobacillus acidophilus.
OG Plasmid pTRK160.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
OC Lactobacillus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11088;
RX MEDLINE; 94113718.
RA Fremaux C., Ahn C., Klaenhammer T.R.;
RT "Molecular analysis of the lactacin F operon.";
RL Appl. Environ. Microbiol. 59:3906-3915(1993).
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CC -----
DR EMBL; M57961; AAA16635.1; -.
KW Hypothetical protein; Plasmid.
FT NON_TER 1 1
SQ SEQUENCE 188 AA; 21073 MW; D7A1FABE073C1081 CRC64;

Query Match 70.9%; Score 39; DB 1; Length 188;
Best Local Similarity 70.0%; Pred. No. 2.2;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WVAKVKSGG 10
   ||| : |||
Db 70 WVAHVDQGG 79

Query Match 67.3%; Score 37; DB 1; Length 117;

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```

RESULT 4
HV56_MOUSE STANDARD; PRT; 97 AA.
ID HV56_MOUSE
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
   the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0504; HVMS91.
DR PFAM; PF00047; ig; 1.
KW Immunoglobulin V region.
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

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Query Match 69.1%; Score 38; DB 1; Length 97;
Best Local Similarity 66.7%; Pred. No. 1.8;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 WVAKVKSGG 9
   ||| : |||
Db 47 WVASISGG 55

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RESULT 5
HV58_MOUSE STANDARD; PRT; 117 AA.
ID HV58_MOUSE
AC P18529;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 5-76 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
   the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0506; HVMS57.
DR PFAM; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-76.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12991 MW; 93A04782B78B8FA0 CRC64;

```

```

Query Match 67.3%; Score 37; DB 1; Length 117;

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```
Best Local Similarity 66.7%; Pred. No. 3.3;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAVKSGG 9
Db 66 WVAISSGG 74

RESULT 6
CB4B_LYCES
ID CB4B_LYCES STANDARD; PRT; 256 AA.
AC P27525;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE CHLOROPHYLL A-B BINDING PROTEIN CP24 10B PRECURSOR (CAB-10B)
DE (LHCP).
GN CAP10B.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Asteridae; euasterids I; Solanales; Solanaceae;
OC Solanum.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91355849.
RA Schwartz E., Pichersky E.;
RT "Sequence of two tomato nuclear genes encoding chlorophyll
a/b-binding proteins of CP24, a PSII antenna component.";
RL Plant Mol. Biol. 15:157-160(1990).
CC -1- SIMILARITY: TO A FAMILY OF PROTEINS INCLUDING THE CP24/CP29, THE
CC CAB 1/II AND ELIP (EARLY LIGHT-INDUCIBLE PROTEINS) PROTEINS.
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CC -----
CC EMBL; M32606; AAA34146.1; -.
DR PIR; S11878; S11878.
DR PFAM; PF00504; Chloroa_b-bind; 1.
KW Chlorophyll; Photosynthesis; Photosystem II; Thylakoid membrane;
KW Chloroplast; Transit peptide; Multigene family; Transmembrane.
FT TRANSIT 1 45 CHLOROPLAST (POTENTIAL).
FT CHAIN 46 256 CHLOROPHYLL A-B BINDING PROTEIN CP24 10B.
SQ SEQUENCE 256 AA; 27470 MW; 33325E6486496726 CRC64;

Query Match 67.3%; Score 37; DB 1; Length 256;
Best Local Similarity 66.7%; Pred. No. 7.3;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 WVAVKSGG 9
Db 55 WIPAVKSGG 63

RESULT 7
THHS_HORVU
ID THHS_HORVU STANDARD; PRT; 37 AA.
AC P33045;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE ANTFUNGAL PROTEIN S (FRAGMENT).
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
OC Poaceae; Hordeum.
RN [1]

RP SEQUENCE.
RC STRAIN-CV. BOMI RISO 1508;
RX MEDLINE; 92037994.
RA Hejgaard J., Jacobsen S., Svendsen I.;
RT "Two antifungal thaumatin-like proteins from barley grain.";
RL FEBS Lett. 291:127-131(1991).
CC -1- FUNCTION: HAS ANTIFUNGAL ACTIVITY. INHIBITS THE GROWTH OF
CC TRICHODERMA VIRIDAE AND CANDIDA ALBICANS.
CC -1- SIMILARITY: BELONGS TO THE THAUMATIN FAMILY.
DR PIR; S17684; S17684.
DR HSP; P25871; 1AUN.
DR PROSITE; PS00316; THAUMATIN; PARTIAL.
DR PFAM; PF00314; thaumatin; 1.
KW Fungicide.
FT NON_TER 37 37
SQ SEQUENCE 37 AA; 3871 MW; 7BE164ACCB8A9881 CRC64;

Query Match 65.5%; Score 36; DB 1; Length 37;
Best Local Similarity 60.0%; Pred. No. 1.6;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 WVAVKSGG 10
Db 14 WAAAVPAGG 23

RESULT 8
HS77_HUMAN
ID HS77_HUMAN STANDARD; PRT; 247 AA.
AC P48741; P19790;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE HEAT SHOCK 70 KD PROTEIN 7 (HEAT SHOCK 70 KD PROTEIN B) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85270444.
RA Voellmy R., Ahmed A., Schiller P., Bromley P., Runger D.;
RT "Isolation and functional analysis of a human 70,000-dalton heat
shock protein gene segment.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:4949-4953(1985).
CC -1- SIMILARITY: BELONGS TO THE HEAT SHOCK PROTEIN 70 FAMILY.
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CC EMBL; M11236; AAA52696.1; -.
DR PIR; A25773; A25773.
DR HSP; P19120; 1NGI.
DR MIM; 140556; -.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; PARTIAL.
DR PFAM; PF00012; HSP70; 1.
KW ATP-binding; Heat shock; Multigene family.
FT NON_TER 247 247
SQ SEQUENCE 247 AA; 26906 MW; 354EE237F6750DD7 CRC64;

Query Match 65.5%; Score 36; DB 1; Length 247;
Best Local Similarity 70.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

QY 1 WVAKVS GGG 10
 Db 92 WPFKVS GGG 101

RESULT 9

SODF_TETPY STANDARD; PRT; 196 AA.
 AC P19666;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE SUPEROXIDE DISMUTASE [FE] (EC 1.15.1.1).
 OS Tetrahymena pyriformis.
 OC Eukaryota; Alveolata; Ciliophora; Oligohymenophorea; Hymenostomatida;
 OC Tetrahymenina; Tetrahymena.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 91009226.
 RA Barra D., Schinina M.E., Bossa F., Puget K., Guissani A.,
 RA Michelson A.M.;
 RT "A tetrameric iron superoxide dismutase from the eucaryote
 Tetrahymena pyriformis.";
 RL J. Biol. Chem. 265:17680-17687(1990).
 CC -I- FUNCTION: DESTROYS RADICALS WHICH ARE NORMALLY PRODUCED WITHIN THE
 CC CELLS AND ARE TOXIC TO BIOLOGICAL SYSTEMS.
 CC -I- CATALYTIC ACTIVITY: 2 PEROXIDE RADICAL + 2 H(+) = O(2) + H(2)O(2).
 CC -I- COFACTOR: THE TETRAMER CONTAINS 2.5 G ATOMS OF FERRIC IRON.
 CC -I- SUBUNIT: HOMOTETRAMER.
 CC -I- SIMILARITY: BELONGS TO THE IRON/MANGANESE SUPEROXIDE DISMUTASE
 CC FAMILY.
 CC PIR; A39223; A39223.
 DR HSSP; P04179; 1MSD.
 DR PROSITE; PS00088; SOD_MN; 1.
 DR FRAM; PF00081; sodfe; 1.
 KW Oxidoreductase; Iron.
 FT METAL 20 20 IRON (BY SIMILARITY).
 FT METAL 68 68 IRON (BY SIMILARITY).
 FT METAL 157 157 IRON (BY SIMILARITY).
 FT METAL 161 161 IRON (BY SIMILARITY).
 SQ SEQUENCE 196 AA; 22657 MW; FC1F2F67893D8DC7 CRC64;

Query Match 64.5%; Score 35.5; DB 1; Length 196;
 Best Local Similarity 53.3%; Pred. No. 11;
 Matches 8; Conservative 1; Mismatches 1; Indels 5; Gaps 1;

QY 1 WV-----AKVKS GGG 10
 Db 69 WIYNDNLAPVKS GGG 83

RESULT 10

CSG_METFE STANDARD; PRT; 593 AA.
 AC P27373;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE CELL SURFACE GLYCOPROTEIN PRECURSOR (S-LAYER PROTEIN).
 GN SLGA.
 OS Methanothermobacter feravidus.
 OC Archaea; Euryarchaeota; Methanobacteriales; Methanothermaceae;
 OC Methanothermus.
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 23-42.
 RC STRAIN=DSM 2088 / V245;
 RX MEDLINE; 91293115.
 RA Broeckl G., Behr M., Fabry S., Hensel R., Kaudewitz H., Biendl E.,
 RA Koenig H.;
 RT "Analysis and nucleotide sequence of the genes encoding the surface-
 RT layer glycoproteins of the hyperthermophilic methanogens
 RT Methanothermobacter feravidus and Methanothermus sociabilis.";
 RL Eur. J. Biochem. 199:147-152(1991).
 CC -I- SUBUNIT: ASSEMBLE INTO MONO-LAYERED CRYSTALLINE ARRAYS.

RL Eur. J. Biochem. 199:147-152(1991).
 CC -I- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
 CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA.
 CC -I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIA IS COVERED BY A
 CC S-LAYER WITH HEXAGONAL SYMMETRY.
 CC -----
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 CC -----

DR EMBL; X58297; CAA41230.1; -.
 DR PIR; S16225; S16225.
 KW Glycoprotein; Cell wall; S-layer; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 593 CELL SURFACE GLYCOPROTEIN.
 FT CARBOHYD 29 29
 FT CARBOHYD 58 58 POTENTIAL.
 FT CARBOHYD 66 66 POTENTIAL.
 FT CARBOHYD 74 74 POTENTIAL.
 FT CARBOHYD 114 114 POTENTIAL.
 FT CARBOHYD 122 122 POTENTIAL.
 FT CARBOHYD 145 145 POTENTIAL.
 FT CARBOHYD 148 148 POTENTIAL.
 FT CARBOHYD 158 158 POTENTIAL.
 FT CARBOHYD 176 176 POTENTIAL.
 FT CARBOHYD 208 208 POTENTIAL.
 FT CARBOHYD 231 231 POTENTIAL.
 FT CARBOHYD 326 326 POTENTIAL.
 FT CARBOHYD 336 336 POTENTIAL.
 FT CARBOHYD 340 340 POTENTIAL.
 FT CARBOHYD 431 431 POTENTIAL.
 FT CARBOHYD 471 471 POTENTIAL.
 FT CARBOHYD 500 500 POTENTIAL.
 FT CARBOHYD 516 516 POTENTIAL.
 SQ SEQUENCE 593 AA; 65481 MW; E064669967B7611C CRC64;

Query Match 63.6%; Score 35; DB 1; Length 593;
 Best Local Similarity 60.0%; Pred. No. 41;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVS GGG 10
 Db 228 YIANVS GGG 237

RESULT 11

CSG_METSC STANDARD; PRT; 593 AA.
 ID CSG_METSC
 AC P27374;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE CELL SURFACE GLYCOPROTEIN PRECURSOR (S-LAYER PROTEIN).
 GN SLGA.
 OS Methanothermobacter sociabilis.
 OC Archaea; Euryarchaeota; Methanobacteriales; Methanothermaceae;
 OC Methanothermus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 3496 / KF1-FL;
 RX MEDLINE; 91293115.
 RA Broeckl G., Behr M., Fabry S., Hensel R., Kaudewitz H., Biendl E.,
 RA Koenig H.;
 RT "Analysis and nucleotide sequence of the genes encoding the surface-
 RT layer glycoproteins of the hyperthermophilic methanogens
 RT Methanothermobacter feravidus and Methanothermus sociabilis.";
 RL Eur. J. Biochem. 199:147-152(1991).
 CC -I- SUBUNIT: ASSEMBLE INTO MONO-LAYERED CRYSTALLINE ARRAYS.

CC -1- SUBCELLULAR LOCATION: CELL WALL.
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: X58296; CAA41229.1; -
CC PIR: S16375; S16375.
KW Glycoprotein; Cell wall; S-layer; Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 593 CELL SURFACE GLYCOPROTEIN.
FT CARBOHYD 29 29 POTENTIAL.
FT CARBOHYD 58 58 POTENTIAL.
FT CARBOHYD 66 66 POTENTIAL.
FT CARBOHYD 74 74 POTENTIAL.
FT CARBOHYD 114 114 POTENTIAL.
FT CARBOHYD 122 122 POTENTIAL.
FT CARBOHYD 145 145 POTENTIAL.
FT CARBOHYD 148 148 POTENTIAL.
FT CARBOHYD 158 158 POTENTIAL.
FT CARBOHYD 176 176 POTENTIAL.
FT CARBOHYD 208 208 POTENTIAL.
FT CARBOHYD 231 231 POTENTIAL.
FT CARBOHYD 326 326 POTENTIAL.
FT CARBOHYD 336 336 POTENTIAL.
FT CARBOHYD 340 340 POTENTIAL.
FT CARBOHYD 431 431 POTENTIAL.
FT CARBOHYD 471 471 POTENTIAL.
FT CARBOHYD 500 500 POTENTIAL.
FT CARBOHYD 516 516 POTENTIAL.
SQ SEQUENCE 593 AA; 65503 MW; DFCDFB357E10F2EB CRC64;

Query Match 63.6%; Score 35; DB 1; Length 593;
Best Local Similarity 60.0%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 WYAKVSGGG 10
Db 228 YIANVSSGGG 237
RESULT 12
ID POLG_JAEV1 STANDARD; PRT: 3432 AA.
AC P27395; Q82920; Q82921; Q82922; Q82923; Q82924; Q82925; Q82926;
Q82927; Q82928;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last annotation update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
DE PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL
DE PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED
DE RNA POLYMERASE (EC 2.7.7.48) (NS5)].
OS Japanese encephalitis virus (strain SA-14).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90320126.
RA Nitayaphan S., Grant J.A., Chang G.J.J., Trent D.W.;
RT "Nucleotide sequence of the virulent SA-14 strain of Japanese
RT encephalitis virus and its attenuated vaccine derivative,
RT SA-14-14-2";
RL Virology 177:541-552(1990).
CC -1- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE
CC HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
CC NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A

CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: M55506; AAA46248.1; -
CC EMBL: M55506; AAA46249.1; ALT_INIT.
CC PIR: A35519; GNMVJS.
CC HSP: P14336; LSVB.
DR PFAM; PF00869; Flavi_glycoprot; 1.
DR PFAM; PF00948; Flavi_NS1; 1.
DR PFAM; PF00949; Flavi_helicase; 1.
DR PFAM; PF00972; Flavi_NS5; 1.
DR PFAM; PF01002; Flavi_NS2B; 1.
DR PFAM; PF01003; Flavi_capsid; 1.
DR PFAM; PF01004; Flavi_M; 1.
DR PFAM; PF01005; Flavi_NS2A; 1.
DR PFAM; PF01349; Flavi_NS4B; 1.
DR PFAM; PF01350; Flavi_NS4A; 1.
DR PFAM; PF01570; Flavi_propep; 1.
KW Polyprotein; Glycoprotein; Transferase; RNA-directed RNA polymerase;
KW Core protein; Coat protein; Envelope protein; Helicase; ATP-binding;
KW Transmembrane; Nonstructural protein.
FT INIT_MET 1 1
FT CHAIN 1 127
FT PROPEP 128 219
FT CHAIN 220 294
FT CHAIN 295 794
FT CHAIN 795 1206
FT CHAIN 1207 1373
FT CHAIN 1374 1504
FT CHAIN 1505 2123
FT CHAIN 2124 2412
FT CHAIN 2413 2527
FT CHAIN 2528 3432
FT NP_BIND 1698 1705
FT SITE 1789 1792
FT TRANSMEM 44 60
FT TRANSMEM 112 127
FT TRANSMEM 280 294
FT TRANSMEM 774 790
FT DISULFID 297 324
FT DISULFID 354 410
FT DISULFID 368 399
FT DISULFID 386 415
FT DISULFID 484 581
FT DISULFID 598 629
FT CARBOHYD 142 142
FT CARBOHYD 448 448
FT CARBOHYD 924 924
FT CARBOHYD 1001 1001
FT CARBOHYD 1594 1594
FT CARBOHYD 2463 2463
FT CARBOHYD 2491 2491
FT CARBOHYD 2761 2761
FT CARBOHYD 2866 2866
FT CARBOHYD 2904 2904
SQ SEQUENCE 3432 AA; 380205 MW; 11B9423735B1B5FE CRC64;

Query Match 63.6%; Score 35; DB 1; Length 3432;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
Qy 1 WYAKVSGGG 10

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Db 3026 WLSRENSGG 3035
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RESULT 13
POLG_JAEV5      STANDARD;      PRT; 3432 AA.
AC P19110;
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
DE PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL
DE PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED
DE RNA POLYMERASE (EC 2.7.7.48) (NS5)].
OS Japanese encephalitis virus (strain SA(v)).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91280801.
RA Aihara S., Rao C., Yu Y.X., Lee T., Watanabe K., Komiya T.,
RA Sumiyoshi H., Hashimoto H., Nomoto A.;
RT "Identification of mutations that occurred on the genome of Japanese
RL virus Genes 5:95-109(1991).
CC -1- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE
CC HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
CC NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA.
CC
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CC
DR EMBL; D90194; BAA14218.1; -.
DR HSP; P14336; 1SVB.
DR PFAM; PF00869; Flavi_glycoprot; 1.
DR PFAM; PF00948; Flavi_NS1; 1.
DR PFAM; PF00949; Flavi_helicase; 1.
DR PFAM; PF00972; Flavi_NS2; 1.
DR PFAM; PF01002; Flavi_NS2B; 1.
DR PFAM; PF01003; Flavi_capsid; 1.
DR PFAM; PF01004; Flavi_M; 1.
DR PFAM; PF01005; Flavi_NS2A; 1.
DR PFAM; PF01349; Flavi_NS4B; 1.
DR PFAM; PF01350; Flavi_NS4A; 1.
DR PFAM; PF01570; Flavi_propep; 1.
KW Polyprotein; Glycoprotein; Transferase; RNA-directed RNA polymerase;
KW Core protein; Coat protein; Envelope protein; Helicase; ATP-binding;
KW Transmembrane; Nonstructural protein.
FT INIT_MET 1 1
FT CHAIN 1 127
FT PROPEP 128 219
FT CHAIN 220 294
FT CHAIN 295 794
FT CHAIN 795 1206
FT CHAIN 1207 1373
FT CHAIN 1374 1504
FT CHAIN 1505 2123
FT CHAIN 2124 2412
FT CHAIN 2413 2527
FT CHAIN 2528 3432
FT NP_BIND 1698 1705
FT SITE 1789 1792

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FT TRANSMEM 44 60
FT TRANSMEM 112 127
FT TRANSMEM 280 294
FT TRANSMEM 774 790
FT DISULFID 297 324
FT DISULFID 354 410
FT DISULFID 368 399
FT DISULFID 386 415
FT DISULFID 484 581
FT DISULFID 598 629
FT CARBOHYD 142 142
FT CARBOHYD 448 448
FT CARBOHYD 924 924
FT CARBOHYD 1001 1001
FT CARBOHYD 2463 2463
FT CARBOHYD 2491 2491
SQ SEQUENCE 3432 AA; 380176 MW; AE8A63E0C00C4674 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 3432;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAVKVGGG 10
Db 3026 WLSRENSGG 3035
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RESULT 14
POLG_JAEVJ      STANDARD;      PRT; 3432 AA.
AC P32886; P08769;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-JAN-1990 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
DE PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL
DE PROTEINS NS1, NS2A, NS2B, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED
DE RNA POLYMERASE (EC 2.7.7.48) (NS5)].
OS Japanese encephalitis virus (strain Jaovs982).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88072090.
RA Sumiyoshi H., Mori C., Fuke I., Morita K., Kuhara S., Kondou J.,
RA Kikuchi Y., Nagamatsu H., Igarashi A.;
RT "Complete nucleotide sequence of the Japanese encephalitis virus
RT genome RNA."
RL Virology 161:497-510(1987).
RN [2]
RP SEQUENCE OF 1-969 FROM N.A.
RX MEDLINE; 87163522.
RA Sumiyoshi H., Morita K., Mori C., Fuke I., Shiba T., Sakaki Y.,
RA Igarashi A.;
RT "Sequence of 3000 nucleotides at the 5' end of Japanese encephalitis
RT virus RNA."
RL Gene 48:195-201(1986).
CC -1- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE
CC HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
CC NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA.
CC
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CC

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CC -----
DR EMBL; M15337; AAA46247.1; -.
DR EMBL; M18370; AAA81554.1; -.
DR PIR; A27403; GNVVJE.
DR HSP; P14336; 1SVB.
DR PFAM; PF00869; Flavl_glycoprot; 1.
DR PFAM; PF00948; Flavl_Ns1; 1.
DR PFAM; PF00949; Flavl_helicase; 1.
DR PFAM; PF00972; Flavl_NS5; 1.
DR PFAM; PF01002; Flavl_NS2B; 1.
DR PFAM; PF01003; Flavl_capsid; 1.
DR PFAM; PF01004; Flavl_M; 1.
DR PFAM; PF01005; Flavl_NS2A; 1.
DR PFAM; PF01349; Flavl_NS4B; 1.
DR PFAM; PF01350; Flavl_NS4A; 1.
DR PFAM; PF01570; Flavl_propesp; 1.
DR Polyprotein; Glycoprotein; Transferase; RNA-directed RNA polymerase;
KW Core protein; Coat protein; Envelope protein; Helicase; ATP-binding;
KW Transmembrane; Nonstructural protein.
FT INIT_MET 1 1
FT CHAIN 1 127
FT PROPEP 128 219
FT CHAIN 220 294
FT CHAIN 295 794
FT CHAIN 795 1206
FT CHAIN 1207 1373
FT CHAIN 1374 1504
FT CHAIN 1505 2123
FT CHAIN 2124 2412
FT CHAIN 2413 2527
FT CHAIN 2528 3432
FT DOMAIN 392 405
FT NP_BIND 1698 1705
FT SITE 1789 1792
FT TRANSMEM 44 60
FT TRANSMEM 112 127
FT TRANSMEM 280 294
FT TRANSMEM 774 790
FT DISULFID 297 324
FT DISULFID 354 410
FT DISULFID 368 399
FT DISULFID 386 415
FT DISULFID 484 581
FT DISULFID 598 629
FT CARBOHYD 142 142
FT CARBOHYD 448 448
FT CARBOHYD 924 924
FT CARBOHYD 1001 1001
FT CARBOHYD 2463 2463
FT CARBOHYD 2491 2491
SQ SEQUENCE 3432 AA; 380160 MW; EEFA26DBF54BF991 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 3432;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYAKVKSGGG 10
Db 3026 WLSRENSGGG 3035
1::: |||||

RESULT 15
ID NLTP_BOVIN STANDARD; PRT; 121 AA.
AC P07857;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE NONSPECIFIC LIPID-TRANSFER PROTEIN (STEROL CARRIER PROTEIN 2) (SCP-2).
GN SCP2.
OS Bos taurus (Bovine).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE.
RC TISSUE=LIVER;
RX MEDLINE; 85149425.
RA Westerman J., Wirtz K.W.A.;
RT "The primary structure of the nonspecific lipid transfer protein
RT (sterol carrier protein 2) from bovine liver.";
RL Biochem. Biophys. Res. Commun. 127:333-338(1985).
CC -!- FUNCTION: MAMMALIAN TISSUES CONTAIN A NONSPECIFIC LIPID-TRANSFER
CC PROTEIN WHICH MEDIATES IN VITRO THE TRANSFER OF ALL COMMON
CC PHOSPHOLIPIDS, CHOLESTEROL AND GLYCOSIDES BETWEEN MEMBRANES.
CC MAY PLAY A ROLE IN REGULATING STEROIDOGENESIS.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC IN THE LIVER AND ALSO ASSOCIATED
CC WITH MITOCHONDRIA ESPECIALLY IN STEROIDOGENIC TISSUES.
DR PROSITE; PS00342; MICROBODIES_CTER; PARTIAL.
KW Lipid-binding; Transport; Mitochondrion.
FT SITE 70 70 ESSENTIAL FOR TRANSPORT OF LIPIDS.
SQ SEQUENCE 121 AA; 13022 MW; D56457DBD15A4FC9 CRC64;
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Query Match 61.8%; Score 34; DB 1; Length 121;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYAKVKSGGG 10
Db 50 WYVDVKNKGK 59
1::: |||||

Search completed: May 27, 2000, 20:07:10
Job time: 982 sec

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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:38:33 ; Search time 199.56 Seconds
(without alignments)
3.474 Million cell updates/sec

Title: US-09-016-061-54
Perfect score: 55
Sequence: 1 WYAKVSGG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SPTREMBL_12:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	39	70.9	342	12	O55810 meaban viru
2	39	70.9	391	2	O51393 pseudomonas
3	39	70.9	408	2	O06427 mycobacteri
4	38	69.1	509	2	O57079 veillonella
5	38	69.1	691	12	O72120 canine cali
6	38	69.1	907	3	Q00303 botrytis ci
7	37	67.3	186	2	O86545 streptomyce
8	37	67.3	238	10	O04364 oryza sativ
9	37	67.3	289	2	Q9X2P4 mycobacteri
10	37	67.3	345	12	O55828 sepiik virus
11	37	67.3	409	2	O54496 streptomyce
12	37	67.3	1008	2	Q9X082 thermotoga
13	37	67.3	1350	10	O04013 volvox cart
14	37	67.3	1765	11	O88457 rattus norv
15	36.5	66.4	375	10	Q9XH01 arabidopsis
16	36	65.5	71	10	P93234 lycopersico
17	36	65.5	175	10	O81927 cicler arlet
18	36	65.5	225	5	P92048 periplaneta
19	36	65.5	235	5	P92047 periplaneta
20	36	65.5	407	2	Q56584 vibrlo algi

21	36	65.5	411	2	O05012	005012 haemophilus
22	36	65.5	616	10	O81533	081533 nicotiana t
23	36	65.5	1014	5	O77433	077433 drosophila
24	36	65.5	1244	2	O55576	055576 synchocyst
25	36	65.5	1413	5	O23596	023596 caenorhabdl
26	35	63.6	163	1	Q9YBA8	Q9YBA8 aeropyrum p
27	35	63.6	303	10	O42912	042912 malus domes
28	35	63.6	343	12	O55830	055830 spordweni v
29	35	63.6	345	12	O55784	055784 alfuy virus
30	35	63.6	345	12	O55791	055791 cactipacore
31	35	63.6	345	12	O55813	055813 murray vall
32	35	63.6	345	12	O55837	055837 yaounde vir
33	35	63.6	408	2	Q9X4Q8	Q9X4Q8 vibrio chol
34	35	63.6	447	13	O73628	073628 anolis caro
35	35	63.6	520	2	O92F72	092F72 burkholderi
36	35	63.6	1175	5	Q18719	Q18719 caenorhabdl
37	35	63.6	3432	12	O36764	036764 japanese en
38	35	63.6	3432	12	O36765	036765 japanese en
39	35	63.6	3432	12	O82873	082873 japanese en
40	35	63.6	3432	12	O82872	082872 japanese en
41	35	63.6	3432	12	O82919	082919 japanese en
42	35	63.6	3432	12	O90297	090297 japanese en
43	35	63.6	3432	12	O90417	090417 japanese en
44	35	63.6	3432	12	O04091	004091 japanese en
45	35	63.6	3432	12	O92928	092928 japanese en

ALIGNMENTS

RESULT 1
O55810 PRELIMINARY; PRT; 342 AA.
ID O55810;
AC O55810;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE NS5 PROTEIN (FRAGMENT).
GN NS5.
OS Meaban virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BREST ART707;
RX MEDLINE; 98080391.
RA KUNO G., CHANG G.-J., TSUCHIYA K.R., KARABATSOS N., CROPP C.B.;
RT "Phylogeny of the genus Flavivirus."
RL J. Virol. 72:73-83(1998).
DR EMBL; AF013386; AAC58774.1; -.
DR PFAM; PF00972; Flavi_NS5; 1.
FT NON_TER 1
FT NON_TER 342 342
SQ SEQUENCE 342 AA; 38615 MW; B837892D CRC32;

Query Match 70.9%; Score 39; DB 12; Length 342;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYAKVSGGG 10
| : : | | | | |
DB 37 WASREKSGG 46

RESULT 2
Q51393 PRELIMINARY; PRT; 391 AA.
ID Q51393;
AC Q51393;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)
DE ALGJ.

GN ALGJ.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
 OC Pseudomonas.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRD1;
 RA FRANKLIN M.J., OHMAN D.E.;
 RL J. Bacteriol. 178:0-0(0).
 DR EMBL; U50202; AAB09782.1;
 SQ SEQUENCE 391 AA; 43106 MW; 882A5BBD CRC32;

Query Match 70.9%; Score 39; DB 2; Length 391;
 Best Local Similarity 60.0%; Pred. No. 18;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVAVKSGGG 10
 |||:|:|
 Db 371 WVAQLKASGG 380

RESULT 3
 O06427 ID O06427 PRELIMINARY; PRT; 408 AA.

AC O06427;
 DT 01-JUL-1997 (TReMBLrel. 04, Created)
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
 DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
 DE HYPOTHETICAL 43.8 KD PROTEIN.
 GN MTCY25D10.40C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RA BROWN D., CHURCHER C.M.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RA BARRELL B.G., RAJANDREAM M.A.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE; 96181548.
 RA PHILIPP W.J., POULET S., EIGLMEIER K., PASCOPELLA L.,
 RA BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
 RA COLE S.T.;
 RT "An integrated map of the genome of the tubercle bacillus,
 RT Mycobacterium tuberculosis H37RV, and comparison with Mycobacterium
 RT leprae.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:3132-3137(1996).
 DR EMBL; 295558; CAB08972.1;
 DR PFAM; PF01494; FAD-binding_3; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 408 AA; 43869 MW; EB86A5DE CRC32;

Query Match 70.9%; Score 39; DB 2; Length 408;
 Best Local Similarity 70.0%; Pred. No. 19;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAVKSGGG 10
 |||:|:|
 Db 386 WVARVRGGG 395

RESULT 4
 Q57079 ID Q57079 PRELIMINARY; PRT; 509 AA.

AC Q57079;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE ALPHA-SUBUNIT, METHYLMALONYL-COA DECARBOXYLASE.
 OS Veillonella parvula.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Sporomusa subbranch;
 OC Veillonella.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HUDER J.B., DIMROTH P.;
 RL J. Biol. Chem. 0:0-0(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 94043308.
 RA HUDER J.B., DIMROTH P.;
 RT "Sequence of the sodium ion pump methylmalonyl-CoA decarboxylase from
 RT Veillonella parvula.";
 RL J. Biol. Chem. 268:24564-24571(1993).
 DR EMBL; 224754; CAA80872.1;
 DR EMBL; L22208; AAC36820.1;
 DR PFAM; PF01039; Carboxyl_trans; 1.
 SQ SEQUENCE 509 AA; 55100 MW; 21F01040 CRC32;

Query Match 69.1%; Score 38; DB 2; Length 509;
 Best Local Similarity 77.8%; Pred. No. 36;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VAKVSGGG 10
 :|||:|
 Db 15 LAKVAGGG 23

RESULT 5

ID 072120 PRELIMINARY; PRT; 691 AA.
 AC 072120;
 DT 01-AUG-1998 (TReMBLrel. 07, Created)
 DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
 DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
 DE CAPSID PROTEIN PRECURSOR.
 OS Canine calicivirus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 OC Calicivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NO. 48;
 RA ROERINK F., HASHIMOTO M., TOHYA Y., MOCHIZUKI M.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF053720; AAC16446.1;
 DR PFAM; PF00915; Calici_coat; 1.
 SQ SEQUENCE 691 AA; 76181 MW; 2775F4B2 CRC32;

Query Match 69.1%; Score 38; DB 12; Length 691;
 Best Local Similarity 60.0%; Pred. No. 50;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAVKSGGG 10
 |||:|:|
 Db 549 WIAEQSAGG 558

RESULT 6

ID Q00303 PRELIMINARY; PRT; 907 AA.
 AC Q00303;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
 DE NITRATE REDUCTASE.
 GN NIAD.

OS Botrytis cinerea (Botryotinia fuckeliana).
 OC Eukaryota; Fungi; Ascomycota; Euscomycetes; Discomycetes; Leotiales;
 OC Sclerotiniaceae; Botryotinia.

RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-T4;

RA LEVIE C., DUTERTRE M., FORTINI D., BRYGOO Y.;
 Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; U43783; AAC02633.1; -.

DR HSSP; P17571; 2CND.

DR PROSITE; PS00559; MOLYBDOPTERIN_EUK; 1.

DR PRAM; PF00173; heme_1; 1.

DR PRAM; PF00175; oxidore_fad; 1.

DR PRAM; PF00174; oxidore_molyb; 1.

DR PRAM; PF00970; Cyt_reductase; 1.

DR PRINTS; PR00406; CYTB5RODASE.

DR PRINTS; PR00407; EUMOPTERIN.

DR PRINTS; PR00363; CYTOCHROME5.

SQ SEQUENCE 907 AA; 101896 MW; 48DBA5CE CRC32;

Query Match 69.1%; Score 38; DB 3; Length 907;

Best Local Similarity 60.0%; Pred. No. 68;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAVKVSGG 10

DB 494 WMERVKSAGG 503

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RESULT 7

OB6545

ID OB6545 PRELIMINARY; PRT; 186 AA.

AC OB6545;

DT 01-NOV-1998 (TREMBLrel. 08, Created)

DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)

DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)

DE HYPOTHETICAL 19.9 KD PROTEIN.

GN SCLF2.08C.

OS Streptomyces coelicolor.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-A3(2);

RA SEGER K.J.; HARRIS D.;

Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-A3(2);

RA PARKHILL J.; BARRELL B.G.; RAJANDREAM M.A.;

Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN-A3(2);

RA MEDLINE; 97000351.

RA REDENBACH M.; KIESER H.M.; DENAPATE D.; EICHNER A.; CULLUM J.;

KINASHI H.; HOPWOOD D.A.;

"A set of ordered cosmids and a detailed genetic and physical map for

the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

Mol. Microbiol. 21:77-96(1996).

DR EMBL; AL031350; CA20499.1; -.

KW Hypothetical protein.

SQ SEQUENCE 186 AA; 19874 MW; E4B54C0F CRC32;

Query Match 67.3%; Score 37; DB 2; Length 186;

Best Local Similarity 60.0%; Pred. No. 19;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WVAVKVSGG 10

DB 51 WWTVRPGG 60

I: :||| I|

RESULT 8

OB4364

ID OB4364 PRELIMINARY; PRT; 238 AA.

AC OB4364;

DT 01-JUL-1997 (TREMBLrel. 04, Created)

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

DE PATHOGENESIS-RELATED THAUMATIN-LIKE PROTEIN.

GN YPR5.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;

OC Poaceae; Oryza.

RN [1]

RP SEQUENCE FROM N.A.

RA COLE K.C.; VELAZHAHAN R.; ANURATHA C.S.; MUTHUKRISHNAN S.;

Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U77657; AAB53368.1; -.

DR HSSP; P02883; 1THU.

DR MENDEL; 13787; Orysa.Ypr5:13787.

DR PROSITE; PS00316; THAUMATIN; 1.

DR PFAM; PF00314; thaumatidin; 1.

SQ SEQUENCE 238 AA; 24779 MW; 3D0DB704 CRC32;

Query Match 67.3%; Score 37; DB 10; Length 238;

Best Local Similarity 70.0%; Pred. No. 25;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 WVAVKVSGG 10

DB 45 WPAAVPSGG 54

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RESULT 9

OBX2P4

ID OBX2P4 PRELIMINARY; PRT; 289 AA.

AC OBX2P4;

DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)

DE ALKANAL MONOOXYGENASE-LIKE HYPOTHETICAL PROTEIN.

GN AMLP.

OS Mycobacterium smegmatis.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-MC2155;

RA KIM B.-K.; CHOI K.-P.; DANIELS L.;

"The gene for F420-dependent glucose-6-phosphate dehydrogenase (fgd)

and a conserved upstream gene coding for a beta-lactamase-like protein

in Mycobacterium species.";

Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-MC2155;

RA PURWANTINI E.; DANIELS L.;

Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF041061; AAD31326.1; -.

KW Monooxygenase.

SQ SEQUENCE 289 AA; 31631 MW; BDED80D0 CRC32;

Query Match 67.3%; Score 37; DB 2; Length 289;

Best Local Similarity 50.0%; Pred. No. 30;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAVKVSGG 10

DB 203 WYISIRAGG 212

I: :||| I|

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RESULT 10
ID O55828 PRELIMINARY; PRT; 345 AA.
AC O55828;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE NS5 PROTEIN (FRAGMENT).
GN NS5.
OS Sepik virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MK7148;
RX MEDLINE; 98080391.
RA KUNO G., CHANG G.-J., TSUCHIYA K.R., KARABATSOS N., CROPP C.B.;
RT "Phylogeny of the genus Flavivirus.";
RL J. Virol. 72:73-83(1998).
DR EMBL; AF013404; AAC58792.1; -.
DR PFAM; PF00972; FlavI_NS5; 1.
FT NON_TER 1 1
FT NON_TER 345 345
SQ SEQUENCE 345 AA; 39170 MW; ADF64409 CRC32;

Query Match 67.3%; Score 37; DB 12; Length 345;
Best Local Similarity 60.0%; Pred. No. 37;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGG 10
DB 37 WVSRRGSGG 46

RESULT 11
ID Q54496 PRELIMINARY; PRT; 409 AA.
AC Q54496;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE SNO2 PROTEIN.
GN SNO2.
OS Streptomyces nogalater.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 27451;
RA YLIHONKO K.P.J.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 27451;
RX MEDLINE; 96242142.
RA YLIHONKO K., TUUKKANEN J., JUSSILA S., CONG L., MANTSALA P.;
RT "A gene cluster involved in nogalamycin biosynthesis from Streptomyces
nogalater: sequence analysis and complementation of early-block
mutations in the anthracycline pathway.";
RL Mol. Gen. Genet. 251:113-120(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 27451;
RX MEDLINE; 96349102.
RA YLIHONKO K., HAKALA J., KUNNARI T., MANTSALA P.;
RT "Production of hybrid anthracycline antibiotics by heterologous
expression of Streptomyces nogalater nogalamycin biosynthesis genes.";
RL Microbiology 142:1965-1972(1996).
RN [4]
RP SEQUENCE FROM N.A.

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RC STRAIN-ATCC 27451;
RX MEDLINE; 98007868.
RA TORIKELL S., YLIHONKO K., HAKALA J., SKURNIK M., MANTSALA P.;
RT "Characterization of Streptomyces nogalater genes encoding enzymes
involved in glycosylation steps in nogalamycin biosynthesis.";
RL Mol. Gen. Genet. 256:203-209(1997).
DR EMBL; AJ224512; CAAL2018.1; -.
DR HSP; P39435; 1B3N.
DR PFAM; PF00109; ketoacyl-synt; 1.
SQ SEQUENCE 409 AA; 42583 MW; 6555B542 CRC32;

Query Match 67.3%; Score 37; DB 2; Length 409;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVAKVSGG 9
DB 198 WVAQLSGG 206

RESULT 12
Q9X082
ID Q9X082 PRELIMINARY; PRT; 1008 AA.
AC Q9X082;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE CONSERVED HYPOTHETICAL PROTEIN.
GN TM0987.
OS Thermotoga maritima.
OC Bacteria; Thermotogales; Thermotoga.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 99287316.
RA NELSON K.E., CLAYTON R.A., GILL S.R., GWINN M.L., DODSON R.J.,
RA HAFT D.H., HICKEY E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A.,
RA McDONALD L., UTTERBACK T.R., MALEK J.A., LINHER K.D., GARRETT M.M.,
RA STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
RA HEIDELBERG J., SUTTON G.G., FLEISCHMANN R.D., WHITE O., SALZBERG S.L.,
RA SMITH H.O., VENTER J.C., FRASER C.M.;
RT "Evidence for lateral gene transfer between Archaea and bacteria from
genome sequence of Thermotoga maritima.";
RL Nature 399:323-329(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA NELSON K.E., CLAYTON R.A., GILL S.R., GWINN M.L., DODSON R.J.,
RA HAFT D.H., HICKEY E.K., PETERSON J.D., NELSON W.C., KETCHUM K.A.,
RA McDONALD L., UTTERBACK T.R., MALEK J.A., LINHER K.D., GARRETT M.M.,
RA STEWART A.M., COTTON M.D., PRATT M.S., PHILLIPS C.A., RICHARDSON D.,
RA HEIDELBERG J., SUTTON G.G., FLEISCHMANN R.D., WHITE O., SALZBERG S.L.,
RA SMITH H.O., VENTER J.C., FRASER C.M.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE001760; AAD36066.1; -.
SQ SEQUENCE 1008 AA; 115760 MW; 2BDC9F6F CRC32;

Query Match 67.3%; Score 37; DB 2; Length 1008;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVSGG 10
DB 196 WVARVKGKG 205

RESULT 13
O04013
ID O04013 PRELIMINARY; PRT; 1350 AA.
AC O04013;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)

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DE REVERSE TRANSCRIPTASE, GAG, POLYPROTEIN.
OS Volvox carteri.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Volvocaceae; Volvox.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HK10; TRANSPOSON-LUECKENBUESSE;
RA KOEHL G., PUTZ E., SCHMITT R.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U90320; AAB51275.1; -.
DR MENDEL; 15899; Volca; 2432; 15899.
DR PFAM; PF00098; zfc-CCHC; 1.
KW Polyprotein; RNA-directed DNA polymerase.
SQ SEQUENCE 1350 AA; 149847 MW; 00224067 CRC32;

Query Match 67.3%; Score 37; DB 10; Length 1350;
Best Local Similarity 87.5%; Pred. No. 1.6e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WYKVKSG 8
DB 892 WYKVKSG 899
II IIII

RESULT 14
O88457 PRELIMINARY; PRT; 1765 AA.
AC O88457;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE VOLTAGE-GATED NA CHANNEL ALPHA SUBUNIT NAN.
SN S52.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=DORSAL ROOT GANGLIA;
RX MEDLINE; 98338024.
RA DIB-HAJJ S.D., TYRRELL L., BLACK J.A., WAXMAN S.G.;
RT "Nan, a novel voltage-gated Na channel, is expressed preferentially in
RT peripheral sensory neurons and down-regulated after axotomy.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:8963-8968(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=DORSAL ROOT GANGLIA;
RA TATE S.N.;
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=DORSAL ROOT GANGLIA;
RX MEDLINE; 99212311.
RA TATE S.N., BENN S.C., HICK C.A., JOHN V.H.;
RT "Two sodium channels contribute to the TTX-R sodium current in primary
RT sensory neurons.";
RL Nat. Neurosci. 1:653-655(1998).
DR EMBL; AF059030; AAC40199.1; -.
DR EMBL; AJ237852; CAB41850.1; -.
DR PFAM; PF00520; Ion-trans; 4.
DR PRINTS; PR00170; NACHANNEL.
KW Ionic channel.
SQ SEQUENCE 1765 AA; 201844 MW; 7C0819AC CRC32;

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Query Match 67.3%; Score 37; DB 11; Length 1765;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 WYKVKSG 10
DB 1497 WYKVKSG 1506
I:IIIIII

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RESULT 15
O9XH01 PRELIMINARY; PRT; 375 AA.
ID O9XH01
AC O9XH01;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE TIN24.10 PROTEIN.
GN TIN24.10.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA WASHU;
RT "The A. thaliana Genome Sequencing Project.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA MURRAY J., LANGSTON Y., CLARKE K., DRONE K.;
RT "The sequence of A. thaliana TIN24.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA WATERSTON R.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA WATERSTON R.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF149413; AAD40130.1; -.
SQ SEQUENCE 375 AA; 44057 MW; 0FC6294F CRC32;

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Query Match 66.4%; Score 36.5; DB 10; Length 375;
Best Local Similarity 47.4%; Pred. No. 50;
Matches 9; Conservative 0; Mismatches 1; Indels 9; Gaps 1;

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QY 1 WYAK-----VKSGGG 10
    IIII      II III
DB 339 WYAKRDGFYLRIRVKDGG 357

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Search completed: May 27, 2000, 19:38:34
Job time: 2367 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:21:30 ; Search time 148.45 Seconds
(without alignments)
1.596 Million cell updates/sec

Title: US-09-016-061-54
Perfect score: 55
Sequence: 1 WYAKVSGGG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	55	100.0	10	1 W76017	LM609 grafted anti
2	50	90.9	10	1 W76008	LM609 grafted anti
3	50	90.9	117	1 W76001	Vitaxin antibody h
4	50	90.9	117	1 W76003	LM609 antibody hea
5	43	78.2	119	1 W69322	15D3 antibody heav
6	43	78.2	119	1 W73503	Antibody 15D3 heav
7	43	78.2	138	1 R20064	MRK16-H chain. Chi
8	42	76.4	119	1 W11919	Humanised MAb SK48
9	42	76.4	123	1 W66099	anti-CD22 monoclon
10	42	76.4	247	1 W11917	Murine MAb SK48-E2
11	41	74.5	110	1 W06207	Rat antibody heavy
12	41	74.5	118	1 W06208	Xenograft antibody
13	41	74.5	140	1 W06205	Xenograft antibody
14	39	70.9	119	1 R32240	Humanised MAb heav
15	39	70.9	119	1 R32243	Humanised MAb heav
16	39	70.9	119	1 R32244	Humanised MAb heav
17	39	70.9	119	1 W27144	Mature heavy chain
18	39	70.9	120	1 W00240	EGF receptor chime
19	39	70.9	122	1 R25722	Humanised VH regio
20	39	70.9	131	1 R70466	VH sequence of ant
21	39	70.9	138	1 R32242	Chimeric MAb heav
22	39	70.9	138	1 R32246	BR55-2 murine IgG3
23	39	70.9	139	1 R31588	BR55-2 heavy chain
24	39	70.9	139	1 R52773	Murine KC-4 immuno
25	39	70.9	139	1 R52791	Murine KC-4 immuno
26	39	70.9	139	1 R52823	Humanised murine K
27	39	70.9	139	1 R70471	Humanised anti-KC-
28	39	70.9	623	1 W02284	Candida albicans l
29	38	69.1	115	1 R04939	Chelate-specific h
30	38	69.1	115	1 R05039	Metal chelate spec
31	38	69.1	115	1 R54137	CHA255 heavy chain
32	37	67.3	13	1 W86105	Peptide from human
33	37	67.3	13	1 W86092	Peptide from human
34	37	67.3	13	1 W86100	Peptide from human

35	37	67.3	98	1	R72075	OF7H1.19 VH-3 H ch
36	37	67.3	108	1	R95283	Anti-proenkephalin
37	37	67.3	108	1	R91364	Anti-proenkephalin
38	37	67.3	116	1	R79245	Heavy chain variab
39	37	67.3	116	1	R79246	Heavy chain variab
40	37	67.3	117	1	W48865	Murine monoclonal
41	37	67.3	117	1	W48866	Chimeric humanized
42	37	67.3	117	1	W86135	Protein sequence o
43	37	67.3	117	1	W86137	Protein sequence o
44	37	67.3	117	1	W86139	Protein sequence o
45	37	67.3	117	1	W86141	Protein sequence o

ALIGNMENTS

RESULT 1

W76017
ID W76017 standard; Protein; 10 AA.
AC W76017:
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR2 protein fragment #3.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis; primer; V-H region; CDR;
complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
N-PSDB: V49854.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
integrin - and related grafted antibodies based on murine monoclonal
LM609, also related nucleic acid, used to treat, prevent or diagnose
angiogenesis or restenosis
Claim 61: Page 41: 129pp: English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
LM609 heavy and light chain variable region. LM609 and the antibody
vitaxin bind selectively to integrin alphavbeta3 and can be used to
inhibit binding of alphavbeta3 to a ligand and thus block
integrin-mediated signal transduction. This is useful in the treatment,
prevention and diagnosis of alphavbeta3-mediated disease, specifically
angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
arthritis, macular degeneration, osteoporosis etc.). The antibodies
contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00074;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 WYAKVSGGG 10
|||||
Db 1 WYAKVSGGG 10

RESULT 2

W76008
ID W76008 standard; Protein; 10 AA.
AC W76008:
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR2 protein fragment #1.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PR 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49845.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Disclosure: Page 40; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0054;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 DB 1 WVAKVSGGG 10

RESULT 3
 W76001
 ID W76001 standard; Protein; 117 AA.
 AC W76001;
 DT 02-NOV-1998 (first entry)
 DE Vitaxin antibody heavy chain variable region protein fragment.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PR 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49820.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 1; Fig 1a; 129pp; English.
 CC This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated

CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 SQ Sequence 117 AA;

Query Match 90.9%; Score 50; DB 1; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.069;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 DB 47 WVAKVSGGG 56

RESULT 4
 W76003
 ID W76003 standard; Protein; 117 AA.
 AC W76003;
 DT 02-NOV-1998 (first entry)
 DE LM609 antibody heavy chain variable region protein fragment.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PR 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49822.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 43; Fig 2a; 129pp; English.
 CC This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 SQ Sequence 117 AA;

Query Match 90.9%; Score 50; DB 1; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.069;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 WVAKVSGGG 10
 DB 47 WVAKVSGGG 56

RESULT 5
 W69322
 ID W69322 standard; Protein; 119 AA.
 AC W69322;
 DT 19-NOV-1998 (first entry)
 DE 15D3 antibody heavy chain.
 KW Hybridoma 15D3; 15D3 antibody; complementarity-determining region; scFv;

KW single-chain antibody molecule; multidrug-resistant human tumour cell;
 OS MDR tumour; CDR; therapy; heavy chain.
 FH Homo sapiens.
 FT Key Location/Qualifiers
 FT Region 1..30 "HFR1"
 FT Region /note= "HFR1"
 FT Region 31..35
 FT Region /note= "HCDR1"
 FT Region 36..49
 FT Region /note= "HFR2"
 FT Region 50..66
 FT Region /note= "HCDR2"
 FT Region 67..98
 FT Region /note= "HFR3"
 FT Region 99..108
 FT Region /note= "HCDR3"
 FT Region 109..119
 FT Region /note= "HFR4"
 PN US5811267-A.
 PD 22-SEP-1998.
 PF 07-JUN-1995; 475000.
 PR 07-JUN-1995; US-475000.
 PR 29-OCT-1990; US-605399.
 PR 22-OCT-1993; US-141375.
 PR 17-OCT-1994; US-323566.
 PA (CHIR) CHIRON CORP.
 PI Ring DB;
 DR WPI; 98-530873/45.
 DR N-PSDB; V44997.
 PT DNA encoding single-chain antibody molecule - specific for
 PT multidrug-resistant tumour cells, useful in diagnosis or therapy
 PS Disclosure; Fig 1: 26pp; English.
 CC This sequence represents the VH chain of the antibody
 CC produced by hybridoma cell line 15D3. It is part of the nucleic acid of
 CC the invention which encodes a single-chain antibody molecule (scFv)
 CC comprising the heavy-chain complementarity-determining regions (CDRs) of
 CC the monoclonal antibody produced by hybridoma cell line 15D3, where the
 CC monoclonal antibody and scFv are capable of binding to
 CC multidrug-resistant (MDR) human tumour cells. The CDR sequences from both
 CC the heavy and light chains (HCDR1, HCDR2, HCDR3, LCDR1, LCDR2, and LCDR3)
 CC are all used in an expression cassette that can be used in a method for
 CC inducing the production of a polypeptide. The method is useful for
 CC producing recombinant scFv, which can be used for diagnosis or therapy
 CC (e.g. in the form of an immunotoxin) for MDR tumours.
 SQ Sequence 119 AA;
 Query Match 78.2%; Score 43; DB 1; Length 119;
 Best Local Similarity 70.0%; Pred. No. 1.1;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 WVAKVKSGGG 10
 Db 47 WVAATISSGGG 56
 RESULT 6
 ID W73503 standard; Protein; 119 AA.
 AC W73503;
 DT 26-FEB-1999 (first entry)
 DE Antibody 15D3 heavy chain protein sequence.
 KW Antibody; 15D3; human; tumour cell; multiple drug resistance; cancer;
 KW Immunotherapy; heavy chain.
 OS Homo sapiens.
 PN US5849877-A.
 PD 15-DEC-1998.
 PF 07-JUN-1995; 483199.
 PR 07-JUN-1995; US-483199.
 PR 29-OCT-1990; US-605399.
 PR 22-OCT-1993; US-141375.
 PR 17-OCT-1994; US-323566.
 PA (CHIR) CHIRON CORP.

PI Ring DB;
 DR WPI; 99-069805/06.
 DR N-PSDB; V08933.
 PT Monomeric and dimeric poly-peptide(s) - which bind to human tumour
 PT cell displaying multiple drug resistance
 PS Claim 1; Fig 1; 26pp; English.
 CC This sequence represents the heavy chain of the antibody produced by
 CC the hybridoma 15D3. The protein is an example of a monomeric
 CC polypeptide of the invention that binds to a human tumour cell displaying
 CC multiple drug resistance. The polypeptides are used in specific binding
 CC assays, affinity purification, drug or toxin targeting, imaging or
 CC immunotherapy of various cancers.
 SQ Sequence 119 AA;
 Query Match 78.2%; Score 43; DB 1; Length 119;
 Best Local Similarity 70.0%; Pred. No. 1.1;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 WVAKVKSGGG 10
 Db 47 WVAATISSGGG 56
 RESULT 7
 ID R20064 standard; Protein; 138 AA.
 AC R20064;
 DT 27-MAR-1992 (first entry)
 DE MRK16-H chain.
 KW Monoclonal antibody; light; heavy; chain; cancer; drug resistance.
 OS Chimeric Homo sapiens;
 OS Chimeric Mus musculus.
 PN J03254691-A.
 PD 13-NOV-1991.
 PR 02-MAR-1990; 051563.
 PR 02-MAR-1990; JP-051563.
 PA (GANK-) ZH GAN KENKYUKAI.
 PA FUJII-) FUJITA GAKUEN GH.
 DR WPI; 92-002461/01.
 DR N-PSDB; Q20070.
 PT Chimera antibody against drug resistant cancer - comprises
 PT variable region homologous to region in mouse monoclonal antibody
 PT and constant region homologous to region in human immunoglobulin
 PS Disclosure; Fig 4; 20pp; Japanese.
 CC A chimeric antibody against drug-resistant cancer consists of
 CC (1) a variable region having an amino acid sequence homologous to
 CC a variable region in the mouse monoclonal antibody against drug-
 CC resistance and (2) a constant region having an amino acid sequence
 CC homologous to the constant region in human immunoglobulin.
 CC The chimeric antibody selectively inhibits the growth of cancer
 CC cells showing drug resistance or enhances the sensitivity to the
 CC drug. The antibody is very low in immunogenicity.
 CC The MRK16-L chain is shown in Q20071.
 SQ Sequence 138 AA;
 Query Match 78.2%; Score 43; DB 1; Length 138;
 Best Local Similarity 70.0%; Pred. No. 1.3;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 WVAKVKSGGG 10
 Db 66 WVAATISSGGG 75
 RESULT 8
 ID W11919 standard; Protein; 119 AA.
 AC W11919;
 DT 24-JUN-1997 (first entry)
 DE Humanised MAB SK48-E26 heavy chain.
 KW Interleukin-1 beta; IL-1 beta; recombinant antibody;

KW humanised antibody; chimeric antibody; antibody engineering;
 KW monoclonal antibody; MAB; SK48-E26; inflammation; therapy.
 OS Chimeric Homo sapiens;
 OS Chimeric Mus sp.
 FH Key Location/Qualifiers
 FT region 1..30
 FT /label= FR1
 FT /note= "framework region 1"
 FT region 31..35
 FT /label= CDR1
 FT /note= "complementarity determining region 1
 FT (Claim 10, page 48)"
 FT region 36..49
 FT /label= FR2
 FT /note= "framework region 2"
 FT region 50..66
 FT /label= CDR2
 FT /note= "complementarity determining region 2
 FT (Claim 10, page 48)"
 FT region 67..98
 FT /label= FR3
 FT /note= "framework region 3"
 FT region 99..108
 FT /label= CDR3
 FT /note= "complementarity determining region 3
 FT (Claim 10, page 48)"
 FT region 109..119
 FT /label= FR4
 FT /note= "framework region 4"
 FT W09501997-A1.
 PN 19-JAN-1995.
 PD 07-JUL-1994; U07659.
 PF 09-JUL-1993; US-090534.
 PR 04-MAR-1994; US-206190.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PI Gross MS, Hurler MR, Jackson JR, Jonak ZL, Theisen TW;
 PI Young PR;
 PI WPI: 95-066868/09.
 DR N-PSDB; T51438
 DR N-PSDB; T51438
 PT Recombinant and humanised chimeric antibodies against human
 PT interleukin-1-beta - for preventing and treating
 PT interleukin-mediated inflammatory disorders
 PS Claim 39; Page 40-41; 62pp; English.
 CC The heavy chain variable region (W1919) and light chain variable
 CC region (W1920) of humanised anti-human interleukin-1 beta (IL-1
 CC beta) murine monoclonal antibody (MAB) SK48-E26 comprise the
 CC complementarity determining regions from MAB SK48-E26 (see also
 CC W1917-18) grafted into human frameworks. The humanised antibody
 CC can be produced in e.g. COS cells transfected with vectors carrying
 CC humanised heavy and light chain nucleic acids (T51437-39) for use
 CC in the treatment and prevention of IL-1 mediated inflammatory
 CC disorders.
 SQ Sequence 119 AA;

Query Match 76.4%; Score 42; DB 1; Length 119;
 Best Local Similarity 70.0%; Pred. NO. 1.7;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAVKSGGG 10
 III : IIII
 Db 47 WWAYISSGGG 56

RESULT 9

W66099
 ID W66099 standard; Protein; 123 AA.

AC W66099;
 DT 10-DEC-1998 (first entry)
 DE anti-CD22 monoclonal antibody heavy chain variable region.
 KW anti-CD22 monoclonal antibody heavy chain variable region; VL;
 KW Pseudomonas exotoxin; variable heavy chain; VH; variable light chain;
 KW malignant B-cell; immunodiagnosis; RFB4 IgG.

OS Mammalia.
 FH Key Location/Qualifiers
 FT Misc_difference 121
 FT /note= "Encoded by gtc"
 PN W09841641-A1.
 PD 24-SEP-1998.
 PF 19-MAR-1998; U05453.
 PR 20-MAR-1997; US-041437.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PI Fitzgerald D, Kreitman R, Mansfield E, Pastan I;
 DR WPI: 98-521227/44.
 DR N-PSDB; V07642.
 PT Recombinant anti-CD22 antibodies and immuno-conjugates - of
 PT antibodies linked to a therapeutic agent, e.g. Pseudomonas exotoxin
 PT or a label; for inhibiting malignant B-cells
 PS Claim 6; Fig 1; 7lpp; English.
 CC The invention claims for a recombinant immunoconjugate comprising
 CC of a therapeutic agent (e.g. Pseudomonas exotoxin) or a detectable
 CC label peptide bonded to a recombinant anti-CD22 antibody (RFB4 IgG)
 CC having the present variable heavy (VH) chain with a cysteine residue
 CC at amino acid 44 and a variable light (VL; W66098) chain with a
 CC cysteine residue at amino acid 100. The immunoconjugate is claimed
 CC to inhibit the growth of malignant B-cells in vivo, such as rodent,
 CC canine or primate B-cells. The anti-CD22 antibody is claimed useful
 CC for detecting CD22 protein in a sample or in vivo in a mammal, and
 CC can be used in diagnostic kits.
 SQ Sequence 123 AA;

Query Match 76.4%; Score 42; DB 1; Length 123;
 Best Local Similarity 70.0%; Pred. NO. 1.7;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAVKSGGG 10
 III : IIII
 Db 47 WWAYISSGGG 56

RESULT 10

W1917
 ID W1917 standard; Protein; 247 AA.

AC W1917;
 DT 24-JUN-1997 (first entry)
 DE Murine MAb SK48-E26 heavy chain.
 DE Interleukin-1 beta; IL-1 beta; recombinant antibody;
 KW Interleukin-1 beta; chimeric antibody; antibody engineering;
 KW humanised antibody; MAB; SK48-E26; inflammation; therapy.
 OS Homo sapiens.

FH Key Location/Qualifiers
 FT peptide 1..19
 FT /label= Sig_peptide
 FT region 20..49
 FT /label= FR1
 FT /note= "framework region 1"
 FT region 50..54
 FT /label= CDR1
 FT /note= "complementarity determining region 1
 FT (Claim 10, page 48)"
 FT region 55..68
 FT /label= FR2
 FT /note= "framework region 2"
 FT region 69..85
 FT /label= CDR2
 FT /note= "complementarity determining region 2
 FT (Claim 10, page 48)"
 FT region 86..117
 FT /label= FR3
 FT /note= "framework region 3"
 FT region 118..127
 FT /label= CDR3
 FT /note= "complementarity determining region 3
 FT (Claim 10, page 48)"
 FT region 128..138

FT /label= FR4
 FT /note= "framework region 4"
 FT 139..247
 FT /label= Constant_region
 PN W09501997-A1.
 PD 19-JAN-1995.
 PF 07-JUL-1994; U07659.
 PR 09-JUL-1993; US-090534.
 PR 04-MAR-1994; US-206190.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PI GROSS MS, Hurle MR, Jackson JR, Jonak ZL, Theisen TW;
 PI Young PR;
 DR WPI; 95-066868/09.
 DR N-PSDB; T51436.
 PT Recombinant and humanised chimeric antibodies against human
 PT interleukin-1-beta - for preventing and treating
 PT interleukin-mediated inflammatory disorders
 PS Claim 5; Page 36-37; 62pp; English.
 CC Amino acid sequences of the heavy chain (W1917) and light chain
 CC (W11918) of anti-human interleukin-1 beta (IL-1 beta) murine
 CC monoclonal antibody (WAB) SK48-E26 were deduced from nucleic acids
 CC (T51436-37) derived from hybridoma SK48-E26. The heavy and light
 CC chains, esp. the complementarity determining region sequences,
 CC can be utilised in novel recombinant chimeric and humanised
 CC antibodies (see also W11919-20) useful for the treatment and
 CC prevention of IL-1 mediated inflammatory disorders.
 SQ Sequence 247 AA;

Query Match 76.4%; Score 42; DB 1; Length 247;
 Best Local Similarity 70.0%; Pred. No. 3.6;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYAKVSGGG 10
 ||| : |||
 Db 66 WWAYISSGGG 75

RESULT 11
 W06207
 ID W06207 standard; Protein; 110 AA.
 AC W06207;
 DE 17-FEB-1997 (first entry)
 DE Rat antibody heavy chain variable region.
 KW Xenograft rejection; xenotransplantation; organ transplant;
 KW animal model; hamster; monoclonal antibody; HAR-1.
 OS Rattus sp.
 FH Key Location/Qualifiers
 FT region 1..19
 FT /label= Leader
 FT misc_difference 11
 FT /note= "amino acid 11 is Leu in HAR-1 VH encoded
 FT by a cDNA clone"
 FT region 20..49
 FT /label= FR-1
 FT /note= "framework region 1"
 FT region 50..54
 FT /label= CDR-1
 FT /note= "complementarity determining region 1"
 FT region 55..68
 FT /label= FR-2
 FT /note= "framework region 2"
 FT region 69..85
 FT /label= CDR-2
 FT /note= "complementarity determining region 2"
 FT region 86..110
 FT /label= FR-3
 FT /note= "framework region 3"

PN W09636358-A1.
 PD 21-NOV-1996.
 PF 14-MAY-1996; U06804.
 PR 15-MAY-1995; US-440621.
 PA (CEDA-) CEDARS SINAI MEDICAL CENT.

PI Cramer DV, Makowka L, Wu G;
 DR WPI; 97-011852/01.
 DR N-PSDB; T43416.
 PT Inhibiting xenograft rejection by modifying antigen expression of
 PT the graft - prevents binding of anti-donor antibody and prolongs
 PT graft survival
 PS Disclosure; Page 102-103; 135pp; English.
 CC A polypeptide (W06207) comprises the variable heavy chain segment
 CC of a LEW rat antibody, and is encoded by a genomic DNA clone
 CC (T43416) obt'd. from a newborn LEW rat. It differs in 1 position
 CC from the VH region of LEW rat anti-hamster xenograft antibody
 CC HAR-1 (W06205). Evidence is provided that the hyperacute
 CC rejection of xenografts is mediated by polyreactive anti-donor
 CC xenograft antibodies having VH germline configurations.
 SQ Sequence 110 AA;

Query Match 74.5%; Score 41; DB 1; Length 110;
 Best Local Similarity 60.0%; Pred. No. 2.3;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WYAKVSGGG 10
 ||| : |||
 Db 66 WVASISTGGG 75

RESULT 12
 W06208
 ID W06208 standard; Protein; 118 AA.
 AC W06208;
 DT 17-FEB-1997 (first entry)
 DE Xenograft antibody ID12BF3 heavy chain variable region.
 KW Xenograft rejection; xenotransplantation; organ transplant;
 KW animal model; hamster; monoclonal antibody; ID12BF3.
 OS Rattus sp.
 FH Key Location/Qualifiers
 FT region 1..98
 FT /label= VH-Segment
 FT /note= "variable segment of heavy chain variable
 FT region" 99..103
 FT /label= D-Segment
 FT /note= "diversity segment of heavy chain variable
 FT region" 104..118
 FT /label= JH-Segment
 FT /note= "joining segment of heavy chain variable
 FT region" 1..30
 FT /label= FR-1
 FT /note= "framework region 1"
 FT region 31..35
 FT /label= CDR-1
 FT /note= "complementarity determining region 1"
 FT region 36..49
 FT /label= FR-2
 FT /note= "framework region 2"
 FT region 50..66
 FT /label= CDR-2
 FT /note= "complementarity determining region 2"
 FT region 67..98
 FT /label= FR-3
 FT /note= "framework region 3"
 FT region 99..107
 FT /label= CDR-3
 FT /note= "complementarity determining region 3"
 FT region 108..118
 FT /label= FR-4
 FT /note= "framework region 4"
 PN W09636358-A1.
 PD 21-NOV-1996.
 PF 14-MAY-1996; U06804.
 PR 15-MAY-1995; US-440621.

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PA (CEDA-) CEDARS SINAI MEDICAL CENT.
PI Cramer DV, Makowka L, Wu G;
DR N-PSDB; T43417.
DR Inhibiting xenograft rejection by modifying antigen expression of
PT the graft - prevents binding of anti-donor antibody and prolongs
PT graft survival
PS Claim 13; Page 96; 135pp; English.
CC A polypeptide (W06208) comprises the variable heavy chain segment
CC of the LEW rat anti-hamster xenograft monoclonal antibody ID12BF3.
CC It is encoded by a cDNA clone (T43417) obtd. from a ID12BF3
CC hybridoma heavy chain cDNA library; the hybridoma was produced by
CC fusing spleen cells of a LEW rat that had received a hamster heart
CC transplant, with rat myeloma cells. Recombinant fragments, e.g.
CC F(ab')2 and Fab', of the antibody block binding of preformed
CC anti-donor xenograft antibodies in a recipient animal serum to
CC antigen expressed by endothelial cells of the xenograft, i.e. they
CC inhibit antibody-mediated rejection, thereby prolonging the
CC survival of the hamster xenograft in the recipient.
SQ Sequence 118 AA;

Query Match 74.5%; Score 41; DB 1; Length 118;
Best Local Similarity 60.0%; Pred. No. 2.5;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVKGSGG 10
   ||| : |||
DB 47 WVASISTGGG 56

RESULT 13
W06205
ID W06205 standard; Protein; 140 AA.
AC W06205;
DE Xenograft antibody HAR-1 heavy chain variable region.
KW Xenograft rejection; xenotransplantation; organ transplant;
KW animal model; hamster; monoclonal antibody; HAR-1.
OS Rattus sp.
FH Key Location/Qualifiers
FT 1..19
FT /label= Leader
FT misc_difference 11
FT /note= "amino acid 11 is val in HAR-1 VH encoded
FT by a genomic clone"
FT 20..117
FT /label= VH-Segment
FT /note= "variable segment of heavy chain variable
FT region"
FT 118..122
FT /label= D-Segment
FT /note= "diversity segment of heavy chain variable
FT region"
FT 123..140
FT /label= JH-Segment
FT /note= "joining segment of heavy chain variable
FT region"
FT 20..49
FT /note= FR-1
FT /label= "framework region 1"
FT 50..54
FT /label= CDR-1
FT /note= "complementarity determining region 1"
FT 55..68
FT /label= FR-2
FT /note= "framework region 2"
FT 69..85
FT /label= CDR-2
FT /note= "complementarity determining region 2"
FT 86..117
FT /label= FR-3
FT /note= "framework region 3"

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FT region 118..129
FT /label= CDR-3
FT /note= "complementarity determining region 3"
FT 130..140
FT /label= FR-4
FT /note= "framework region 4"
PN W09636358-A1.
PD 21-NOV-1996.
PF 14-MAY-1996; U06804.
PF 15-MAY-1995; US-440621.
PA (CEDA-) CEDARS SINAI MEDICAL CENT.
PI Cramer DV, Makowka L, Wu G;
DR WPI; 97-011852/01.
DR N-PSDB; T43414.
PT Inhibiting xenograft rejection by modifying antigen expression of
PT the graft - prevents binding of anti-donor antibody and prolongs
PT graft survival
PS Claim 9; Page 92-93; 135pp; English.
CC A polypeptide (W06205) comprises the variable heavy chain segment
CC of the LEW rat anti-hamster xenograft monoclonal antibody HAR-1.
CC It is encoded by a cDNA clone (T43414) obtd. from a HAR-1
CC hybridoma heavy chain cDNA library; the hybridoma was produced by
CC fusing spleen cells of a LEW rat that had received a hamster heart
CC transplant, with rat myeloma cells. Recombinant fragments, e.g.
CC F(ab')2 and Fab', of the antibody block binding of preformed
CC anti-donor xenograft antibodies in a recipient animal serum to
CC antigen expressed by endothelial cells of the xenograft, i.e. they
CC inhibit antibody-mediated rejection, thereby prolonging the
CC survival of the hamster xenograft in the recipient.
SQ Sequence 140 AA;

Query Match 74.5%; Score 41; DB 1; Length 140;
Best Local Similarity 60.0%; Pred. No. 3;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 WVAKVKGSGG 10
   ||| : |||
DB 66 WVASISTGGG 75

RESULT 14
R32240
ID R32240 standard; Protein; 119 AA.
AC R32240;
DE Humanised MAB heavy chain variable region H-hu-BR55-2/1 clone.
KW Monoclonal; antibody; MAB; light; heavy; chain; variable; region;
KW human/mouse; chimeric; difucosyl; Lewis; blood group; murine; BR55-2;
KW expression vector; IgG1; IgG3; pVg; pVg3; gamma; kappa; constant;
KW pVg1c; pVg3c; PCR; plasmid; host cell; sp2/O-Ag 14; electroporation;
KW antigen; Y-6; B-7-2; binding specificity; erythrocyte; diagnosis;
KW cancer; epithelial; breast; colorectal; ovarian; prostate; pancreatic;
KW gastric; small cell lung; immunotherapy; HIV; pVg2; pVg3h; pVg4.
OS Synthetic.
FH Key Location/Qualifiers
FT 31..35
FT /label= CDR1
FT /note= "Claim 8"
FT 50..66
FT /label= CDR2
FT /note= "Claim 8"
FT 99..108
FT /label= CDR3
FT /note= "Claim 8"
PN EP-528767-A.
PD 24-FEB-1993.
PF 18-AUG-1992; 810633.
PR 21-AUG-1991; GB-018013.
PR 02-MAR-1992; GB-004514.
PA (SANO ) SANDOZ LTD.
PA (SANO ) SANDOZ PATENT GMBH.
PA (SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.

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PI Co MS, Loibner H;
 DR WPI: 93-060580/08.
 PT Human-mouse chimeric monoclonal antibodies - recognise di:fucoyl
 PT Lewis blood group antigens Y-6 and B-7-2, useful for treating
 PT cancer and HIV infection
 PS Claim 7: Page 20; 65pp; English.
 CC The sequences given in R32239-40 and R32243-44 represent the light and
 CC heavy chain variable regions respectively from a humanised chimeric
 CC monoclonal antibody (MAB) which recognises the difucosyl Lewis blood
 CC group. The murine MAB BR55-2 was used as a basis for the construction
 CC of this chimeric MAB. Separate expression vectors were used to
 CC express the chimeric human BR55-2 IgG1 and IgG3 antibody light and
 CC heavy chains: pVg for the light chain, pVg1h for the gamma 1 heavy
 CC chain and pVg2, pVg3h and pVg4 for the human gamma-2, -3 and -4 heavy
 CC chains respectively. The actual expressed chimeric BR55-2 light
 CC and pVg1c (or pVg3c) respectively and the variable regions were
 CC constructed by PCR. The resulting plasmids were used to transfect the
 CC host cell line sp2/O-Ag 14 by electroporation. The resulting MABs
 CC recognise the difucosyl Lewis blood group antigens Y-6 and B-7-2 but
 CC do not induce human anti-mouse antibody response. The MABs show a
 CC restricted binding specificity which is associated with a lack of
 CC cross-reactivity to related antigens expressed on blood cells eg.
 CC erythrocytes. This allows the MABs to be particularly useful for
 CC therapeutic use in humans. The MABs are useful in the diagnosis and
 CC treatment of cancer of epithelial origin, eg. breast, colorectal,
 CC ovarian, prostate, pancreatic or gastric cancer and small cell lung
 CC cancer. The MABs are also useful for immunotherapy of HIV infections
 CC since the Lewis Y antigen is also selectively expressed on HIV
 CC infected cells.
 SQ Sequence 119 AA;

Query Match 70.9%; Score 39; DB 1; Length 119;
 Best Local Similarity 60.0%; Pred. No. 5.6;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 WVAKVSGGG 10
 ||||:||||
 Db 47 WVAISNGGG 56

RESULT 15
 R32243
 ID R32243 standard; Protein; 119 AA.
 AC R32243;
 DT 09-JUN-1993 (first entry)
 DE Humanised MAB heavy chain variable region H-hu-BR55-2/2 clone.
 KW Monoclonal; antibody; MAB; light; heavy; chain; variable; region;
 KW human/mouse; chimeric; difucosyl; Lewis; blood group; murine; BR55-2;
 KW expression vector; IgG1; IgG3; pVg; pVg3; gamma; kappa; constant;
 KW pVg1c; pVg3c; PCR; plasmid; host cell; sp2/O-Ag 14; electroporation;
 KW antigen; Y-6; B-7-2; binding specificity; erythrocyte; diagnosis;
 KW cancer; epithelial; breast; colorectal; ovarian; prostate; pancreatic;
 KW gastric; small cell lung; immunotherapy; HIV; pVg2; pVg3h; pVg4.
 OS Synthetic.
 FH Key
 FT region 31..35 Location/Qualifiers
 FT /label= CDR1
 FT /note= "Claim 8"
 FT region 50..66
 FT /label= CDR2
 FT /note= "Claim 8"
 FT region 99..108
 FT /label= CDR3
 FT /note= "Claim 8"
 PN EP-528767-A.
 PD 24-FEB-1993.
 PF 18-AUG-1992; 810633.
 PR 21-AUG-1991; GB-018013.
 PR 02-MAR-1992; GB-004514.
 PA (SANO) SANDOZ LTD.

PA (SANO) SANDOZ PATENT GMBH.
 PI (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
 Co MS, Loibner H;
 DR WPI: 93-060580/08.
 PT Human-mouse chimeric monoclonal antibodies - recognise di:fucoyl
 PT Lewis blood group antigens Y-6 and B-7-2, useful for treating
 PT cancer and HIV infection
 PS Claim 7: Page 20; 65pp; English.
 CC The sequences given in R32239-40 and R32243-44 represent the light and
 CC heavy chain variable regions respectively from a humanised chimeric
 CC monoclonal antibody (MAB) which recognises the difucosyl Lewis blood
 CC group. The murine MAB BR55-2 was used as a basis for the construction
 CC of this chimeric MAB. Separate expression vectors were used to
 CC express the chimeric human BR55-2 IgG1 and IgG3 antibody light and
 CC heavy chains: pVg for the light chain, pVg1h for the gamma 1 heavy
 CC chain and pVg2, pVg3h and pVg4 for the human gamma-2, -3 and -4 heavy
 CC chains respectively. The actual expressed chimeric BR55-2 light
 CC chain gene and the heavy chain gene consist of two adjacent parts.
 CC The kappa/gamma constant regions were built into the vectors pVg
 CC and pVg1c (or pVg3c) respectively and the variable regions were
 CC constructed by PCR. The resulting plasmids were used to transfect the
 CC host cell line sp2/O-Ag 14 by electroporation. The resulting MABs
 CC recognise the difucosyl Lewis blood group antigens Y-6 and B-7-2 but
 CC do not induce human anti-mouse antibody response. The MABs show a
 CC restricted binding specificity which is associated with a lack of
 CC cross-reactivity to related antigens expressed on blood cells eg.
 CC erythrocytes. This allows the MABs to be particularly useful for
 CC therapeutic use in humans. The MABs are useful in the diagnosis and
 CC treatment of cancer of epithelial origin, eg. breast, colorectal,
 CC ovarian, prostate, pancreatic or gastric cancer and small cell lung
 CC cancer. The MABs are also useful for immunotherapy of HIV infections
 CC since the Lewis Y antigen is also selectively expressed on HIV
 CC infected cells.
 SQ Sequence 119 AA;

Query Match 70.9%; Score 39; DB 1; Length 119;
 Best Local Similarity 60.0%; Pred. No. 5.6;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 WVAKVSGGG 10
 ||||:||||
 Db 47 WVAISNGGG 56

Search completed: May 27, 2000, 19:21:31
 Job time: 1585 sec

CC immunoglobulin E (IgE) receptor, MAb. The humanised, semi-chimeric
CC or chimeric MAb can be used to treat or prevent diseases,
CC specifically allergies, associated with the receptor, and has very
CC low antigenicity in humans.
SQ Sequence 117 AA;

Query Match 79.2%; Score 42; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.79;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
|||||
Db 57 STYYPDTVKG 66

RESULT 15
W27354
ID W27354 standard; Protein; 117 AA.
AC W27354;
DT 16-DEC-1997 (first entry)
DE Heavy chain variable region of human CRA2 antibody.
KW Complementarity determining region; CDR; murine; mouse; human;
KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
KW IgE; MAb; heavy chain; variable region; humanised; semi-chimeric;
KW chimeric; treatment; prevention; disease; allergy; CRA2.
OS Homo sapiens.
PN J09191886-A.
PD 29-JUL-1997.
PF 19-JAN-1996; 024816.
PR 19-JAN-1996; JP-024816.
PA (ASAK) ASahi BREWERIES LTD.
PA (NIKK-) NIKKA WHISKEY KK.
PA (TORI) TORII YAKUHIIN KK.
PA (TSUR/) TSURA T.
DR WPI; 97-429186/40.
DR N-PSDB; T90025.
PT Humanised, semi-chimeric and chimeric antibodies against human
PT high-affinity IgE receptor - useful medicinally and have low
PT antigenicity in humans
PS Disclosure; Fig 1; 26pp; Japanese.
CC The cDNA encoding the present sequence, the heavy chain variable
CC region of the human antibody (Ab) CRA2, was used in the preparation
CC of a humanised or semi-chimeric monoclonal Ab (MAb), comprising
CC complementarity determining regions (CDR) from a murine, anti-human
CC high affinity immunoglobulin E (IgE) receptor, MAb. The humanised,
CC semi-chimeric or chimeric MAb can be used to treat or prevent
CC diseases, specifically allergies, associated with the receptor, and
CC has very low antigenicity in humans.
SQ Sequence 117 AA;

Query Match 79.2%; Score 42; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.79;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
|||||
Db 57 STYYPDTVKG 66

Search completed: May 27, 2000, 19:21:33
Job time: 1587 sec


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Query Match      79.2%; Score 42; DB 1; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.09;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTRVEG 10
    ||||| |||||
Db 8 STYYPDTRVKG 17

RESULT 12
R79155
ID R79155 standard; peptide; 117 AA.
AC R79155;
DT 04-MAR-1996 (first entry)
DE Human IgE receptor-binding antibody-related peptide heavy chain.
KW Immunoglobulin E; antibody; receptor; monoclonal; detection;
KW Complementarity determining region.
OS Mus sp.
FH Key
FT region
FT 31..35
FT /label= CDR1H
FT /note="all CDR regions are claimed"
FT region
FT 50..66
FT /label= CDR2H
FT /note="all CDR regions are claimed"
FT region
FT 99..106
FT /label= CDR3H
FT /note="all CDR regions are claimed"
FT J07165799-A.
PN 27-JUN-1995.
PD 22-OCT-1993; 264792.
PR 22-OCT-1993; JP-264792.
PA (ASAK ) ASAKI BREWERIES LTD.
PA (NIKK-) NIKKA WHISKEY KK.
PA (TORI ) TORII YAHUKIN KK.
PA (TSUR/) TSURA T.
DR WPI: 95-261292/34.
DR N-PSDB; Q96282.
PT Novel monoclonal antibody against human high-affinity IgE receptor -
PT and DNA fragment encoding the MAb, for the specific identification
PT of human Fc-epsilon RI
PS Claim 3; Page 13; 20pp; Japanese.
CC Polypeptides which specifically recognise human IgE receptor (Fc-
CC epsilon-RI) have been isolated and sequenced. The new peptides are
CC related to a monoclonal antibody against Fc-epsilon-RI and are
CC either heavy or light chain molecules. The heavy chain molecules
CC have the general formula FR1-CDR1H-FR2-CDR2H-FR3-CDR3H-FR4 (corresp.
CC to R79153, R79155, R79157, R79159 and R79161) and are encoded by
CC Q96280, Q96282, Q96284, Q96286 and Q96288. FR1 is a polypeptide
CC having 29-36 amino acids (aa), FR2 is a 10-16 aa polypeptide, FR3 is
CC a 33-35 aa polypeptide and FR4 is a 12-14 aa polypeptide. Similarly
CC the light chains have the general formula FR5-CDR1L-FR6-CDR2L-FR7-
CC CDR3L-FR8, (corresp. to R79154, R79156, R79158, R79160 and R79162)
CC and are encoded by Q96281, Q96283, Q96285, Q96287 and Q96289. FR5
CC is a 23-28 aa polypeptide, FR6 is a 14-16 aa polypeptide, FR7 is a
CC 30-34 aa polypeptide and FR8 is a 9-11 aa polypeptide. All the
CC peptides are derived from mouse hybridoma cells and are useful in
CC the detection of the human Fc-epsilon-RI or for the elucidation of
CC an antigen recognising region of a monoclonal antibody against
CC human Fc-epsilon-RI.
SQ Sequence 117 AA;

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Query Match      79.2%; Score 42; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.79;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTRVEG 10
    ||||| |||||
Db 57 STYYPDTRVKG 66

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RESULT 13
W27357
ID W27357 standard; Protein; 117 AA.
AC W27357;
DT 16-DEC-1997 (first entry)
DE Heavy chain variable region of chimeric human CRA2 antibody.
KW Complementarity determining region; CDR; murine; mouse; human;
KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
KW IgE; MAb; heavy chain; variable region; humanised; semi-chimeric;
KW chimeric; treatment; prevention; disease; allergy; CRA2.
OS Chimeric - Homo sapiens.
OS Chimeric - Mus spp.
OS Synthetic.
PN J09191886-A.
PD 29-JUL-1997.
PR 19-JAN-1996; 024816.
PR 19-JAN-1996; JP-024816.
PA (ASAK ) ASAKI BREWERIES LTD.
PA (NIKK-) NIKKA WHISKEY KK.
PA (TORI ) TORII YAHUKIN KK.
PA (TSUR/) TSURA T.
DR WPI: 97-429186/40.
PT Humanised, semi-chimeric and chimeric antibodies against human
PT high-affinity IgE receptor - useful medicinally and have low
PT antigenicity in humans
PS Claim 8; Page 15; 26pp; Japanese.
CC The present sequence, the heavy chain variable region of a
CC chimeric human CRA2 antibody (Ab), comprises complementarity
CC determining regions (CDR) from a murine, anti-human high affinity
CC immunoglobulin E (IgE) receptor, monoclonal Ab (MAb). The
CC humanised chimeric MAb can be used to treat or prevent diseases,
CC specifically allergies, associated with the receptor, and has very
CC low antigenicity in humans.
SQ Sequence 117 AA;

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Query Match      79.2%; Score 42; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.79;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTRVEG 10
    ||||| |||||
Db 57 STYYPDTRVKG 66

RESULT 14
W27526
ID W27526 standard; Protein; 117 AA.
AC W27526;
DT 16-DEC-1997 (first entry)
DE Heavy chain variable region of human CRA2 antibody.
KW Complementarity determining region; CDR; murine; mouse; human;
KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
KW IgE; MAb; heavy chain; variable region; humanised; semi-chimeric;
KW chimeric; treatment; prevention; disease; allergy; CRA2.
OS Homo sapiens.
PN J09191886-A.
PD 29-JUL-1997.
PR 19-JAN-1996; 024816.
PR 19-JAN-1996; JP-024816.
PA (ASAK ) ASAKI BREWERIES LTD.
PA (NIKK-) NIKKA WHISKEY KK.
PA (TORI ) TORII YAHUKIN KK.
PA (TSUR/) TSURA T.
DR WPI: 97-429186/40.
PT Humanised, semi-chimeric and chimeric antibodies against human
PT high-affinity IgE receptor - useful medicinally and have low
PT antigenicity in humans
PS Claim 2; Page 13; 26pp; Japanese.
CC The present sequence, the heavy chain variable region of the human
CC antibody (Ab) CRA2, was used in the preparation of a humanised or
CC semi-chimeric monoclonal Ab (MAb), comprising complementarity
CC determining regions (CDR) from a murine, anti-human high affinity

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PT New polypeptide including sequence from single antibody chain and
PT able to penetrate a cell - used as vector for delivering attached
PT components, e.g. nucleic acid or antigen, to cells, useful in gene
PT therapy and vaccination
PS Example 2; Page 21; 36pp; French.
CC This sequence corresponds to a peptide derived from the complementary
CC determining region 2 (CDR2) of an immunoglobulin IgG2a protein and is
CC used in the production of a polypeptide that (i) comprises a unique or
CC repeated peptide motif; (ii) includes a sequence consisting of one or
CC more different antibody fragments and (iii) can penetrate into cells.
CC The polypeptides are vectors for delivering a substance to cells
CC (in vivo, in vitro or ex vivo), particularly for use as pharmaceutical
CC (gene therapy, or where the substance is an antigen, for vaccination,
CC in which case the polypeptide acts effectively as an adjuvant).
SQ Sequence 31 AA;

Query Match      81.1%; Score 43; DB 1; Length 31;
Best Local Similarity 80.0%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
   |||| ||||:|
Db 11 STYYSDTVKG 20

RESULT 9
W99571
ID W99571 standard; peptide; 33 AA.
AC W99571;
DT 22-JUN-1999 (first entry)
DE Immunoglobulin IgG2a CDR2-derived peptide #7.
KW Primer; PCR; amplification; immunoglobulin; IgG2a; repeat motif;
KW antibody; cell penetration; vector; gene therapy; antigen; vaccination.
OS Synthetic.
OS Homo sapiens.
PN FR2766826-A1.
PD 05-FEB-1999.
PF 04-AUG-1997; 009972.
PR 04-AUG-1997; FR-009972.
PA (INSP ) INST PASTEUR.
PI Avrameas A, Avrameas S, Buttin G, Ternynck T;
DR WPI; 99-156194/14.
PT New polypeptide including sequence from single antibody chain and
PT able to penetrate a cell - used as vector for delivering attached
PT components, e.g. nucleic acid or antigen, to cells, useful in gene
PT therapy and vaccination
PS Example 2; Page 20; 36pp; French.
CC This sequence corresponds to a peptide derived from the complementary
CC determining region 2 (CDR2) of an immunoglobulin IgG2a protein and is
CC used in the production of a polypeptide that (i) comprises a unique or
CC repeated peptide motif; (ii) includes a sequence consisting of one or
CC more different antibody fragments and (iii) can penetrate into cells.
CC The polypeptides are vectors for delivering a substance to cells
CC (in vivo, in vitro or ex vivo), particularly for use as pharmaceutical
CC (gene therapy, or where the substance is an antigen, for vaccination,
CC in which case the polypeptide acts effectively as an adjuvant).
SQ Sequence 33 AA;

Query Match      81.1%; Score 43; DB 1; Length 33;
Best Local Similarity 80.0%; Pred. No. 0.12;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
   |||| ||||:|
Db 10 STYYSDTVKG 19

RESULT 10
W99573
ID W99573 standard; peptide; 49 AA.
AC W99573;

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DT 22-JUN-1999 (first entry)
DE Immunoglobulin IgG2a CDR2-3 derived peptide CDR2-3-PL19.
KW Primer; PCR; amplification; immunoglobulin; IgG2a; repeat motif;
KW antibody; cell penetration; vector; gene therapy; antigen; vaccination.
OS Synthetic.
OS Homo sapiens.
PN FR2766826-A1.
PD 05-FEB-1999.
PF 04-AUG-1997; 009972.
PR 04-AUG-1997; FR-009972.
PA (INSP ) INST PASTEUR.
PI Avrameas A, Avrameas S, Buttin G, Ternynck T;
DR WPI; 99-156194/14.
PT New polypeptide including sequence from single antibody chain and
PT able to penetrate a cell - used as vector for delivering attached
PT components, e.g. nucleic acid or antigen, to cells, useful in gene
PT therapy and vaccination
PS Example 5; Page 23; 36pp; French.
CC This sequence corresponds to a peptide derived from the complementary
CC determining region 2/3 (CDR2/3) of an immunoglobulin IgG2a protein and
CC is used in the production of a polypeptide that (i) comprises a unique
CC or repeated peptide motif; (ii) includes a sequence consisting of one
CC or more different antibody fragments and (iii) can penetrate into cells.
CC The polypeptides are vectors for delivering a substance to cells
CC (in vivo, in vitro or ex vivo), particularly for use as pharmaceutical
CC (gene therapy, or where the substance is an antigen, for vaccination,
CC in which case the polypeptide acts effectively as an adjuvant).
SQ Sequence 49 AA;

Query Match      81.1%; Score 43; DB 1; Length 49;
Best Local Similarity 80.0%; Pred. No. 0.19;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
   |||| ||||:|
Db 29 STYYSDTVKG 38

RESULT 11
W27342
ID W27342 standard; peptide; 17 AA.
AC W27342;
DT 13-DEC-1997 (first entry)
DE CDR2 from murine anti-human IgE receptor antibody heavy chain.
KW Complementarity determining region; CDR2; murine; mouse; human;
KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
KW IgE; MAb; heavy chain; variable region; humanised; semi-chimeric;
KW chimeric; treatment; prevention; disease; allergy.
OS Mus spp.
PN J09191886-A.
PD 29-JUL-1997.
PF 19-JAN-1996; 024816.
PR 19-JAN-1996; JP-024816.
PA (ASAK ) ASAHU BREWERIES LTD.
PA (NIKK ) NIKKA WHISKEY KK.
PA (TORI ) TORII YAKUHHN KK.
PA (TSUR) TSURA T.
DR WPI; 97-429186/40.
PT Humanised, semi-chimeric and chimeric antibodies against human
PT high-affinity IgE receptor - useful medicinally and have low
PT antigenicity in humans
PS Claim 1; Page 12; 26pp; Japanese.
CC The present complementarity determining region 2 (CDR2), which is
CC from a murine, anti-human high affinity immunoglobulin E (IgE)
CC receptor, monoclonal antibody (MAb) heavy chain variable region,
CC can be used in the preparation of humanised or semi-chimeric
CC anti-human high affinity IgE receptor MAB. The MAB can be used to
CC treat or prevent diseases, specifically allergies, associated with
CC the receptor. The humanised, semi-chimeric or chimeric MAB have
CC very low antigenicity in humans.
SQ Sequence 17 AA;

```

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SW, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB; V49855.
PT Humanised antibody. Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 61; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 81.1%; Score 43; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.032;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
 ||||| :|||:
Db 1 STYYPTVQ 10

RESULT 6
W99565
ID W99565 standard; peptide; 21 AA.
AC W99565;
DE 22-JUN-1999 (first entry)
DE Immunoglobulin IgG2a CDR2-derived peptide #1.
KW Primer; PCR; amplification; immunoglobulin; IgG2a; repeat motif;
KW antibody; cell penetration; vector; gene therapy; antigen; vaccination.
OS Synthetic.
OS Homo sapiens.
PN FR2766826-A1.
PD 05-FEB-1999.
PF 04-AUG-1997; 009972.
PR 04-AUG-1997; FR-009972.
PA (INSP) INST PASTEUR.
PI Avrameas A, Avrameas S, Buttin G, Ternynck T;
DR WPI: 99-156194/14.
PT New polypeptide including sequence from single antibody chain and
PT able to penetrate a cell - used as vector for delivering attached
PT components, e.g. nucleic acid or antigen, to cells, useful in gene
PT therapy and vaccination
PS Example 2; Page 20; 36pp; French.
CC This sequence corresponds to a peptide derived from the complementary
CC determining region 2 (CDR2) of an immunoglobulin IgG2a protein and is
CC used in the production of a polypeptide that (i) comprises a unique or
CC repeated peptide motif; (ii) includes a sequence consisting of one or
CC more different antibody fragments and (iii) can penetrate into cells.
CC The polypeptides are vectors for delivering a substance to cells
CC (in vivo, in vitro or ex vivo), particularly for use as pharmaceutical
CC (gene therapy, or where the substance is an antigen, for vaccination,
CC in which case the polypeptide acts effectively as an adjuvant).

CC in which case the polypeptide acts effectively as an adjuvant).
SQ Sequence 21 AA;

Query Match 81.1%; Score 43; DB 1; Length 21;
Best Local Similarity 80.0%; Pred. No. 0.075;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
 ||||| :|||:
Db 10 STYYSDTVKG 19

RESULT 7
W99570
ID W99570 standard; peptide; 30 AA.
AC W99570;
DE 22-JUN-1999 (first entry)
DE Immunoglobulin IgG2a CDR2-derived peptide #6.
KW Primer; PCR; amplification; immunoglobulin; IgG2a; repeat motif;
KW antibody; cell penetration; vector; gene therapy; antigen; vaccination.
OS Synthetic.
OS Homo sapiens.
PN FR2766826-A1.
PD 05-FEB-1999.
PF 04-AUG-1997; 009972.
PR 04-AUG-1997; FR-009972.
PA (INSP) INST PASTEUR.
PI Avrameas A, Avrameas S, Buttin G, Ternynck T;
DR WPI: 99-156194/14.
PT New polypeptide including sequence from single antibody chain and
PT able to penetrate a cell - used as vector for delivering attached
PT components, e.g. nucleic acid or antigen, to cells, useful in gene
PT therapy and vaccination
PS Example 2; Page 20; 36pp; French.
CC This sequence corresponds to a peptide derived from the complementary
CC determining region 2 (CDR2) of an immunoglobulin IgG2a protein and is
CC used in the production of a polypeptide that (i) comprises a unique or
CC repeated peptide motif; (ii) includes a sequence consisting of one or
CC more different antibody fragments and (iii) can penetrate into cells.
CC The polypeptides are vectors for delivering a substance to cells
CC (in vivo, in vitro or ex vivo), particularly for use as pharmaceutical
CC (gene therapy, or where the substance is an antigen, for vaccination,
CC in which case the polypeptide acts effectively as an adjuvant).

Query Match 81.1%; Score 43; DB 1; Length 30;
Best Local Similarity 80.0%; Pred. No. 0.11;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
 ||||| :|||:
Db 10 STYYSDTVKG 19

RESULT 8
W99572
ID W99572 standard; peptide; 31 AA.
AC W99572;
DE 22-JUN-1999 (first entry)
DE Immunoglobulin IgG2a CDR2-derived peptide #8.
KW Primer; PCR; amplification; immunoglobulin; IgG2a; repeat motif;
KW antibody; cell penetration; vector; gene therapy; antigen; vaccination.
OS Synthetic.
OS Homo sapiens.
PN FR2766826-A1.
PD 05-FEB-1999.
PF 04-AUG-1997; 009972.
PR 04-AUG-1997; FR-009972.
PA (INSP) INST PASTEUR.
PI Avrameas A, Avrameas S, Buttin G, Ternynck T;
DR WPI: 99-156194/14.

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB: V49846.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Disclosure: Page 40; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 94.3%; Score 50; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0017; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 1;

QY 1 STYYLDTVEG 10
 |||||
 Db 1 STYYLDTVQG 10

RESULT 3
 W76001
 ID W76001 standard; Protein; 117 AA.

DT 02-NOV-1998 (first entry)
 DE Vitaxin antibody heavy chain variable region protein fragment.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB: V49820.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 1; Fig 1a; 129pp; English.
 CC This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated

CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 SQ Sequence 117 AA;

Query Match 94.3%; Score 50; DB 1; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.027; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 1;

QY 1 STYYLDTVEG 10
 |||||
 Db 57 STYYLDTVQG 66

RESULT 4
 W76003
 ID W76003 standard; Protein; 117 AA.

AC W76003;
 DT 02-NOV-1998 (first entry)
 DE LM609 antibody heavy chain variable region protein fragment.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB: V49822.

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 43; Fig 2a; 129pp; English.
 CC This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 SQ Sequence 117 AA;

Query Match 94.3%; Score 50; DB 1; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.027; 0; Indels 0; Gaps 0;
 Matches 9; Conservative 1; Mismatches 1;

QY 1 STYYLDTVEG 10
 |||||
 Db 57 STYYLDTVQG 66

RESULT 5
 W76018
 ID W76018 standard; Protein; 10 AA.

AC W76018;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR2 protein fragment #4.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2000, 19:21:33 ; Search time 148.45 Seconds
(without alignments)
1.596 Million cell updates/sec

Title: US-09-016-061-58
Perfect score: 53
Sequence: 1 STYYLDTVVEG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	53	100.0	10	1 W76019	LM609 grafted anti
2	50	94.3	10	1 W76009	LM609 grafted anti
3	50	94.3	117	1 W76001	Vitaxin antibody h
4	50	94.3	117	1 W76003	LM609 antibody hea
5	43	81.1	10	1 W76018	LM609 grafted anti
6	43	81.1	21	1 W99565	Immunoglobulin IgG
7	43	81.1	30	1 W99570	Immunoglobulin IgG
8	43	81.1	31	1 W99572	Immunoglobulin IgG
9	43	81.1	33	1 W99571	Immunoglobulin IgG
10	43	81.1	49	1 W99573	Immunoglobulin IgG
11	42	79.2	17	1 W27342	CDR2 from murine a
12	42	79.2	117	1 W79155	Human IgE receptor
13	42	79.2	117	1 W27357	Heavy chain variab
14	42	79.2	117	1 W27526	Heavy chain variab
15	42	79.2	117	1 W27354	Heavy chain variab
16	42	79.2	118	1 R79161	Human IgE receptor
17	42	79.2	120	1 W00240	EGF receptor chime
18	42	79.2	127	1 R47510	LS2H241 heavy chai
19	42	79.2	139	1 W21652	Humanised reshaped
20	42	79.2	139	1 W21656	Chimeric MAB 15 PC
21	42	79.2	140	1 W21654	Mouse MAB 15 heavy
22	42	79.2	158	1 W19577	Mouse anti-idiotyp
23	42	79.2	158	1 W19579	Mouse anti-idiotyp
24	42	79.2	239	1 W73874	Human antiFc epsil
25	42	79.2	242	1 W73876	Human antiFc epsil
26	42	79.2	260	1 R77617	Anti-C5 MAB N19/8
27	41	77.4	13	1 W86109	Peptide from human
28	41	77.4	13	1 W86083	Peptide from human
29	41	77.4	117	1 W48865	Murine monoclonal
30	41	77.4	117	1 W48866	Chimeric humanized
31	41	77.4	117	1 W86135	Protein sequence o
32	41	77.4	117	1 W86137	Protein sequence o
33	41	77.4	117	1 W86139	Protein sequence o
34	41	77.4	117	1 W86141	Protein sequence o

35 41 77.4 136 1 R56962 MAB A33 heavy chai
36 41 77.4 237 1 W95440 A33/212 single-cha
37 41 77.4 241 1 W95441 A33/218 single-cha
38 41 77.4 245 1 W97891 A33/218 single cha
39 41 77.4 264 1 W73049 Humanised A33 scab
40 41 77.4 532 1 W73051 Z330CH2.z chimeric
41 41 77.4 643 1 W73048 A33 chimeric recep
42 41 77.4 643 1 W73050 Z33g2G237A2 chimer
43 40 75.5 17 1 W16651 Anti-cancer specif
44 40 75.5 62 1 R76969 HSV-neutralising a
45 40 75.5 95 1 W35098 Product of target

ALIGNMENTS

RESULT 1
W76019
ID W76019 standard; Protein; 10 AA.
AC W76019;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR2 protein fragment #5.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49856.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angio genesis or restenosis
PS Claim 61; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
CC inhibit binding of alphaVbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 100.0%; Score 53; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00048;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 STYYLDTVVEG 10
Db 1 STYYLDTVVEG 10

RESULT 2
W76009
ID W76009 standard; Protein; 10 AA.
AC W76009;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR2 protein fragment #2.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 YYLDTVEG 10

Db 927 YWLTIDG 934

RESULT 13

ID 075732 PRELIMINARY; PRT; 82 AA.

AC 075732;

DT 01-NOV-1998 (TReMBLrel. 08, Created)

DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)

DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)

DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).

GN VH

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-INTESTINE;

RA FISCHER M., KUEPPERS R.;

RT "Human IGA and IGM secreting intestinal plasma cells carry heavily

RT mutated VH region genes.";

RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AJ009529; CAA08736.1; -

DR HSP; P01772; 2IG2.

FT NON_TER 1

FT NON_TER 82

SQ SEQUENCE 82 AA; 9387 MW; 440D63F2 CRC32;

Query Match

Best Local Similarity 64.2%; Score 34; DB 4; Length 82;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10

Db 24 STYADSVKG 33

RESULT 14

ID 09X319 PRELIMINARY; PRT; 227 AA.

AC 09X319;

DT 01-NOV-1999 (TReMBLrel. 12, Created)

DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)

DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)

DE PX01-49.

OS Bacillus anthracis.

OG Plasmid virulence plasmid PX01.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OC Bacillus/Staphylococcus group; Bacillus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-STERNE;

RA OKINAKA R.T., CLOUD K., HAMTON O., HOFFMASTER A., HILL K.K., KEIM P.,

RA KOEHLER T., LAMKE G., KUMANO S., MAHTILON J., MANTER D., MARTINEZ Y.,

RA RICKE D.O., SVENSSON R., JACKSON P.J.;

RT "The sequence and organization of px01, the large Bacillus anthracis

plasmid harboring the Anthrax toxin genes.";

RL J. Bacteriol. 0:0-0(1999).

DR EMBL: AF065404; AAD32353.1; -

KW Plasmid.

SQ SEQUENCE 227 AA; 27180 MW; 390811C4 CRC32;

Query Match

Best Local Similarity 64.2%; Score 34; DB 2; Length 227;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TYLDTVEG 10

Db 166 TYALDKVEG 174

RESULT 15

P94454

ID P94454 PRELIMINARY; PRT; 259 AA.

AC P94454;

DT 01-MAY-1997 (TReMBLrel. 03, Created)

DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)

DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)

DE MODIFICATION METHYLASE F511 (EC 2.1.1.72) (ADENINE-SPECIFIC

DE METHYLTRANSFERASE F511) (M.F511).

GN F511M.

OS Bacillus stearothermophilus.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OC Bacillus/Staphylococcus group; Bacillus.

RN [1]

RP SEQUENCE FROM N.A., AND FUNCTION.

RC STRAIN-F5;

RX MEDLINE: 97254473

RA DEGIYAREV S.K., NETESOVA N.A., ABDURASHITOV M.A., SHEVCHENKO A.V.;

RT "Primary structure and strand specificity of BstF51-1 DNA

RT methyltransferase which recognizes 5'-GGATG-3'.";

RL Gene 187:217-219(1997).

CC -1- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE

CC GGATG, CAUSES SPECIFIC METHYLATION ON A-2, AND PROTECTS THE DNA

CC FROM CLEAVAGE BY THE MFS11 ENDONUCLEASE.

CC -1- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA ADENINE = S-

CC ADENOSYL-L-HOMOCYSTEINE + DNA 6-METHYLAMINOPURINE.

DR EMBL: X97069; CAA65779.1; -

DR HSP; P11409; 1BOO.

DR PROSITE: PS00092; N6_MTASE; 1.

DR PFAM: PF01555; N6_N4_Mtase; 1.

DR PRINTS: PR00506; D21N6MTFRASE.

DR PRINTS: PR00508; S21N4MTFRASE.

KW Transferase; Methyltransferase.

SQ SEQUENCE 259 AA; 30387 MW; 6FA5ABDA CRC32;

Query Match

Best Local Similarity 64.2%; Score 34; DB 2; Length 259;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TYLDTVEG 10

Db 25 TYCLDCVEG 33

Search completed: May 27, 2000, 19:38:37

Job time: 2370 sec

RA TABATA S.;
 RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RC SEQUENCE FROM N.A.
 RP STRAIN=PC6803;
 RX MEDLINE; 96127529.
 RA KANEKO T., TANAKA A., SATO S., KOTANI H., SAZUKA T., MIYAJIMA N.,
 RA SUGIURA M., TABATA S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT *Synechocystis* sp. strain PC6803. I. Sequence features in the 1 Mb
 RT region from map positions 64% to 92% of the genome.";
 RL DNA Res. 2:153-166(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PC6803;
 RX MEDLINE; 97061201.
 RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
 RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
 RA HOSOUCHI T., MATSUO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
 RA SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
 RA TABATA S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT *Synechocystis* sp. strain PC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 DR EMBL; D64001; BAA10314.1; -.
 DR PFAM; PF00004; AAA: 1.
 KW Hypothetical protein.
 SQ SEQUENCE 499 AA; 55974 MW; 6CCDE23 CRC32;

Query Match 66.0%; Score 35; DB 2; Length 499;
 Best Local Similarity 70.0%; Pred. No. 60;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
 I I I I I
 Db 43 SVYYWDFVEG 52

RESULT 10
 O48573
 ID O48573 PRELIMINARY; PRT; 1170 AA.
 AC O48573;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE PUTATIVE DISEASE RESISTANCE PROTEIN.
 GN T19K24.2.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 OC Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
 RA SYKES S.M., KAUL S., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
 RA SOMERVILLE C.R., VENTER J.C.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC002342; AAC79134.1; -.
 DR MENDEL; 27856; Arath;3338;27856.
 DR PFAM; PF00360; LRR: 4.
 DR PFAM; PF00931; NB-ARC: 1.
 DR PRINTS; PRO0364; DISPASERSIST.
 SQ SEQUENCE 1170 AA; 133397 MW; 9B32952B CRC32;

Query Match 66.0%; Score 35; DB 10; Length 1170;
 Best Local Similarity 75.0%; Pred. No. 1.6e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TYVLDTVE 9
 I I I I I
 Db 41 TYVIDTEE 48

RESULT 11
 P78509 PRELIMINARY; PRT; 3460 AA.
 ID P78509;
 AC P78509;
 DT 01-MAY-1997 (TrEMBLrel. 03, Created)
 DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE REELIN.
 GN RELN.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA DESILVA U., D'ARCANGELO G., BRADEN V.V., CHEN J., MIAO G.G.,
 RA CURRAN T., GREEN E.D.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 194-430 FROM N.A.
 RA LAMAR B., WAMSLEY P., GIBSON A.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U79716; AAC51105.1; -.
 DR EMBL; AC000121; AAB46357.1; -.
 DR HSP; P00743; IAP0.
 DR PFAM; PF00008; EGF: 5.
 KW Glycoprotein.
 SQ SEQUENCE 3460 AA; 388399 MW; C8D817E9 CRC32;

Query Match 66.0%; Score 35; DB 4; Length 3460;
 Best Local Similarity 60.0%; Pred. No. 5.9e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
 I I I I I
 Db 2077 STYYAGTMQG 2086

RESULT 12
 O33954 PRELIMINARY; PRT; 4472 AA.
 ID O33954;
 AC O33954;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE TYLACTONE SYNTHASE STARTER MODULE AND MODULES 1 & 2.
 GN TYLG.
 OS Streptomyces fradiae.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA DEHOFF B.S., SUTTON K.L., ROSTECK P.R. JR.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U78289; AAB66504.1; -.
 DR HSP; P47227; IBD8.
 DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 2.
 DR PROSITE; PS00606; E_KETOACYL-SYNTHASE; 2.
 DR PFAM; PF00550; pp-binding; 3.
 DR PFAM; PF00109; ketoacyl-synt; 3.
 DR PFAM; PF00698; Acyl_transf; 3.
 DR PFAM; PF00106; adh_short; 1.
 KW Transferase.
 SQ SEQUENCE 4472 AA; 463281 MW; 0D3F1FE0 CRC32;

Query Match 66.0%; Score 35; DB 2; Length 4472;
 Best Local Similarity 62.5%; Pred. No. 7.9e+02;

RESULT 6
P91438 PRELIMINARY; PRT; 934 AA.
AC P91438;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE CODED FOR BY C. ELEGANS CDNA YK29C11.5.
GN T07F8.3.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
[1]
RN
RP
RC STRAIN-BRISTOL N2;
RC MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKIN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALLDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.; III of C.
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RN Nature 368:32-38(1994).
[2]
RN
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA PAULEY A.;
[3]
RN
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U80954; AAB38098.1; -.
SQ SEQUENCE 934 AA; 106811 MW; 2A889EC8 CRC32;

Query Match 67.9%; Score 36; DB 5; Length 934;
Best Local Similarity 70.0%; Pred. No. 79;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STYYLDTVVEG 10
| | | | | | | |
Db 234 STYYVDQVLG 243

RESULT 7
O18547 PRELIMINARY; PRT; 214 AA.
AC O18547;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE ARROWHEAD.
GN AWH.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Prtergota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN-OREGON R;
RA CURTISS J., HEILIG J.S.;
RL Dev. Biol. 0:0-0(1997).
DR EMBL; U82539; AAB71337.1; -.
HSSP; P10037; IAU7.

DR FLYBASE; FBgn0013751; Awh.
DR PROSITE; PS00478; LIM_DOMAIN_1; 1.
DR PFAM; PF00046; homeobox; 1.
DR PFAM; PF00412; LIM; 2.
KW LIM motif; Metal-binding; Zinc.
SQ SEQUENCE 214 AA; 24243 MW; F7C6AF44 CRC32;

Query Match 66.0%; Score 35; DB 5; Length 214;
Best Local Similarity 75.0%; Pred. No. 22;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 YYLDTVVEG 10
| | | | | | | |
Db 122 HYLDTVVEG 129

RESULT 8
O68786 PRELIMINARY; PRT; 328 AA.
AC O68786;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1999 (TReMBLrel. 11, Last sequence update)
DT 01-AUG-1999 (TReMBLrel. 11, Last annotation update)
DE PUTATIVE TRANSPOSASE (YHGA HOMOLOG).
GN Y1072.
OS Yersinia pestis.
OG Plasmid pMT-1, and Plasmid pMT1.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Yersinia.
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN-KIM10+;
RX MEDLINE; 99043898.
RA LINDLER L.E., PLANO G.V., BURLAND V., MAYHEW G.F., BLATTNER F.R.;
RT "Complete DNA sequence and detailed analysis of the Yersinia pestis
RT KIM5 plasmid encoding murine toxin and capsular antigen.";
RL Infect. Immun. 66:5731-5742(1998).
[2]
RN
RP SEQUENCE OF 44-328 FROM N.A.
RC STRAIN-KIM;
RA HU P., ELLIOTT J., MCCREADY P., SKOWRONSKI E., GARNES J.,
RA KOBAYASHI A., CARRANO A.V., BRUBAKER R., GARCIA E.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF074611; AAC82732.1; -.
DR EMBL; AF053947; AAC13235.1; -.
KW Plasmid.
SQ SEQUENCE 328 AA; 37143 MW; E2CC90FF CRC32;

Query Match 66.0%; Score 35; DB 2; Length 328;
Best Local Similarity 87.5%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YYLDTVVEG 10
| | | | | | | |
Db 82 YSLDTVEG 89

RESULT 9
Q55174 PRELIMINARY; PRT; 499 AA.
AC Q55174;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JAN-1999 (TReMBLrel. 09, Last annotation update)
DE HYPOTHETICAL 56.0 KD PROTEIN.
GN YCF46.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
[1]
RN
RP SEQUENCE FROM N.A.
RC STRAIN-PCC6803;

```

ID O50210 PRELIMINARY; PRT; 473 AA.
AC O50210;
DT 01-JUN-1998 (TReMBLrel. 06, Created)
DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE GLUTAMINE SYNTHETASE.
GN GLNA.
OS Synecococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
NC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
RC SEQUENCE FROM N.A.
RP STRAIN=PCC 7942;
RA COHEN-KUPIEC R.;
RL Thesis (1993), Unknown Institution.
RN [2]
RP PARTIAL SEQUENCE FROM N.A.
RC STRAIN=PCC 7942;
RA PHUNG L.T.;
RL Thesis (1997), Unknown Institution.
RN [3]
RP SEQUENCE OF 1-4 FROM N.A.
RC STRAIN=PCC 7942;
RX MEDLINE; 94064573.
RA COHEN-KUPIEC R., GUREVITZ M., ZILBERSTEIN A.;
RT "Expression of glna in the cyanobacterium Synecococcus sp. strain PCC
RT 7942 is initiated from a single nif-like promoter under various
RT nitrogen conditions.";
RL J. Bacteriol. 175:7727-7731(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7942;
RA PHUNG L.T., COHEN-KUPIEC R.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF031129; AAB87965.1; -.
DR HSSP; P06201; 2LGS.
DR PFAM; PF00120; gln-synt; 1.
SQ SEQUENCE 473 AA; 53045 MW; 79A9CADB CRC32;

Query Match 71.7%; Score 38; DB 2; Length 473;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
| | | | |
DB 150 SYYYDSIEG 159

RESULT 3
O62534 PRELIMINARY; PRT; 752 AA.
ID O62534
AC O62534;
DT 01-AUG-1998 (TReMBLrel. 07, Created)
DT 01-AUG-1998 (TReMBLrel. 07, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE SERINE/THREONINE PROTEIN KINASE
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RA MACDOUGALL C.N.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y07908; CAA69216.1; -.
DR HSSP; P05132; 1FMQ.
DR FLYBASE; FBgn0020386; pk61C.
DR PFAM; PF00069; pkkinase; 1.
KW Serine/threonine-protein kinase.
SQ SEQUENCE 752 AA; 85423 MW; D432AE72 CRC32;

Query Match 69.8%; Score 37; DB 5; Length 752;

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Best Local Similarity 77.8%; Pred. No. 39;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TYYLDTVEG 10
| | | | |
DB 655 TYLDDPEG 663

RESULT 4
O75741 PRELIMINARY; PRT; 77 AA.
ID O75741
AC O75741;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=INTESTINE;
RA FISCHER M., KUEPPERS R.;
RT "Human IGA and Igm secreting intestinal plasma cells carry heavily
RT mutated VH region genes.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ009540; CAA08745.1; -.
DR HSSP; P01772; 2IG2.
DR NON_TER 1
FT NON_TER 77
SQ SEQUENCE 77 AA; 8734 MW; 1F7F9E8E CRC32;

Query Match 67.9%; Score 36; DB 4; Length 77;
Best Local Similarity 66.7%; Pred. No. 4.2;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TYYLDTVEG 10
| | | | |
DB 26 TYADSVKG 34

RESULT 5
O32822 PRELIMINARY; PRT; 339 AA.
ID O32822
AC O32822;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
DE HYPOTHETICAL 39.7 KD PROTEIN (FRAGMENT).
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Listeria.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EGD;
RA BOROVOK I., MISLOVATI M., COHEN G., AHARONOWITZ Y.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF009622; AAB63803.1; -.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 339 AA; 39702 MW; 1ECE3268 CRC32;

Query Match 67.9%; Score 36; DB 2; Length 339;
Best Local Similarity 70.0%; Pred. No. 24;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
| | | | |
DB 148 SSYVLGDVEG 157

```

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:38:36 ; Search time 199.56 Seconds
(without alignments)
3.474 Million cell updates/sec

Title: US-09-016-061-58
Perfect score: 53
Sequence: 1 STYVLDVTVEG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 segs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SPTREMBL12.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	75.5	1642	13	Q91132
2	38	71.7	473	2	O50210
3	37	69.8	752	5	O62534
4	36	67.9	77	4	O75741
5	36	67.9	339	2	O32822
6	36	67.9	934	5	P91438
7	35	66.0	214	5	O18547
8	35	66.0	328	2	O68786
9	35	66.0	499	2	O55174
10	35	66.0	1170	10	O48573
11	35	66.0	3460	4	P78509
12	35	66.0	4472	2	O33954
13	34	64.2	82	4	O75732
14	34	64.2	227	2	Q9X319
15	34	64.2	259	2	P94454
16	34	64.2	308	5	O16503
17	34	64.2	324	2	Q9Z834
18	34	64.2	329	2	O84436
19	34	64.2	522	1	O27026
20	34	64.2	641	1	O58238

21	34	54.2	665	3	Q07799
22	34	54.2	671	11	Q63711
23	34	54.2	705	11	Q63710
24	34	54.2	949	3	O14093
25	34	54.2	985	5	O01590
26	34	54.2	3209	13	O93574
27	34	54.2	3461	11	Q60841
28	33	62.3	50	10	Q41998
29	33	62.3	77	4	O75726
30	33	62.3	191	2	O86039
31	33	62.3	204	10	Q9ZVG4
32	33	62.3	242	6	O46604
33	33	62.3	268	6	O46603
34	33	62.3	274	10	Q9XH68
35	33	62.3	329	10	Q40138
36	33	62.3	329	10	O49079
37	33	62.3	330	11	Q63241
38	33	62.3	331	11	Q63239
39	33	62.3	332	10	Q40459
40	33	62.3	332	10	O81917
41	33	62.3	353	11	Q63242
42	33	62.3	357	6	O18872
43	33	62.3	357	11	Q63238
44	33	62.3	366	4	Q12922
45	33	62.3	443	2	O84169

ALIGNMENTS

RESULT 1
Q91132 PRELIMINARY; PRT: 1642 AA.
ID Q91132;
AC Q91132;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE COBRA VENOM FACTOR PRECURSOR.
OS Naja naja (Indian cobra).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Lepidosauria;
OC Squamata; Scleroglossa; Serpentes; Colubroidea; Elapidae; Elapinae;
OC Naja.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-VENOM GLAND;
RX MEDLINE; 95108041.
RA FRITZINGER D.C., BREDEHORST R., VOGEL C.W.;
RT "Molecular cloning and derived primary structure of cobra venom factor."
RL Proc. Natl. Acad. Sci. U.S.A. 91:12775-12779(1994).
DR EMBL; U09969; AAA68989.1; -.
DR HSSP; P01024; 1C3D.
DR PROSITE; PS00477; ALPHA_2_MACROGLOBULIN; 1.
DR PFAM; PF00207; A2M; 1.
DR PRINTS; PR00004; ANAPHYLATOXN.
KW Signal.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 648 ALPHA CHAIN OF COBRA VENOM FACTOR.
FT CHAIN 1264 1642 BETA CHAIN OF COBRA VENOM FACTOR.
SQ SEQUENCE 1642 AA; 184516 MW; DC8042EA CRC32;

Query Match 75.5%; Score 40; DB 13; Length 1642;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYVLDVTVE 9
:|||||
Db 1007 ATYVLDTTE 1015

RESULT 2
O50210

```
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE; 97426617.
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RA Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M.,
RA Federspiel N., Hyman R., Kalman S., Kemp C., Kurdai O., Lew H., Lin D.,
RA Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; AE000160; AAC73645.1; -.
DR EMBL; U82598; AAB40741.1; -.
DR ECOGENE; EG13627; ybck.
KW Hypothetical protein.
SQ SEQUENCE 508 AA; 57526 MW; F85C07DBF45105CD CRC64;

Query Match 66.0%; Score 35; DB 1; Length 508;
Best Local Similarity 75.0%; Pred. No. 20;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTV 8
Db 36 SDYYLDTI 43
```

Search completed: May 27, 2000, 20:07:12
Job time: 984 sec

Query Match 67.9%; Score 36; DB 1; Length 523;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
| | | | | | | |
Db 441 STYRLDSAE 450

RESULT 12
HV02_CANFA STANDARD; PRT; 117 AA.
AC P01785;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION MOO.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RP SEQUENCE OF 1-112.
RX MEDLINE; 77242268.
RA Wasserman R.L., Capra J.D.;
RT "Primary structure of the variable regions of two canine
RT immunoglobulin heavy chains";
RL Biochemistry 16:3160-3168(1977).
RN [2]
RP SEQUENCE OF 113-117.
RX MEDLINE; 80077682.
RA McCumber L.J., Capra J.D.;
RT "The complete amino-acid sequence of a canine mu chain.";
RL Mol. Immunol. 16:565-570(1979).
CC -I- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A02068; MHDGMO.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12703 MW; FCE07309E0A84B35 CRC64;

Query Match 66.0%; Score 35; DB 1; Length 117;
Best Local Similarity 66.7%; Pred. No. 3.7;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TYYYLDTVEG 10
| | | | | | | |
Db 57 TYYADAVKG 65

RESULT 13
HV3L_HUMAN STANDARD; PRT; 119 AA.
AC P01773;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION BUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE (MYELOMA PROTEIN BUR).
RX MEDLINE; 79151016.
RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
RT "Primary structure of a human IgA1 immunoglobulin. IV. Streptococcal
RT IgA1 protease, digestion, Fab and Fc fragments, and the complete
RT amino acid sequence of the alpha 1 heavy chain.";
RL J. Biol. Chem. 254:2865-2874(1979).
DR PIR; A02056; AIHUBR.
DR HSSP; P01772; 21G2.

DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Glycoprotein.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 22 96
FT CARBOHYD 28 28
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;

Query Match 66.0%; Score 35; DB 1; Length 119;
Best Local Similarity 66.7%; Pred. No. 3.8;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 TYYYLDTVEG 10
| | | | | | | |
Db 58 TYYADSVRG 66

RESULT 14
YK27_AQUAE STANDARD; PRT; 364 AA.
ID YK27_AQUAE
AC O67821;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HYPOTHETICAL PROTEIN AQ_2027.
GN AQ_2027.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VF5;
RX MEDLINE; 98196666.
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Huber R.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Swanson R.V.;
RT Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus";
RL Nature 392:353-358(1998).
CC -I- SIMILARITY: TO B.BURGDORFERI BB0374.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AE000768; AAC07788.1; -.
KW Hypothetical protein.
SQ SEQUENCE 364 AA; 42016 MW; 4022756E079B7276 CRC64;

Query Match 66.0%; Score 35; DB 1; Length 364;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
| | | | | | | |
Db 203 SFYYLDSITG 212

RESULT 15
YBCK_ECOLI STANDARD; PRT; 508 AA.
ID YBCK_ECOLI
AC P77698;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 57.5 KD PROTEIN IN EMRE-RUS INTERGENIC REGION.
GN YBCK.
OS Escherichia coli.

```

RESULT 9
GLNA_SYN2P STANDARD; PRT; 473 AA.
AC P28605;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GLUTAMINE SYNTHETASE (EC 6.3.1.2) (GLUTAMATE--AMMONIA LIGASE).
GN GLNA.
OS Synechococcus sp. (strain PCC 7002) (Agmenellum quadruplicatum).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=PR-6;
RX MEDLINE; 93139025.
RA Wagner S.J., Thomas S.P., Kaufman R.I., Nixon B.T., Stevens S.E. Jr.;
RT "The glna gene of the cyanobacterium Agmenellum quadruplicatum PR-6
RL J. Bacteriol. 175:604-612(1993).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) -> ADP + GLUTAMINE +
CC ORTHOPHOSPHATE.
CC -1- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
CC HEXAGON.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; Z13965; CAA78366.1; -.
CC PIR; S23852; S23852.
CC PIR; A47050; A47050.
CC HSSP; P06201; 2LGS.
CC PROSITE; PS00180; GLNA_1; 1.
CC PROSITE; PS00181; GLNA_ATP; 1.
CC PFAM; PF00120; gln-synt; 1.
CC Ligase.
KW Ligase.
SQ SEQUENCE 473 AA; 53030 MW; 495C6C7A1EDBC576 CRC64;

Query Match 69.8%; Score 37; DB 1; Length 473;
Best Local Similarity 75.0%; Pred. No. 7.3;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLDTVEG 10
Db 152 YVDSVEG 159
II:|:|:|

RESULT 10
GLNA_ANASP STANDARD; PRT; 473 AA.
AC P00964;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE GLUTAMINE SYNTHETASE (EC 6.3.1.2) (GLUTAMATE--AMMONIA LIGASE).
GN GLNA.
OS Anabaena sp. (strain PCC 7120).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
RN [1]
RP SEQUENCE FROM N.A.
RX Tumer N.E., Robinson S.J., Haselkorn R.;
RT "Different promoters for the Anabaena glutamine synthetase gene
RL during growth using molecular or fixed nitrogen.";
RL Nature 306:337-342(1983).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) -> ADP + GLUTAMINE +
CC ORTHOPHOSPHATE.

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CC -1- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
CC HEXAGON.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- MISCELLANEOUS: IN ANABAENA, IT IS PRESENT IN AMMONIA-GROWN
CC VEGETATIVE CELLS AS WELL AS IN HETEROCYSTIS (FOR NITROGEN
CC FIXATION).
CC -1- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
CC -----
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CC -----
CC EMBL; X00147; CAA24982.1; -.
CC PIR; A01192; AJAIQ.
CC HSSP; P06201; 2LGS.
CC PROSITE; PS00180; GLNA_1; 1.
CC PROSITE; PS00181; GLNA_ATP; 1.
CC PROSITE; PS00182; GLNA_ADENYLATION; 1.
CC PFAM; PF00120; gln-synt; 1.
CC Nitrogen fixation; Ligase.
KW Nitrogen fixation; Ligase.
FT INIT_MET 0
FT CONFLICT 106 106 BY SIMILARITY.
FT SEQUENCE 473 AA; 53005 MW; 373C7F949443A4E9 CRC64;

Query Match 67.9%; Score 36; DB 1; Length 473;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 YLDTVEG 10
Db 150 YFLDSVEG 157
I:|:|:|

RESULT 11
YB34_YEAST STANDARD; PRT; 523 AA.
ID YB34_YEAST
AC P38299;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HYPOTHETICAL 60.6 KD PROTEIN IN SMPI-MBAI INTERGENIC REGION.
GN YB184W OR YB11306.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=S288C;
RX MEDLINE; 95176710.
RA Demolis N., Jacquet M., Mallet L.;
RT "A 12.5 kb fragment of the yeast chromosome II contains two adjacent
RT genes encoding ribosomal proteins and six putative new genes, one of
RT which encodes a putative transcriptional factor.";
RL Yeast 10:1511-1525(1994).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U02073; AAB60278.1; -.
CC EMBL; Z36053; CAA85145.1; -.
CC PIR; S46056; S46056.
KW Hypothetical protein.
SQ SEQUENCE 523 AA; 60642 MW; 9BFFBD192C85472F CRC64;

```

Query Match 71.7%; Score 38; DB 1; Length 97;
Best Local Similarity 70.0%; Pred. No. 0.76;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
DB 56 STYYPDSVKG 65
|||||:|:|

RESULT 6
HV3F_HUMAN
ID HV3F_HUMAN STANDARD; PRT; 115 AA.
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION BUT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE; 78137069.
RA Torano A., Putnam F.W.;
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
RT IgA2 immunoglobulin of the A2m (2) allotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C
CC REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
DR PIR; A02050; A2HUBU.
DR PFAM; PF00047; ig; 1.
KW Immunoglobulin V region.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DCF4 CRC64;

Query Match 69.8%; Score 37; DB 1; Length 115;
Best Local Similarity 60.0%; Pred. No. 1.5;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
DB 56 TTYVADSVKG 65
|||||:|:|

RESULT 7
HV3C_HUMAN
ID HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION VH26 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81101090.
RA Matthysens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
RT heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC -----
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CC -----
DR EMBL; J00236; AAA53516.1; -.

DR EMBL; M35415; AAA58735.1; -.
DR PIR; A02047; H3HU26.
DR PFAM; PF00047; ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V-III REGION VH26.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 69.8%; Score 37; DB 1; Length 117;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
DB 76 STYYGDSVKG 85
|||||:|:|

RESULT 8
GLNA_FREDI
ID GLNA_FREDI STANDARD; PRT; 470 AA.
AC P33035;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GLUTAMINE SYNTHETASE (EC 6.3.1.2) (GLUTAMATE--AMMONIA LIGASE).
GN GLNA.
OS Freymella diplosiphon (Calothrix PCC 7601).
OC Bacteria; Cyanobacteria; Nostocales; Rivulariaceae; Freymella.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93129187.
RA Elmorjani K., Liotenberg S., Houmard J., de Marsac N.T.;
RT "Molecular characterization of the gene encoding glutamine synthetase
RT in the cyanobacterium Calothrix sp. PCC 7601.";
RL Biochem. Biophys. Res. Commun. 189:1296-1302(1992).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + NH(3) = ADP + GLUTAMINE +
CC ORTHOPHOSPHATE.
CC -1- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
CC HEXAGON.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
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CC -----
DR EMBL; L05609; AAA23288.1; -.
DR PIR; JCI403; JCI403.
DR HSP; P06201; 2LGS.
DR PROSITE; PS00180; GLNA_1; 1.
DR PROSITE; PS00181; GLNA_ATP; 1.
DR PROSITE; PS00182; GLNA_ADENYLATION; 1.
DR PFAM; PF00120; gln-synt; 1.
KW Ligase.
FT INIT_MET 0 0 BY SIMILARITY.
SQ SEQUENCE 470 AA; 52919 MW; ADD7B49A7789E832 CRC64;

Query Match 69.8%; Score 37; DB 1; Length 470;
Best Local Similarity 75.0%; Pred. No. 7.2;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 YYLDTVEG 10
DB 150 YYVDSVEG 157
|||:|:|

```

RX STRAIN=BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0505; HVMS84.
KW PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 79.2%; Score 42; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.15;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 STYYLDTVEG 10
    ||||| |||:|
Db 76 STYYPTVKG 85

RESULT 3
HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 345 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0502; HVMS34.
KW PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;

Query Match 79.2%; Score 42; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.15;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 STYYLDTVEG 10
    ||||| |||:|
Db 76 STYYPTVKG 85

```

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RESULT 4
HV05_CARAU STANDARD; PRT; 116 AA.
AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 5A PRECURSOR.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Cyprinidae; Carassius.
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE; 88144476.
RA Wilson M.R., Middleton D., Warr G.W.;
RT "Immunoglobulin heavy chain variable region gene evolution: structure
RT and family relationships of two genes and a pseudogene in a teleost
RT fish.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
DR PIR; B28966; B28966.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 116 IG HEAVY CHAIN V REGION 5A.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 85 116 FRAMEWORK 3.
FT DISULFID 41 114 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match 75.5%; Score 40; DB 1; Length 116;
Best Local Similarity 70.0%; Pred. No. 0.37;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 STYYLDTVEG 10
    ||||| |||:|
Db 75 STYYADSVKG 84

RESULT 5
HV56_MOUSE STANDARD; PRT; 97 AA.
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RT the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0504; HVMS91.
KW PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;

```


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OM protein - protein search, using sw model

Run on: May 27, 2000, 20:07:11 ; Search time 69.28 Seconds
(without alignments)
4.396 Million cell updates/sec

Title: US-09-016-061-58
Perfect score: 53
Sequence: 1 STYLDTEG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues
Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	79.2	117	1 HV53_MOUSE	P18524 mus musculu
2	42	79.2	117	1 HV54_MOUSE	P18526 mus musculu
3	42	79.2	117	1 HV55_MOUSE	P18526 mus musculu
4	40	75.5	116	1 HV05_CARAU	P19181 carassius a
5	38	71.7	97	1 HV56_MOUSE	P18527 mus musculu
6	37	69.8	115	1 HV3F_HUMAN	P01767 homo sapien
7	37	69.8	117	1 HV3C_HUMAN	P01764 homo sapien
8	37	69.8	470	1 GLNA_FREDI	P33035 fremyella d
9	37	69.8	473	1 GLNA_SYN2	P28605 synechococc
10	36	67.9	473	1 GLNA_ANASP	P00964 anabaena sp
11	36	67.9	523	1 YB34_YEAST	P38299 saccharomyc
12	35	66.0	117	1 HV02_CANFA	P01785 canis famli
13	35	66.0	119	1 HV3L_HUMAN	P01773 homo sapien
14	35	66.0	364	1 YK27_AQUAE	O67821 aquifex aco
15	35	66.0	508	1 YBCK_ECOLI	P77698 escherichia
16	35	66.0	1062	1 CERU_MOUSE	O61147 mus musculu
17	34	64.2	98	1 HV57_MOUSE	P18528 mus musculu
18	34	64.2	117	1 HV58_MOUSE	P18529 mus musculu
19	34	64.2	117	1 HV59_MOUSE	P18530 mus musculu
20	34	64.2	353	1 GBQ_LYMS	P38411 lymnaea sta
21	34	64.2	711	1 YRFF_ECOLI	P45800 escherichia
22	34	64.2	4488	1 RRPV_CVMJH	P19751 murine coro
23	33	62.3	117	1 HV3J_HUMAN	P01771 homo sapien
24	33	62.3	318	1 ALYS_BPHB3	P32762 streptococc
25	33	62.3	318	1 ALYS_STREN	P06653 streptococc
26	33	62.3	329	1 PSBO_PEA	P14226 pisum sativ
27	33	62.3	332	1 PSBO_ARATH	P23321 arabidopsis
28	33	62.3	332	1 PSBO_SPTOL	P12359 spinacia oi
29	33	62.3	333	1 PSBO_SOLTU	P26320 solanum tub
30	33	62.3	471	1 TNAE_ECOLI	P00913 escherichia
31	33	62.3	473	1 GLNA_SYNY3	P77961 synechocyst
32	33	62.3	654	1 BFR2_HUMAN	Q01742 homo sapien
33	33	62.3	821	1 FGR2_HUMAN	P21802 homo sapien
34	33	62.3	821	1 FGR2_MOUSE	P21803 mus musculu

35	33	62.3	823	1 CEK3_CHICK	P18461 gallus gall
36	33	62.3	1008	1 DPOL_HSVE2	P52367 equine herp
37	32	60.4	250	1 LFA3_HUMAN	P19256 homo sapien
38	32	60.4	332	1 GBAL_HAEIN	P31766 haemophilus
39	32	60.4	354	1 GBQ_LOLFO	P38412 loligo forb
40	32	60.4	457	1 YMS9_YEAST	Q03648 saccharomyc
41	32	60.4	553	1 DPOL_BPPRD	P10479 bacterioph
42	32	60.4	631	1 OE66_NPVLS	P89558 leucania se
43	32	60.4	813	1 FGR2_XENLA	Q03364 xenopus lae
44	32	60.4	1005	1 MANA_DICDI	P34098 dictyosteli
45	32	60.4	1077	1 XNYV_CLOTM	P51584 clostridium

ALIGNMENTS

RESULT 1
HV53_MOUSE
ID HV53_MOUSE STANDARD; PRT; 117 AA.
AC P18524;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION RF PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS; THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0503; HVMSRF.
DR PFAM; PF00047; ig: 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT CHAIN 1 19
FT DOMAIN 20 117 IG HEAVY CHAIN V REGION RF.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;

Query Match 79.2%; Score 42; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.15;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYLDTEG 10
Db 76 STYLDTEG 85

RESULT 2
HV54_MOUSE
ID HV54_MOUSE STANDARD; PRT; 117 AA.
AC P18525;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 5-84 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.

|||||:|:|
Db 48 TTYLDSVKG 56

RESULT 13
I47200
Ig heavy chain variable VDJ region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 23-Jul-1999
C:Accession: I47200
R:Sun, J.; Kacskovics, I.; Brown, W.R.; Butler, J.E.
J. Immunol. 153, 5618-5627, 1994
A:Title: Expressed swine VH genes belong to a small VH gene family homologous to human V
A:Reference number: I47177; MUID:95081609
A:Accession: I47200
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-150 <SUN>
A:Cross-references: EMBL:U15459; NID:g571404; PIDN:AAA67025.1; PID:g571405
C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 77.4%; Score 41; DB 2; Length 150;
Best Local Similarity 77.8%; Pred. No. 1.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TTYLDTVEG 10
|||||:|:|
Db 79 TTYLDSVKG 87

RESULT 14
S24248
Ig heavy chain V region (VH26) - human
C:Species: Homo sapiens (man)
C:Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S24248
R:Stewart, A.K.; Huang, C.; Stollar, B.D.; Schwartz, R.S.
submitted to the EMBL Data Library, June 1992
A:Description: A single VH gene predominates in the rearranged and expressed human B cell
A:Reference number: S24247
A:Accession: S24248
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <STE>
A:Cross-references: EMBL:X67069; NID:g38395; PIDN:CAA47454.1; PID:g38396
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 75.5%; Score 40; DB 2; Length 90;
Best Local Similarity 70.0%; Pred. No. 1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
|||||:|:|
Db 56 STYYADSVKG 65

RESULT 15
S26935
Ig heavy chain V region (DP-42) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S26935
R:Tomlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of
A:Reference number: S26885; MUID:93021117
A:Accession: S26935
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-97 <TOM>

A:Cross-references: EMBL:Z12342; NID:g32905; PIDN:CAA78212.1; PID:g32906
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-97/Domain: immunoglobulin homology <IMM>

Query Match 75.5%; Score 40; DB 2; Length 97;
Best Local Similarity 70.0%; Pred. No. 1.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVEG 10
|||||:|:|
Db 56 STYYADSVKG 65

Search completed: May 27, 2000, 19:26:38
Job time: 1761 sec

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVFEG 10
 |||| |||:|

Db 76 STYYPDVTKG 85

RESULT 8
 HVM534
 Ig heavy chain precursor V region (345) - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
 C:Accession: J0502
 R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
 J. Exp. Med. 169, 2007-2019, 1989
 A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
 A:Reference number: J0501; MUID:89279149
 A:Accession: J0502
 A:Status: translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-117 <LEV>
 A:Experimental source: strain BALB/cJ
 A:Note: this sequence belongs to the VH7183 subfamily
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-117/Product: Ig heavy chain V region (345) #status predicted <WAT>
 F:34-117/Domain: immunoglobulin homology <IMM>
 F:41-115/Disulfide bonds: #status predicted

Query Match 79.2%; Score 42; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 0.57;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVFEG 10
 |||| |||:|

Db 76 STYYPDVTKG 85

RESULT 9
 PHI552
 Ig H chain V region (clone 16E4) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PHI552
 R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
 J. Exp. Med. 177, 1105-1116, 1993
 A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
 A:Reference number: PHI528; MUID:93210465
 A:Accession: PHI552
 A:Molecule type: mRNA
 A:Residues: 1-117 <MUK>
 A:Note: the stop codon X appears in residue 87
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin

Query Match 79.2%; Score 42; DB 2; Length 117;
 Best Local Similarity 80.0%; Pred. No. 0.57;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVFEG 10
 |||| |||:|

Db 57 STYYPDVTKG 66

RESULT 10
 PHI548
 Ig H chain V region (clone 12F4) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PHI548

R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
 J. Exp. Med. 177, 1105-1116, 1993
 A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
 A:Reference number: PHI528; MUID:93210465
 A:Accession: PHI548
 A:Molecule type: mRNA
 A:Residues: 1-119 <MUK>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 42; DB 2; Length 119;
 Best Local Similarity 80.0%; Pred. No. 0.58;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVFEG 10
 |||| |||:|

Db 57 STYYPDVTKG 66

RESULT 11
 PHI549
 Ig H chain V region (clone 13F1) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PHI549
 R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
 J. Exp. Med. 177, 1105-1116, 1993
 A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
 A:Reference number: PHI528; MUID:93210465
 A:Accession: PHI549
 A:Molecule type: mRNA
 A:Residues: 1-119 <MUK>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 42; DB 2; Length 119;
 Best Local Similarity 80.0%; Pred. No. 0.58;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYLDTVFEG 10
 |||| |||:|

Db 57 STYYPDVTKG 66

RESULT 12
 S56009
 Ig heavy chain variable region against dystrophin - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
 C:Accession: S56009
 R:Morris, G.E.; Nguyen, C.; Man, N.T.
 Biochem. J. 309, 355-359, 1995
 A:Title: Specificity and V(H) sequence of two monoclonal antibodies against the N-ter
 A:Reference number: S56008; MUID:95344393
 A:Accession: S56009
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-92 <MOR>
 A:Cross-references: EMBL:Z46661
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:6-86/Domain: immunoglobulin homology <IMM>

Query Match 77.4%; Score 41; DB 2; Length 92;
 Best Local Similarity 77.8%; Pred. No. 0.68;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYLLDTVEG 10

Db 57 STYYPDTVKG 66
||||| |||:|

RESULT 3

Ig heavy chain V region (clone ph62) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 23-Jul-1999
C:Accession: S02717
R:Sollazzo, M.; Hasemann, C.A.; Meek, K.D.; Glotz, D.; Capra, J.D.; Zanetti, M.
submitted to the EMBL Data Library, February 1989
A:Reference number: S02717

A:Accession: S02717
A:Molecule type: DNA
A:Residues: 1-113 <SOL>
A:Cross-references: EMBL:Y00744; NID:g52472; PIDN:CAA68713.1; PID:s6964; PID:g1334095
A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 42; DB 2; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.54;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 STYYLDTVEG 10
||||| |||:|

RESULT 4

Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26468
R:Kavaler, J.
submitted to the EMBL Data Library, April 1991

A:Reference number: S26459
A:Accession: S26468
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <KAV>
A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 42; DB 2; Length 113;
Best Local Similarity 80.0%; Pred. No. 0.54;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 STYYLDTVEG 10
||||| |||:|

RESULT 5

Ig H chain V region (clone 13G12) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1538
R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
J. Exp. Med. 177, 1105-1116, 1993
A:Title: Molecular characterization of the humoral responses to *Cryptococcus neoformans*
A:Reference number: PH1528; MUID:93210465
A:Accession: PH1538
A:Molecule type: mRNA
A:Residues: 1-115 <MUK>

A:Note: the stop codons X appear in residues 82, 85 and 106
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match

Best Local Similarity 79.2%; Score 42; DB 2; Length 115;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 STYYLDTVEG 10
||||| |||:|

Db 56 STYYPDTVKG 65

RESULT 6

HVMSRF
Ig heavy chain precursor V region (RF) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
C:Accession: JT0503
J:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
A:Reference number: JT0501; MUID:89279149
A:Accession: JT0503
A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>
A:Experimental source: strain BALB/cJ

A:Note: this sequence belongs to the VH7183 subfamily
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; hybridoma; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-117/Product: Ig heavy chain V region (RF) #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>
F:41-115/Disulfide bonds: #status predicted

Query Match 79.2%; Score 42; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.57;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 1 STYYLDTVEG 10
||||| |||:|

Db 76 STYYPDTVKG 85

RESULT 7

HVMS84
Ig heavy chain precursor V region (5-84) - mouse

C:Species: Mus musculus (house mouse)
C>Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
C:Accession: JT0505

J:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary

A:Reference number: JT0501; MUID:89279149

A:Accession: JT0505

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A:Note: this sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:41-115/Disulfide bonds: #status predicted

Query Match 79.2%; Score 42; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.57;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:26:38 ; Search time 163.56 Seconds
(without alignments)
3.585 Million cell updates/sec

Title: US-09-016-061-58
Perfect score: 53
Sequence: 1 STYYLDTVEG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_63:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	43	81.1	83	2 S21593	Ig heavy chain V r
2	42	79.2	111	2 S51211	Ig heavy chain V r
3	42	79.2	113	2 S02717	Ig heavy chain V r
4	42	79.2	113	2 S26468	Ig heavy chain V r
5	42	79.2	115	2 PH1538	Ig H chain V regio
6	42	79.2	117	1 HVMSRF	Ig heavy chain pre
7	42	79.2	117	1 HVMS84	Ig heavy chain pre
8	42	79.2	117	1 HVMS34	Ig heavy chain pre
9	42	79.2	117	2 PH1552	Ig H chain V regio
10	42	79.2	119	2 PH1548	Ig H chain V regio
11	42	79.2	119	2 PH1549	Ig H chain V regio
12	41	77.4	92	2 S56009	Ig heavy chain var
13	41	77.4	150	2 I47200	Ig heavy chain var
14	40	75.5	90	2 S24248	Ig heavy chain V r
15	40	75.5	97	2 S26935	Ig heavy chain V r
16	40	75.5	97	2 S46462	Ig heavy chain V r
17	40	75.5	98	2 S26929	Ig heavy chain V r
18	40	75.5	98	2 S26889	Ig heavy chain V r
19	40	75.5	98	2 S54856	Ig heavy chain V r
20	40	75.5	99	2 S24259	Ig heavy chain V r
21	40	75.5	100	2 S24258	Ig heavy chain V r
22	40	75.5	101	2 S24257	Ig heavy chain V r
23	40	75.5	102	2 S24260	Ig heavy chain V r
24	40	75.5	104	2 S24255	Ig heavy chain V r
25	40	75.5	105	2 S24249	Ig heavy chain V r
26	40	75.5	106	2 S24256	Ig heavy chain V r
27	40	75.5	108	2 PH1648	Ig heavy chain V r
28	40	75.5	109	2 PH1649	Ig heavy chain V r
29	40	75.5	109	2 S24254	Ig heavy chain V r
30	40	75.5	109	2 S24253	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S21593
Ig heavy chain V region (10C5) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: S21593
R:Kaartinen, M.
submitted to the EMBL Data Library, May 1992
A:Reference number: S21591
A:Accession: S21593
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-83 <KAA>
A:Cross-references: EMBL:X66457; NID:g51598; PIDN:CAA47072.1; PID:g51599
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 81.1%; Score 43; DB 2; Length 83;
Best Local Similarity 80.0%; Pred. No. 0.25;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVEG 10
|||||
Db 27 STYYSDTVKG 36

RESULT 2

S51211
Ig heavy chain V region (AC7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Aug-1995 #sequence_revision 01-Dec-1995 #text_change 30-May-1997
C:Accession: S51211; S58929
R:Jarrin, A.; Andrieux, A.; Chapel, A.; Buchou, T.; Marguerie, G.
FEBS Lett. 354: 169-172, 1994
A:Title: A synthetic peptide with anti-platelet activity derived from a CDR of an ant
A:Reference number: S51210; MUID:95046326
A:Accession: S51211
A:Molecule type: mRNA
A:Residues: 9-111 <JAR>
A:Accession: S58929
A:Molecule type: protein
A:Residues: 1-20 <JAR2>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 42; DB 2; Length 111;
Best Local Similarity 80.0%; Pred. No. 0.53;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 STYYLDTVEG 10

Key	Location/Qualifiers
Peptide	1..22
FT	/note= "signal peptide"
FT	23..242
Protein	/note= "mature protein"
FT	
J11000174-A.	
PN	
PD	06-JAN-1999.
PF	13-JUN-1997; 171232.
PR	13-JUN-1997; JP-171232.
PA	(ASAK) ASAHI BREWERIES LTD.
PA	(NIKK-) NIKKA WHISKEY KK.
PA	(TORI) TORII YAKUJIN KK.
PA	(TSUR/) TSURA T.
PA	WPI: 99-124394/11.
DR	N-PSDB; X01216.
PT	Preparing an antibody Fab fragment using yeast - in high yield
PS	Claim 6; Page 9-10; 13pp; Japanese.
CC	This sequence represents a human antiFc epsilon RI alpha chain antibody,
CC	produced using the method of the invention. The method is for preparing
CC	an antibody Fab fragment using the yeast Pichia pastoris as the host
CC	cell. The method can prepare an antibody Fab fragment cost efficiently
CC	and in high yield.
SQ	Sequence 242 AA;

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FT EP-745612-A1. /note= "mouse constant IgG1 region"
PN 04-DEC-1996.
PD 14-MAY-1996; 107651.
PR 26-MAY-1995; EP-107967.
PA (MERE ) MERCK PATENT GMBH.
PI Adan J, Carceller A, Gomez A, Piulats J, Rosell E;
DR WPI; 97-013659/02.
DR N-PSDB; T70808.
PT Monoclonal anti-idiotypic antibodies mimicking epidermal growth
PT factor receptor - useful for tumour therapy
PS Claim 6; Fig 5C; 28pp; English.
CC Murine monoclonal anti-idiotypic antibodies, 15H8, 3B6 and 5A6 are
CC new. They induce an immune response against epidermal growth factor
CC receptor (EGFR). The sequences of the heavy and light chain variable
CC regions of these antibodies are given in the specification. The
CC antibodies are used for the manufacture of drugs directed against
CC tumours that express EGFR on their surface, including melanomas,
CC gliomas and carcinomas.
SQ Sequence 158 AA;

Query Match 92.9%; Score 52; DB 1; Length 158;
Best Local Similarity 90.0%; Pred. No. 0.014;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDVTQVG 10
DB 76 STYYPDVTQVG 85

RESULT 13
W19579
ID W19579 standard; Protein; 158 AA.
AC W19579;
DE Mouse anti-idiotypic antibody 5A6 heavy chain variable region.
KW Anti-idiotypic; anti-EGFR; epidermal growth factor receptor; tumour;
KW cancer; neoplasia; glioma; melanoma; carcinoma; drug manufacture; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT peptide 1..19
FT region /label= sig_peptide
FT /label= FR1
FT /note= "framework region 1"
FT region 50..54
FT /label= CDR1
FT /note= "complementarity determining region 1"
FT region 55..68
FT /label= FR2
FT /note= "framework region 2"
FT region 69..85
FT /label= CDR2
FT /note= "complementarity determining region 2"
FT region 86..117
FT /label= FR3
FT /note= "framework region 3"
FT region 118..133
FT /label= CDR3
FT /note= "complementarity determining region 3"
FT region 134..144
FT /label= FR4
FT /note= "framework region 4"
FT region 145..158
FT /note= "mouse constant IgG1 region"
PN EP-745612-A1.
PD 04-DEC-1996.
PR 14-MAY-1996; 107651.
PR 26-MAY-1995; EP-107967.
PA (MERE ) MERCK PATENT GMBH.
PI Adan J, Carceller A, Gomez A, Piulats J, Rosell E;
DR WPI; 97-013659/02.

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DR N-PSDB; T70810.
PT Monoclonal anti-idiotypic antibodies mimicking epidermal growth
PT factor receptor - useful for tumour therapy
PS Claim 6; Fig 5E; 28pp; English.
CC Murine monoclonal anti-idiotypic antibodies, 15H8, 3B6 and 5A6 are
CC new. They induce an immune response against epidermal growth factor
CC receptor (EGFR). The sequences of the heavy and light chain variable
CC regions of these antibodies are given in the specification. The
CC antibodies are used for the manufacture of drugs directed against
CC tumours that express EGFR on their surface, including melanomas,
CC gliomas and carcinomas.
SQ Sequence 158 AA;

Query Match 92.9%; Score 52; DB 1; Length 158;
Best Local Similarity 90.0%; Pred. No. 0.014;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDVTQVG 10
DB 76 STYYPDVTQVG 85

RESULT 14
W73874
ID W73874 standard; Protein; 239 AA.
AC W73874;
DE 31-MAR-1999 (first entry)
DE Human antiFc epsilon RI alpha chain antibody #2.
KW AntiFc epsilon RI alpha chain antibody; antibody production; human.
OS Homo sapiens.
FH Key Location/Qualifiers
FT peptide 1..19
FT Protein /note= "signal peptide"
FT /note= "mature protein"
FT J11000174-A.
PN 06-JAN-1999.
PD 13-JUN-1997; 171232.
PR 13-JUN-1997; JP-171232.
PA (ASAK ) ASAKI BREWERIES LTD.
PA (NIKK ) NIKKA WHISKY KK.
PA (TORI ) TORII YAKUHUIN KK.
PA (TSUR ) TSURA T.
DR WPI; 99-124394/11.
DR N-PSDB; X01214.
PT Preparing an antibody Fab fragment using yeast - in high yield
PS Claim 6; Page 7; 13pp; Japanese.
CC This sequence represents a human antiFc epsilon RI alpha chain antibody,
CC produced using the method of the invention. The method is for preparing
CC an antibody Fab fragment using the yeast Pichia pastoris as the host
CC cell. The method can prepare an antibody Fab fragment cost efficiently
CC and in high yield.
SQ Sequence 239 AA;

Query Match 92.9%; Score 52; DB 1; Length 239;
Best Local Similarity 90.0%; Pred. No. 0.023;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDVTQVG 10
DB 76 STYYPDVTQVG 85

RESULT 15
W73876
ID W73876 standard; Protein; 242 AA.
AC W73876;
DE 31-MAR-1999 (first entry)
DE Human antiFc epsilon RI alpha chain antibody #4.
KW AntiFc epsilon RI alpha chain antibody; antibody production; human.
OS Homo sapiens.

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FT /label= CDR1
FT /note= "complementarity determining region 1"
FT 55. .68
FT /label= Framework-2
FT 69. .86
FT /label= CDR2
FT /note= "complementarity determining region 2"
FT 87. .117
FT /label= Framework-3
FT 118. .128
FT /label= CDR3
FT /note= "complementarity determining region 3"
FT 129. .138
FT /label= Framework-4
FT EP-781847-A1.
FT 02-JUL-1997.
FT 25-OCT-1996; 117154.
FT 06-NOV-1995; EP-117407.
FT (MERE ) MERCK PATENT GMBH.
FT Bendig M, Jones T, Saldana J;
FT WPI: 97-334904/31.
FT N-PSDB; T72269.
FT Humanised form of murine monoclonal antibody MAb 15 - useful for
FT treating lung cancer
FT Example 1; Fig 5; 71pp; English.
FT This polypeptide comprises the heavy chain variable region VH
FT of murine monoclonal antibody (Mab) 15 (DSM ACC2117). It is
FT encoded by a Mab 15 VH cDNA sequence (T72269) modified for the
FT expression of chimeric antibody. The VL sequence was similarly
FT obtained (see W21655). The modified VH and VL sequences were used
FT in a claimed process to model and design novel humanised, reshaped
FT Mab 15 having humanised, reshaped VH and VL sequences (see W21652
FT and W21651), which can be used for treating tumours, especially
FT lung cancer, and for the manufacture of a drug related to tumours,
FT especially lung cancer.
FT Sequence 139 AA;
SQ

Query Match 92.9%; Score 52; DB 1; Length 139;
Best Local Similarity 90.0%; Pred. No. 0.013;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
Db 76 STYYPDTVKG 85
|||||||:|

RESULT 11
W21654
ID W21654 standard; Protein; 140 AA.
AC W21654;
DT 03-JAN-1998 (first entry)
DE Mouse Mab 15 heavy chain variable region.
KW Humanised antibody; monoclonal antibody; Mab 15; tumour;
KW lung cancer; therapy.
OS Mus musculus.
FH Key Location/Qualifiers
FT Peptide 1. .19
FT /label= Sig_peptide
FT Protein 20. .140
FT /label= Mat_protein
FT Region 20. .49
FT /label= Framework-1
FT Region 50. .53
FT /label= CDR1
FT /note= "complementarity determining region 1"
FT Region 54. .68
FT /label= Framework-2
FT Region 69. .86
FT /label= CDR2
FT /note= "complementarity determining region 2"
FT Region 87. .117
FT /label= Framework-3

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FT Region 118. .128
FT /label= CDR3
FT /note= "complementarity determining region 3"
FT 129. .139
FT /label= Framework-4
FT EP-781847-A1.
FT 02-JUL-1997.
FT 25-OCT-1996; 117154.
FT 06-NOV-1995; EP-117407.
FT (MERE ) MERCK PATENT GMBH.
FT Bendig M, Jones T, Saldana J;
FT WPI: 97-334904/31.
FT N-PSDB; T72267.
FT Humanised form of murine monoclonal antibody MAb 15 - useful for
FT treating lung cancer
FT Example 1; Fig 2; 71pp; English.
FT This polypeptide comprises the heavy chain variable region VH
FT of murine monoclonal antibody (Mab) 15 (DSM ACC2117), a Mab that
FT shows a therapeutic effect on human tumour cells, especially human
FT lung cancer. Its sequence was deduced from an isolated cDNA
FT cloner (see T72267). The Mab 15 VL region sequence (W21653)
FT has also been determined. Amplified VH and VL cDNA sequences were
FT used in a claimed process for the production of novel humanised,
FT reshaped Mab 15 having humanised, reshaped VH and VL regions (see
FT W21652 and W21651), which can be used for treating tumours,
FT especially lung cancer, and for the manufacture of a drug related
FT to tumours, especially lung cancer.
FT Sequence 140 AA;
SQ

Query Match 92.9%; Score 52; DB 1; Length 140;
Best Local Similarity 90.0%; Pred. No. 0.013;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
Db 76 STYYPDTVKG 85
|||||||:|

RESULT 12
W19577
ID W19577 standard; Protein; 158 AA.
AC W19577;
DT 30-JUL-1997 (first entry)
DE Mouse anti-idiotypic antibody 3B6 heavy chain variable region.
KW Anti-idiotypic; anti-EGFR; epidermal growth factor receptor; tumour;
KW cancer; neoplasia; glioma; melanoma; carcinoma; drug manufacture; ss.
OS Mus musculus.
FH Key Location/Qualifiers
FT Peptide 1. .19
FT /label= sig_peptide
FT Region 20. .49
FT /label= FR1
FT /note= "framework region 1"
FT Region 50. .53
FT /label= CDR1
FT /note= "complementarity determining region 1"
FT Region 54. .68
FT /label= FR2
FT /note= "framework region 2"
FT Region 69. .85
FT /label= CDR2
FT /note= "complementarity determining region 2"
FT Region 86. .117
FT /label= FR3
FT /note= "framework region 3"
FT Region 118. .133
FT /label= CDR3
FT /note= "complementarity determining region 3"
FT Region 134. .144
FT /label= FR4
FT /note= "framework region 4"
FT Region 145. .158

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QY 1 STYYPDVTQVQ 10
 Db 55 STYYPDVTQVG 64

RESULT 8
 W00240
 ID W00240 standard; Protein; 120 AA.
 AC W00240;
 DT 22-NOV-1996 (first entry)
 DE EGF receptor chimeric MAb chMint5 VH chain.
 KW Mouse-human chimeric antibody; monoclonal antibody; chMint5;
 KW epidermal growth factor receptor; EGF-R; diagnosis; therapy;
 KW immunotoxin; immunocytokine; tumour; cancer.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT region 31..35
 FT /label= CDR1
 FT region 51..66
 FT /label= CDR2
 FT region 99..109
 FT /label= CDR3
 PN W09627010-A1.
 PD 06-SEP-1996.
 PF 01-MAR-1996; E00805.
 PR 01-MAR-1995; IT-FI0036.
 PA (ITUV-) ITAL MIN UNIV RICERCA SCI & TECNOLOGICA.
 PI Anastasi AM, Colnaghi MI, De Santis R, Di Massimo AM;
 PI Ferrer Marsal C, Mele A;
 DR WPI; 96-412776/41.
 DR N-PSDB; T33445.
 PT Murine/human chimeric monoclonal antibody, chMint5 specific for
 PT EGF-R - shows a lower immunogenicity when administered to humans
 PS Claim 7: Page 15; 28pp; English.
 CC The amino acid sequence (W00240) of the heavy chain variable region
 CC (VH) of the epidermal growth factor receptor (EGF-R)-specific mouse-
 CC human chimeric antibody chMint5 was deduced from a cDNA clone
 CC (T33445) obtd. by PCR amplification of murine Mint5 hybridoma DSM
 CC ACC2150 cDNA. chMint5 comprises Mint5 VH and VL regions fused
 CC to human C-gamma1 and CK regions. Constructs were expressed in
 CC CHO cell transfectants. chMint5 shows lower immunogenicity than
 CC Mint5 when administered to humans. It can be used in diagnostic
 CC assays or used to produce immunotoxins or immunocytokines useful
 CC for tumour therapy.
 SQ Sequence 120 AA;

Query Match 92.9%; Score 52; DB 1; Length 120;
 Best Local Similarity 90.0%; Pred. No. 0.011;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDVTQVQ 10
 Db 57 STYYPDVTQVG 66

RESULT 9
 W21652
 ID W21652 standard; Protein; 139 AA.
 AC W21652;
 DT 03-JAN-1998 (first entry)
 DE Humanised reshaped MAB 15 heavy chain variable region..
 DE Humanised antibody; monoclonal antibody; MAB 15; tumour;
 KW lung cancer; therapy.
 KW Chimeric Mus musculus.
 OS Chimeric Homo sapiens.
 OS Chimeric synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= Sig_peptide
 FT Protein 20..139
 FT /label= Mat_protein
 FT Region 20..49

FT Region /label= Framework-1
 FT 50..54
 FT /label= CDR1
 FT /note= "complementarity determining region 1"
 FT 55..68
 FT /label= Framework-2
 FT 69..85
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT 86..117
 FT /label= Framework-3
 FT 118..128
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 FT 129..138
 FT /label= Framework-4
 PN EP-781847-A1.
 PD 02-JUL-1997.
 PF 25-OCT-1996; 117154.
 PR 06-NOV-1995; EP-117407.
 PA (MERE) MERCK PATENT GMBH.
 PI Bendig M, Jones T, Saldana J;
 DR WPI; 97-334904/31.
 DR N-PSDB; T72237.
 PT Humanised form of murine monoclonal antibody MAB 15 - useful for
 PT treating lung cancer
 PS Claim 2: Fig 12; 7lpp; English.
 CC This polypeptide comprises the heavy chain variable region VH
 CC of humanised reshaped monoclonal antibody (MAB) 15 comprising
 CC complementarity determining regions of murine MAB 15 (DSM ACC2117),
 CC and reshaped human 30P1 framework regions. It is expressed by a
 CC cDNA clone (see T72237) prepared using PCR mutagenesis methods. A
 CC claimed process for preparation of humanised reshaped MAB 15
 CC involves: cloning and sequencing murine MAB 15 VL and VH regions
 CC (see W21653 and W21654); constructing, expressing and analysing
 CC chimeric MAB 15 antibody (see W21655-56); modelling the structure
 CC of murine MAB 15 variable regions; designing reshaped human MAB 15
 CC variable regions; preparing an oligonucleotide sequence which codes
 CC for the constant regions of the light and heavy chain of a human
 CC immunoglobulin; and constructing, expressing and analysing the
 CC complete reshaped human MAB 15. The humanised MAB can be used for
 CC treating tumours, especially lung cancer, and for the manufacture
 CC of a drug related to tumours, especially lung cancer.
 SQ Sequence 139 AA;

Query Match 92.9%; Score 52; DB 1; Length 139;
 Best Local Similarity 90.0%; Pred. No. 0.013;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDVTQVQ 10
 Db 76 STYYPDVTQVG 85

RESULT 10
 W21656
 ID W21656 standard; Protein; 139 AA.
 AC W21656;
 DT 03-JAN-1998 (first entry)
 DE Chimeric MAB 15 PCR-modified heavy chain variable region..
 DE Humanised antibody; monoclonal antibody; MAB 15; tumour;
 KW lung cancer; therapy.
 KW Chimeric Mus musculus.
 OS Chimeric synthetic.
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT /label= Sig_peptide
 FT Protein 25..139
 FT /label= Mat_protein
 FT Region 20..49
 FT /label= Framework-1
 FT 50..54

W27526
ID W27526 standard; Protein; 117 AA.
AC W27526;
DE 16-DEC-1997 (first entry)
DT Heavy chain variable region of human CRA2 antibody.
KW Complementarity determining region; CDR; murine; mouse; human;
KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
KW IgE; MAb; heavy chain; variable region; humanised; semi-chimeric;
KW chimeric; treatment; prevention; disease; allergy; CRA2.
OS Homo sapiens.
PN J09191886-A.
PD 29-JUL-1997.
PF 19-JAN-1996; 024816.
PR 19-JAN-1996; JP-024816.
PA (ASAK) ASahi BREWERIES LTD.
PA (NIKK-) NIKKA WHISKEY KK.
PA (TORI) TORII YAKUHIIN KK.
PA (TSUR/) TSURA T.
DR WPI; 97-429186/40.
PT Humanised, semi-chimeric and chimeric antibodies against human
PT high-affinity IgE receptor - useful medicinally and have low
PT antigenicity in humans
PS Claim 2; Page 13; 26pp; Japanese.
CC The present sequence, the heavy chain variable region of the human
CC antibody (Ab) CRA2, was used in the preparation of a humanised or
CC semi-chimeric monoclonal Ab (MAb), comprising complementarity
CC determining regions (CDR) from a murine, anti-human high affinity
CC immunoglobulin E (IgE) receptor, MAb. The humanised, semi-chimeric
CC or chimeric MAb can be used to treat or prevent diseases,
CC specifically allergies, associated with the receptor, and has very
CC low antigenicity in humans.
SQ Sequence 117 AA;

Query Match 92.9%; Score 52; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. NO. 0.01;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
| | | | | | | | | |
DB 57 STYYPDTVKG 66

RESULT 6
W27354
ID W27354 standard; Protein; 117 AA.
AC W27354;
DE 16-DEC-1997 (first entry)
DT Heavy chain variable region of human CRA2 antibody.
KW Complementarity determining region; CDR; murine; mouse; human;
KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
KW IgE; MAb; heavy chain; variable region; humanised; semi-chimeric;
KW chimeric; treatment; prevention; disease; allergy; CRA2.
OS Homo sapiens.
PN J09191886-A.
PD 29-JUL-1997.
PF 19-JAN-1996; 024816.
PR 19-JAN-1996; JP-024816.
PA (ASAK) ASahi BREWERIES LTD.
PA (NIKK-) NIKKA WHISKEY KK.
PA (TORI) TORII YAKUHIIN KK.
PA (TSUR/) TSURA T.
DR WPI; 97-429186/40.
DR N-PSDB; T90025.
PT Humanised, semi-chimeric and chimeric antibodies against human
PT high-affinity IgE receptor - useful medicinally and have low
PT antigenicity in humans
PS Disclosure; Fig 1; 26pp; Japanese.
CC The cDNA encoding the present sequence, the heavy chain variable
CC region of the human antibody (Ab) CRA2, was used in the preparation
CC of a humanised or semi-chimeric monoclonal Ab (MAb), comprising
CC complementarity determining regions (CDR) from a murine, anti-human
CC high affinity immunoglobulin E (IgE) receptor, MAb. The humanised,

CC semi-chimeric or chimeric MAb can be used to treat or prevent
CC diseases, specifically allergies, associated with the receptor, and
CC has very low antigenicity in humans.
SQ Sequence 117 AA;

Query Match 92.9%; Score 52; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. NO. 0.01;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
| | | | | | | | | |
DB 57 STYYPDTVKG 66

RESULT 7
R79161
ID R79161 standard; peptide; 118 AA.
AC R79161;
DE 04-MAR-1996 (first entry)
DT Human IgE receptor-binding antibody-related peptide heavy chain.
KW Immunoglobulin E; antibody; receptor; monoclonal; detection;
KW Complementarity determining region.
OS Mus sp.
FH Key Location/Qualifiers
FT region 29..33 /label= CDR1H
FT /note= "all CDR regions are claimed"
FT region 48..64 /label= CDR2H
FT /note= "all CDR regions are claimed"
FT region 97..107 /label= CDR3H
FT /note= "all CDR regions are claimed"

J07165799-A.
PN 27-JUN-1995.
PD 22-OCT-1993; 264792.
PR 22-OCT-1993; JP-264792.
PA (ASAK) ASahi BREWERIES LTD.
PA (NIKK-) NIKKA WHISKEY KK.
PA (TORI) TORII YAKUHIIN KK.
PA (TSUR/) TSURA T.
DR WPI; 95-261292/34.
DR N-PSDB; Q96288.
PT Novel monoclonal antibody against human high-affinity IgE receptor -
PT and DNA fragment encoding the MAb, for the specific identification
PT of human Fc-epsilon RI
PS Claim 9; Page 16; 20pp; Japanese.
CC Polypeptides which specifically recognise human IgE receptor (Fc-
CC epsilon-RI) have been isolated and sequenced. The new peptides are
CC related to a monoclonal antibody against Fc-epsilon-RI and are
CC either heavy or light chain molecules. The heavy chain molecules
CC have the general formula FRI-CDR1H-FR2-CDR2H-FR3-CDR3H-FR4 (corresp.
CC to R79153, R79155, R79157, R79159 and R79161) and are encoded by
CC Q96280, Q96282, Q96284, Q96286 and Q96288. FRI is a polypeptide
CC having 29-36 amino acids (aa), FR2 is a 10-16 aa polypeptide, FR3 is
CC a 33-35 aa polypeptide and FR4 is a 12-14 aa polypeptide. Similarly
CC the light chains have the general formula FR5-CDR1L-FR6-CDR2L-FR7-
CC CDR3L-FR8, (corresp. to R79154, R79156, R79158, R79160 and R79162)
CC and are encoded by Q96281, Q96283, Q96285, Q96287 and Q96289. FR5
CC is a 23-28 aa polypeptide, FR6 is a 14-16 aa polypeptide, FR7 is a
CC 30-34 aa polypeptide and FR8 is a 9-11 aa polypeptide. All the
CC peptides are derived from mouse hybridoma cells and are useful in
CC the detection of the human Fc-epsilon-RI or for the elucidation of
CC an antigen recognising region of a monoclonal antibody against
CC human Fc-epsilon-RI.
SQ Sequence 118 AA;

Query Match 92.9%; Score 52; DB 1; Length 118;
Best Local Similarity 90.0%; Pred. NO. 0.01;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
 KW IgE; MAb; heavy chain; variable region; humanised; semi-chimeric;
 KW chimeric; treatment; prevention; disease; allergy.
 OS Mus spp.
 PN J09191886-A.
 PD 29-JUL-1997. 024816.
 PR 19-JAN-1996; JP-024816.
 PR (ASAK) ASAKI BREWERIES LTD.
 PA (NIKK-) NIKKA WHISKEY KK.
 PA (TORI) TORII YAKUHIIN KK.
 PA (TSUR/) TSURA T.
 DR WPI; 97-429186/40.
 PT Humanised, semi-chimeric and chimeric antibodies against human
 PT high-affinity IgE receptor - useful medicinally and have low
 PT antigenicity in humans
 PS Claim 1; Page 12; 26pp; Japanese.
 CC The present complementarity determining region 2 (CDR2), which is
 CC from a murine, anti-human high affinity immunoglobulin E (IgE)
 CC receptor, monoclonal antibody (MAB) heavy chain variable region,
 CC can be used in the preparation of humanised or semi-chimeric
 CC anti-human high affinity IgE receptor MAB. The MAB can be used to
 CC treat or prevent diseases, specifically allergies, associated with
 CC the receptor. The humanised, semi-chimeric or chimeric MAB have
 CC very low antigenicity in humans.
 SQ Sequence 17 AA;

Query Match 92.9%; Score 52; DB 1; Length 17;
 Best Local Similarity 90.0%; Pred. No. 0.0012;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDVTVOG 10
 Db 8 STYYPDVTVGK 17
 |||||:|

RESULT 3

ID R79155 standard; peptide; 117 AA.
 AC R79155;
 DT 04-MAR-1996 (first entry)
 DE Human IgE receptor-binding antibody-related peptide heavy chain.
 KW Immunoglobulin E; antibody; receptor; monoclonal; detection;
 KW complementarity determining region.
 OS Mus sp.
 FH Key Location/Qualifiers
 FT region 31..35
 FT /label= CDR1H
 FT /note= "all CDR regions are claimed"
 FT region 50..66
 FT /label= CDR2H
 FT /note= "all CDR regions are claimed"
 FT region 99..106
 FT /label= CDR3H
 FT /note= "all CDR regions are claimed"

J07165799-A.

27-JUN-1995.

22-OCT-1993; 264792.

22-OCT-1993; JP-264792.

(ASAK) ASAKI BREWERIES LTD.

(NIKK-) NIKKA WHISKEY KK.

(TORI) TORII YAKUHIIN KK.

(TSUR/) TSURA T.

WPI; 95-261292/34.

N-PSDB; Q96282.

PT Novel monoclonal antibody against human high-affinity IgE receptor -
 PT and DNA fragment encoding the MAb, for the specific identification
 PT of human Fc-epsilon RI

Claim 3; Page 13; 20pp; Japanese.

CC Polypeptides which specifically recognise human IgE receptor (Fc-
 CC epsilon-RI) have been isolated and sequenced. The new peptides are
 CC related to a monoclonal antibody against Fc-epsilon-RI and are

CC either heavy or light chain molecules. The heavy chain molecules
 CC have the general formula FR1-CDR1H-FR2-CDR2H-FR3-CDR3H-FR4 (corresp.
 CC to R79153, R79155, R79157, R79159 and R79161) and are encoded by
 CC Q96280, Q96282, Q96284, Q96286 and Q96288. FR1 is a polypeptide
 CC having 29-36 amino acids (aa), FR2 is a 10-16 aa polypeptide, FR3 is
 CC a 33-35 aa polypeptide and FR4 is a 12-14 aa polypeptide. Similarly
 CC the light chains have the general formula FR5-CDR1L-FR6-CDR2L-FR7-
 CC CDR3L-FR8, (corresp. to R79154, R79156, R79158, R79160 and R79162)
 CC and are encoded by Q96281, Q96283, Q96285, Q96287 and Q96289. FR5
 CC is a 23-28 aa polypeptide, FR6 is a 14-16 aa polypeptide, FR7 is a
 CC 30-34 aa polypeptide and FR8 is a 9-11 aa polypeptide. All the
 CC peptides are derived from mouse hybridoma cells and are useful in
 CC the detection of the human Fc-epsilon-RI or for the elucidation of
 CC an antigen recognising region of a monoclonal antibody against
 CC human Fc-epsilon-RI.
 SQ Sequence 117 AA;

Query Match 92.9%; Score 52; DB 1; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.01;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDVTVOG 10
 Db 57 STYYPDVTVGK 66
 |||||:|

RESULT 4

ID W27357 standard; Protein; 117 AA.

AC W27357;

DT 16-DEC-1997 (first entry)

DE Heavy chain variable region of chimeric human CRA2 antibody.

KW Complementarity determining region; CDR; murine; mouse; human;

KW high affinity; immunoglobulin E; receptor; monoclonal antibody;

KW IgE; MAB; heavy chain; variable region; humanised; semi-chimeric;

KW chimeric; treatment; prevention; disease; allergy; CRA2.

OS Chimeric - Homo sapiens.

OS Chimeric - Mus spp.

OS Synthetic.

PN J09191886-A.

PD 29-JUL-1997.

PF 19-JAN-1996; 024816.

PR 19-JAN-1996; JP-024816.

PA (ASAK) ASAKI BREWERIES LTD.

PA (NIKK-) NIKKA WHISKEY KK.

PA (TORI) TORII YAKUHIIN KK.

PA (TSUR/) TSURA T.

DR WPI; 97-429186/40.

PT Humanised, semi-chimeric and chimeric antibodies against human

PT high-affinity IgE receptor - useful medicinally and have low

PT antigenicity in humans

PS Claim 8; Page 15; 26pp; Japanese.

CC The present sequence, the heavy chain variable region of a

CC chimeric human CRA2 antibody (Ab), comprises complementarity

CC determining regions (CDR) from a murine, anti-human high affinity

CC immunoglobulin E (IgE) receptor, monoclonal Ab (MAB). The

CC humanised chimeric MAB can be used to treat or prevent diseases,

CC specifically allergies, associated with the receptor, and has very

CC low antigenicity in humans.

SQ Sequence 117 AA;

Query Match 92.9%; Score 52; DB 1; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.01;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDVTVOG 10
 Db 57 STYYPDVTVGK 66
 |||||:|

RESULT 5

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2000, 19:21:31 ; Search time 148.45 Seconds
(without alignments)
1.596 Million cell updates/sec

Title: US-09-016-061-56
Perfect score: 56
Sequence: 1 STYPTVQV 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	10	1 W76018	LM609 grafted anti
2	52	92.9	17	1 W7342	CDR2 from murine a
3	52	92.9	117	1 W79155	Human IgE receptor
4	52	92.9	117	1 W27357	Heavy chain variab
5	52	92.9	117	1 W27526	Heavy chain variab
6	52	92.9	117	1 W27354	Heavy chain variab
7	52	92.9	118	1 W79161	Human IgE receptor
8	52	92.9	120	1 W00240	EGF receptor chime
9	52	92.9	139	1 W21652	Humanised reshaped
10	52	92.9	139	1 W21656	Chimeric MAb 15 PC
11	52	92.9	140	1 W21654	Mouse MAb 15 heavy
12	52	92.9	158	1 W19577	Mouse anti-idiotyp
13	52	92.9	158	1 W19579	Mouse anti-idiotyp
14	52	92.9	239	1 W73874	Human antiFc epsil
15	52	92.9	242	1 W73876	Human antiFc epsil
16	52	92.9	260	1 R77617	Anti-C5 MAb N19/8
17	50	89.3	117	1 R79157	Human IgE receptor
18	49	87.5	98	1 R36526	Heavy chain VH 718
19	49	87.5	123	1 W66099	anti-CD22 monoclon
20	49	87.5	136	1 R06251	Variable region of
21	48	85.7	119	1 W11919	Humanised MAb SK48
22	48	85.7	121	1 R60626	ME1-14 heavy chain
23	48	85.7	121	1 W16648	Anti-cancer specif
24	48	85.7	121	1 W22951	Monoclonal antibod
25	48	85.7	121	1 W86124	Protein sequence o
26	48	85.7	121	1 W86125	Protein sequence o
27	48	85.7	121	1 W86122	Protein sequence o
28	48	85.7	121	1 W86120	Protein sequence o
29	48	85.7	121	1 W86118	Murine 340 Vh amin
30	48	85.7	130	1 R86318	Anti-IL-8 MAb 5.12
31	48	85.7	130	1 W23785	Monoclonal antibod
32	48	85.7	130	1 W31575	Anti IL-8 monoclon
33	48	85.7	130	1 W42318	Anti IL-8 antibody
34	48	85.7	130	1 W33740	Anti IL-8 monoclon

35	48	85.7	130	1 W40121	Murine monoclonal
36	48	85.7	130	1 W69306	Murine anti-IL-8 M
37	48	85.7	138	1 W03722	Anti-human gp39 MA
38	48	85.7	139	1 R27053	Anti-CEA specific
39	48	85.7	139	1 R30480	bCEA specific mous
40	48	85.7	144	1 R61239	Monoclonal antibod
41	48	85.7	247	1 W11917	Murine MAb SK48-E2
42	48	85.7	251	1 R86320	Anti-IL-8 MAB 5.12
43	48	85.7	251	1 W23787	Chimeric monoclonal
44	48	85.7	251	1 W31577	Chimeric anti IL-8
45	48	85.7	251	1 W42320	Murine variable an

ALIGNMENTS

RESULT 1

W76018	ID	W76018 standard; Protein; 10 AA.
AC	W76018;	
DT	02-NOV-1998	(first entry)
DE	LM609 grafted antibody V-H region CDR2 protein fragment #4.	
KW	Vitaxin; antibody; variable region; heavy chain; light chain; integrin;	
KW	LM609; inhibitor; integrin-mediated signal transduction; treatment;	
KW	diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;	
KW	neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;	
KW	macular degeneration; osteoporosis; primer; V-H region; CDR;	
KW	complementarity determining region.	
OS	Mus sp.	
PN	W09833919-A2.	
PD	06-AUG-1998.	
PF	30-JAN-1998: U01826.	
PR	30-JAN-1997: US-791391.	
PA	(IXSY-) IXSY INC.	
PI	Glaser SM, Huse WD;	
DR	WPI; 98-437472/37.	
DR	N-PSDB: V49855.	
PT	Humanised antibody, Vitaxin, that binds selectively to alphavbeta3	
PT	integrin - and related grafted antibodies based on murine monoclonal	
PT	LM609, also related nucleic acid, used to treat, prevent or diagnose	
PS	angiogenesis or restenosis	
PS	Claim 61: Page 41; 129pp: English.	
CC	W76007-W76040 are protein fragments of the grafted monoclonal antibody	
CC	LM609 heavy and light chain variable region. LM609 and the antibody	
CC	vitaxin bind selectively to integrin alphavbeta3 and can be used to	
CC	inhibit binding of alphavbeta3 to a ligand and thus block	
CC	integrin-mediated signal transduction. This is useful in the treatment,	
CC	prevention and diagnosis of alphavbeta3-mediated disease, specifically,	
CC	angiogenesis and restenosis (but also e.g. (non-)immune inflammation,	
CC	diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid	
CC	arthritis, macular degeneration, osteoporosis etc.). The antibodies	
CC	contain non-murine framework regions so are suitable for use in humans.	
CC	Enhanced types of LM609 have affinity more than 90 times greater than	
CC	that of parent the parent antibody.	
SQ	Sequence 10 AA;	

Query Match 100.0%; Score 56; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYPTVQV 10
Db 1 STYPTVQV 10
|||||

RESULT 2

W27342	ID	W27342 standard; peptide; 17 AA.
	AC	W27342;
	DT	12-DEC-1997 (first entry)
	DE	CDR2 from murine anti-human IgE receptor antibody heavy chain.
	KW	Complementarity determining region; CDR2; murine; mouse; human;

```

DE SALIVARY GLAND SECRETION PROTEIN (FRAGMENT).
GN SGS-1.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidae; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RA ROTH G.E., WATTLER S., BORNSCHNEIN H., LEHMANN M., KORGE G.;
RT "Structure and regulation of the salivary gland secretion protein gene
RT Sgs-1 of Drosophila melanogaster.";
RL Genetics 0:0-0(1999).
DR EMBL; AF156227; AAD43809.1; -.
DR NON_TER 258 258
SQ SEQUENCE 258 AA; 27832 MW; D925EFDC CRC32;

Query Match 62.5%; Score 35; DB 5; Length 258;
Best Local Similarity 85.7%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 YPDPVQ 9
DB 47 YPDPVQ 53

RESULT 13
O74693 PRELIMINARY; PRT; 731 AA.
AC O74693; Q01308;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE CLOCK-CONTROLLED PROTEIN 9.
GN CCG-9.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycetes; Euascomycetes; Pyrenomycetes;
OC Sordariales; Sordariaceae; Neurospora.
RN [1]
RP SEQUENCE FROM N.A., AND INDUCTION.
RX STRAIN=FRQ7;
RX MEDLINE; 97075124.
RA BELL-PEDERSEN D., SHINOHARA M.L., LOROS J.J., DUNLAP J.C.;
RT "Circadian clock-controlled genes isolated from Neurospora crassa are
RT late night- to early morning-specific.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:13096-13101(1996).
RN [2]
RP REVISIONS.
RA SHINOHARA M.L., BELL-PEDERSEN D., LOROS J.J., DUNLAP J.C.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -1- INDUCTION: EXPRESSION LEVELS MAY BE INFLUENCED BY CIRCADIAN
CC RHYTHMS.
CC -1- SIMILARITY: TO G.FRONDOSA TREHALOSE SYNTHASE.
DR EMBL; AF088906; AAC64285.1; -.
DR EMBL; U46088; AAA98472.1; ALT_FRAME.
DR PFAM; PF00534; Glycos_transf_1; 1.
SQ SEQUENCE 731 AA; 81834 MW; 78A09452 CRC32;

Query Match 62.5%; Score 35; DB 3; Length 731;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TYYPDTVQ 9
DB 535 TYYPDLIR 542

RESULT 14
O9Y2R2 PRELIMINARY; PRT; 807 AA.
AC O9Y2R2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)

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DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE PROTEIN TYROSINE PHOSPHATASE HOMOLOG (EC 3.1.3.48).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA LIU T., ZHANG J., FU G., ZHANG Q., YE M., ZHOU J., WU J., SHEN Y.,
RA YU M., CHEN S., MAO M., CHEN Z.;
RT "Human protein tyrosine phosphatase (70zpep) homolog.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF077031; AAD27764.1; -.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
KW Hydrolase.
SQ SEQUENCE 807 AA; 91708 MW; 5C10AAEF CRC32;

Query Match 62.5%; Score 35; DB 4; Length 807;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYPDTVQ 9
DB 722 STSYPDTE 730

RESULT 15
O95063 PRELIMINARY; PRT; 808 AA.
AC O95063;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DE 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE LYMPHOID PHOSPHATASE LYPI (EC 3.1.3.48).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA ROIFMAN C.M.;
RT "Human cDNA of Lyp1 Protein Tyrosine Phosphatase.";
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001846; AAD00904.1; -.
DR HSP; P18052; IYFO.
DR PROSITE; PS00383; TYR_PHOSPHATASE_1; 1.
KW Hydrolase.
SQ SEQUENCE 808 AA; 91763 MW; 204C9CB9 CRC32;

Query Match 62.5%; Score 35; DB 4; Length 808;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYPDTVQ 9
DB 723 STSYPDTE 731

Search completed: May 27, 2000, 19:38:36
Job time: 2369 sec

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Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TYYPDTVQG 10
||| |::|
Db 26 TYIADSVKG 34

RESULT 9

O16565 PRELIMINARY; PRT; 194 AA.

AC O16565

DT 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DE B0047.2 PROTEIN.

GN B0047.2.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;

OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN-BRISTOL N2;

RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULTON J.,

RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P., III of C.

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RT elegans.";

RL Nature 368:32-38(1994).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RA PAULEY A., GOELA D., OZERSKY P.;

RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RA WATERSTON R.;

RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF016658; AAB66042.1; -.

SQ SEQUENCE 194 AA; 22602 MW; E82C2F36 CRC32;

Query Match 64.3%; Score 36; DB 5; Length 194;

Best Local Similarity 75.0%; Pred. No. 19;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 STIYPTDV 8
||| |::|
Db 93 STIYPTDI 100

RESULT 10

O17863 PRELIMINARY; PRT; 326 AA.

AC O17863

DT 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DE F37H8.4 PROTEIN.

GN F37H8.4.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;

OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

RN [1]

RP SEQUENCE FROM N.A.

RA GREGORY J.;

RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE; 94150718.

RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULTON J.,

RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RT elegans.";

RL Nature 368:32-38(1994).

DR EMBL; Z81534; CAB04347.1; -.

SQ SEQUENCE 326 AA; 36733 MW; C4CDF53F CRC32;

Query Match 64.3%; Score 36; DB 5; Length 326;

Best Local Similarity 85.7%; Pred. No. 35;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STIYPTD 7
||| |::|
Db 80 STIYPTD 86

RESULT 11

O05938 PRELIMINARY; PRT; 352 AA.

ID O05938

DT 01-JUL-1997 (TrEMBLrel. 04, Created)

DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)

DT 01-AUG-1998 (TrEMBLrel. 07, Last annotation update)

DE LIPASE HELPER PROTEIN.

GN LPWB.

OS Pseudomonas wisconsinensis.

OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;

OC Pseudomonas.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-LMG P-15151;

RA ANDRE C., CHARMOILLE L., CORNELIS P., HAZBON M.H.;

RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; U88907; AAB53648.1; -.

SQ SEQUENCE 352 AA; 39574 MW; 149A3E5C CRC32;

Query Match 64.3%; Score 36; DB 2; Length 352;

Best Local Similarity 87.5%; Pred. No. 39;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TYYPDTVQ 9
||| |::|
Db 273 TYVDPDTVQ 280

RESULT 12

O9YOE9

ID O9YOE9 PRELIMINARY; PRT; 258 AA.

AC O9YOE9

DT 01-NOV-1999 (TrEMBLrel. 12, Created)

DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)

DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)


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RX MEDLINE: 95159428.
RA SIMON-MATEO C., FREIJE J.M., ANDRES G., LOPEZ-OTIN C., VINUELA E.;
RT "Mapping and sequence of the gene encoding protein p17, a major
RL African swine fever virus structural protein.";
RL Virology 206:1140-1144(1995).
RN [23]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE: 92263807.
RA GARCIA-BEATO R., FREIJE J.M., LOPEZ-OTIN C., BLASCO R., VINUELA E.,
RA SALAS M.L.;
RT "A gene homologous to topoisomerase II in African swine fever virus.";
RL Virology 188:938-947(1992).
RN [24]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE: 94091056.
RA FREIJE J.M., LAIN S., VINUELA E., LOPEZ-OTIN C.;
RT "Nucleotide sequence of a nucleoside triphosphate phosphohydrolase
RT gene from African swine fever virus.";

Query Match 66.1%; Score 37; DB 12; Length 962;
Best Local Similarity 60.0%; Pred. No. 79; Mismatches 2; Indels 0; Gaps 0;
Matches 6; Conservative 2;

QY 1 STYYPDVTQV 10
Db 110 STHYPMILG 119

RESULT 6
O93574 PRELIMINARY; PRT; 3209 AA.
AC O93574
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE EXTRACTED CELLULAR REELIN (FRAGMENT).
GN REELN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RA BERNIER B., GOFFINET A.M.;
RT "Comparative study of reelin in vertebrates.";
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF090441; AAC35559.1; -.
DR PFAM; PF00008; EGF; 5.
KW Glycoprotein.
FT NON_TER 1 1
SQ SEQUENCE 3209 AA; 361288 MW; E574CD3A CRC32;

Query Match 66.1%; Score 37; DB 13; Length 3209;
Best Local Similarity 70.0%; Pred. No. 3.1e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 STYYPDVTQV 10
Db 1826 STYTGTTQ 1835

RESULT 7
Q60841 PRELIMINARY; PRT; 3461 AA.
AC Q60841
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE REELIN (REELER PROTEIN).
GN REELN OR REELN OR RL.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CEREBELLUM;
RX MEDLINE: 95231649.
RA D'ARCANDELO G., MIAO G.G., CHEN S.C., SOARES H.D., MORGAN J.I.,
RA CURRAN T.;
RT "A protein related to extracellular matrix proteins deleted in the
RT mouse mutant reeler.";
RL Nature 374:719-723(1995).
RN [2]
RP SEQUENCE OF 2581-3461 FROM N.A.
RC STRAIN=BALB/C; TISSUE=BRAIN;
RX MEDLINE: 95375789.
RA HIROTSUNE S., TAKAHARA T., SASAKI N., HIROSE K., YOSHIKI A.,
RA OHASHI T., KUSAKABE M., MURAKAMI Y., MURAMATSU M., WATANABE S.,
RA NAKAO K., KATSUKI M., HAYASHIZAKI Y.;
RT "The reeler gene encodes a protein with an EGF-like motif expressed by
RT pioneer neurons.";
RL Nat. Genet. 10:77-83(1995).
RN [3]
RP SEQUENCE OF 2581-3461 FROM N.A.
RC STRAIN=BALB/C; TISSUE=BRAIN;
RX MEDLINE: 96021025.
RA CURRAN T., D'ARCANDELO G., GOFFINET A., HAYASHIZAKI Y.;
RT "Reeler gene discrepancies.";
RL Nat. Genet. 11:12-13(1995).
DR EMBL; U24703; AAB91599.1; -.
DR EMBL; D63520; BAA09788.1; -.
DR MGD; MGI:103022; Reln.
DR PFAM; PF00008; EGF; 7.
KW Glycoprotein.
SQ SEQUENCE 3461 AA; 387510 MW; 0EB2E5DD CRC32;

Query Match 66.1%; Score 37; DB 11; Length 3461;
Best Local Similarity 70.0%; Pred. No. 3.4e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 STYYPDVTQV 10
Db 2078 STYVAGTTQ 2087

RESULT 8
O75741 PRELIMINARY; PRT; 77 AA.
AC O75741
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=INTESTINE;
RA FISCHER M., KUEPPERS R.;
RT "Human IGA and IGM secreting intestinal plasma cells carry heavily
RT mutated VH region genes.";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ009540; CAA08745.1; -.
DR HSSP; P01772; 2IG2.
FT NON_TER 1 1
SQ SEQUENCE 77 AA; 8734 MW; 1F7F9E8E CRC32;

Query Match 64.3%; Score 36; DB 4; Length 77;
Best Local Similarity 66.7%; Pred. No. 6.8;

```

RL J. Virol. 64:2073-2081(1990).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE: 90219204.
RA ALMENDRAL J.M., ALMAZAN F., BLASCO R., VINUELA E.;
RT "Multigene families in African swine fever virus: family 110.";
RL J. Virol. 64:2064-2072(1990).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE: 91134988.
RA CAMACHO A., VINUELA E.;
RT "protein p22 of African swine fever virus: an early structural protein
that is incorporated into the membrane of infected cells.";
RL Virology 181:251-257(1991).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE: 94187118.
RA RODRIGUEZ J.M., YANEZ R.J., PAN R., RODRIGUEZ J.F., SALAS M.L.,
RA VINUELA E.;
RT "Multigene families in African swine fever virus: family 505.";
RL J. Virol. 68:2746-2751(1994).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE: 93346971.
RA YANEZ R.J., RODRIGUEZ J.M., RODRIGUEZ J.F., SALAS M.L., VINUELA E.;
RT "African swine fever virus thymidylate kinase gene: sequence and
transcriptional mapping.";
RL J. Gen. Virol. 74:1633-1638(1993).
RN [9]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE: 94065656.
RA ALCAMI A., ANGULO A., VINUELA E.;
RT "Mapping and sequence of the gene encoding the African swine fever
virion protein of M(r) 11500.";
RL J. Gen. Virol. 74:2317-2324(1993).
RN [10]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE: 93277388.
RA MUNOZ M., FREIJE J.M., SALAS M.L., VINUELA E., LOPEZ-OTIN C.;
RT "Structure and expression in E. coli of the gene coding for protein
p10 of African swine fever virus.";
RL Arch. Virol. 130:93-107(1993).
RN [11]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE: 90357780.
RA BLASCO R., LOPEZ-OTIN C., MUNOZ M., BOCKAMP E.O., SIMON-MATEO C.,
RA VINUELA E.;
RT "Sequence and evolutionary relationships of African swine fever virus
thymidine kinase.";
RL Virology 178:301-304(1990).
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE: 93281390.
RA YANEZ R.J., BOURSNEILL M., NOGAL M.L., YUSTE L., VINUELA E.;
RT "African swine fever virus encodes two genes which share significant
homology with the two largest subunits of DNA-dependent RNA
polymerases.";
RL Nucleic Acids Res. 21:2423-2427(1993).
RN [13]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE: 93353606.
RA RODRIGUEZ J.M., YANEZ R.J., ALMAZAN F., VINUELA E., RODRIGUEZ J.F.;
RT "African swine fever virus encodes a CD2 homolog responsible for the
adhesion of erythrocytes to infected cells.";
RL J. Virol. 67:5312-5320(1993).
RN [14]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE: 94085774.
RA YANEZ R.J., RODRIGUEZ J.M., BOURSNEILL M., RODRIGUEZ J.F., VINUELA E.;
RT "Two putative African swine fever virus helicases similar to yeast
'DBAH' pre-mRNA processing proteins and vaccinia virus ATPases D11L
and D6R.";
RL Gene 134:161-174(1993).
RN [15]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE: 90223993.
RA LOPEZ-OTIN C., FREIJE J.M., PARRA F., MENDEZ E., VINUELA E.;
RT "Mapping and sequence of the gene coding for protein p72, the major
capsid protein of African swine fever virus.";
RL Virology 175:477-484(1990).
RN [16]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE: 94123986.
RA RODRIGUEZ J.M., YANEZ R.J., RODRIGUEZ J.F., VINUELA E., SALAS M.L.;
RT "The DNA polymerase-encoding gene of African swine fever virus:
sequence and transcriptional analysis.";
RL Gene 136:103-110(1993).
RN [17]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE: 93327788.
RA SIMON-MATEO C., ANDRES G., VINUELA E.;
RT "Polyprotein processing in African swine fever virus: a novel gene
expression strategy for a DNA virus.";
RL EMBO J. 12:2977-2987(1993).
RN [18]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE: 93233210.
RA PRADOS F.J., VINUELA E., ALCAMI A.;
RT "Sequence and characterization of the major early phosphoprotein p32
of African swine fever virus.";
RL J. Virol. 67:2475-2485(1993).
RN [19]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE: 92260660.
RA ALCAMI A., ANGULO A., LOPEZ-OTIN C., MUNOZ M., FREIJE J.M.,
RA CARRASCOA A.L., VINUELA E.;
RT "Amino acid sequence and structural properties of protein p12, an
African swine fever virus attachment protein.";
RL J. Virol. 66:3860-3868(1992).
RN [20]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE: 93174976.
RA YANEZ R.J., VINUELA E.;
RT "African swine fever virus encodes a DNA ligase.";
RL Virology 193:531-536(1993).
RN [21]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;
RX MEDLINE: 93174941.
RA PENA L., YANEZ R.J., REVILLA Y., VINUELA E., SALAS M.L.;
RT "African swine fever virus guanylyltransferase.";
RL Virology 193:319-328(1993).
RN [22]
RP SEQUENCE FROM N.A.
RC STRAIN=BA71V;

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 [1]
 RN SEQUENCE FROM N.A.
 RA DESILVA U., D'ARCANGELO G., BRADEN V.V., CHEN J., MIAO G.G.,
 RA CURRAN T., GREEN E.D.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 [2]
 RN SEQUENCE OF 194-430 FROM N.A.
 RA LAMAR B., WAMSLEY P., GIBSON A.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U79716; AAC51105.1; -.
 DR EMBL; AC000121; AAB46357.1; -.
 DR HSSP; P00743; IAP0.
 DR PFAM; PF00008; EGF; 5.
 KW Glycoprotein.
 SQ SEQUENCE 3460 AA; 388399 MW; C8D817E9 CRC32;

Query Match 67.1%; Score 38; DB 4; Length 3460;
 Best Local Similarity 70.0%; Pred. No. 2.2e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 STYDPDTVQG 10
 ||||| |:
 Db 2077 STYAGTMOG 2086

RESULT 3
 ID Q63206 PRELIMINARY; PRT; 517 AA.
 AC Q63206;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE FGR MRNA.
 GN FGR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-F344; TISSUE=LEUKEMIA;
 RA YUE C.C., LABASH J.D., JAYE M.;
 RL Nucleic Acids Res. 0:0-0(1990).
 DR EMBL; X57018; CAA40337.1; -.
 DR HSSP; P00523; 2PTK.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PFAM; PF00069; pkinase; 1.
 DR PFAM; PF00017; SH2; 1.
 DR PFAM; PF00018; SH3; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 SQ SEQUENCE 517 AA; 58792 MW; 285CE487 CRC32;

Query Match 66.1%; Score 37; DB 11; Length 517;
 Best Local Similarity 75.0%; Pred. No. 39;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 YYPDPTVQG 10
 ||||| |:
 Db 32 YYPDPTQG 39

RESULT 4
 ID Q61404 PRELIMINARY; PRT; 517 AA.
 AC Q61404;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE GARDNER-RASHEED FELINE SARCOMA VIRAL (FGR) ONCOGENE HOMOLOG
 DE (C-FGR MRNA).
 GN FGR OR C-FGR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 90191719.
 RA KING F.J., COLE M.D.;
 RT "Molecular cloning and sequencing of the murine c-fgr gene."
 RL Oncogene 5:337-344(1990).
 DR EMBL; X52191; CAA36437.1; -.
 DR HSSP; P00523; 2PTK.
 DR MGD; MGI:95527; Fgr.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PFAM; PF00069; pkinase; 1.
 DR PFAM; PF00017; SH2; 1.
 DR PFAM; PF00018; SH3; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PRINTS; PR00452; SH3DOMAIN.
 SQ SEQUENCE 517 AA; 58882 MW; 0B8F985B CRC32;

Query Match 66.1%; Score 37; DB 11; Length 517;
 Best Local Similarity 75.0%; Pred. No. 39;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 YYPDPTVQG 10
 ||||| |:
 Db 32 YYPDPTQG 39

RESULT 5
 ID Q89443 PRELIMINARY; PRT; 962 AA.
 AC Q89443;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE HELICASE.
 GN B962L.
 OS African swine fever virus (ASFV).
 OC Viruses; dsDNA viruses, no RNA stage;
 OC African swine fever-like viruses.
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE; 96036500.
 RA YANEZ R.J., RODRIGUEZ J.M., NOGAL M.L., YUSTE L., ENRIQUEZ C.,
 RA RODRIGUEZ J.F., VINUELA E.;
 RT "Immune protection conferred by the baculovirus-related glycoprotein
 of Thogoto virus (orthomyxoviridae).";
 RL Virology 208:249-278(1995).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE; 94333765.
 RA LA VEGA I., GONZALEZ A., BLASCO R., CALVO V., VINUELA E.;
 RT "Nucleotide sequence and variability of the inverted terminal
 repetitions of African swine fever virus DNA.";
 RL Virology 201:152-156(1994).
 [3]
 RN SEQUENCE FROM N.A.
 RC STRAIN=BA71V;
 RX MEDLINE; 90219205.
 RA GONZALEZ A., CALVO V., ALMAZAN F., ALMENDRAL J.M., RAMIREZ J.C.,
 RA LA VEGA I., BLASCO R., VINUELA E.;
 RT "Multigene families in African swine fever virus: family 360.";

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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:38:34 ; Search time 199.56 Seconds
(without alignments)
3.474 Million cell updates/sec

Title: US-09-016-061-56
Perfect score: 56
Sequence: 1 STYYPDTVQG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

SPTREMBL12:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	40	71.4	77	4	O75728
2	38	67.9	3460	4	P78509
3	37	66.1	517	11	Q63206
4	37	66.1	517	11	Q61404
5	37	66.1	962	12	Q89443
6	37	66.1	3209	13	Q93574
7	37	66.1	3461	11	Q60841
8	36	64.3	77	4	O75741
9	36	64.3	194	5	O16565
10	36	64.3	326	5	O17863
11	36	64.3	352	2	O05938
12	35	62.5	258	5	O9Y0E9
13	35	62.5	731	3	O74693
14	35	62.5	807	4	O9Y2R2
15	35	62.5	808	4	O95063
16	35	62.5	1252	2	Q9ZA93
17	35	62.5	3097	5	O15943
18	34	60.7	82	4	O75732
19	34	60.7	129	2	Q60111
20	34	60.7	129	12	P89125

21	34	60.7	129	12	P89130
22	34	60.7	141	12	Q9WRY2
23	34	60.7	141	12	Q9WRY1
24	34	60.7	141	12	Q9WRW3
25	34	60.7	141	12	Q9WRW1
26	34	60.7	244	2	O50296
27	34	60.7	292	12	Q9YLL5
28	34	60.7	318	1	O58278
29	34	60.7	372	1	Q9Y966
30	34	60.7	559	12	O90026
31	34	60.7	652	2	P71994
32	34	60.7	662	5	O62139
33	34	60.7	732	4	O43607
34	34	60.7	792	4	P78313
35	34	60.7	934	5	P91438
36	34	60.7	1224	4	P78311
37	34	60.7	1265	4	P78312
38	34	60.7	3070	12	O89906
39	34	60.7	3074	12	Q08534
40	33	58.9	115	11	O64186
41	33	58.9	141	12	O5WRX0
42	33	58.9	141	12	Q9W9R6
43	33	58.9	160	2	O53974
44	33	58.9	193	1	O51987
45	33	58.9	265	5	P90819

ALIGNMENTS

RESULT 1
O75728 PRELIMINARY; PRT; 77 AA.
AC O75728;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE IG HEAVY CHAIN VARIABLE REGION (FRAGMENT).
GN VH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=INTESTINE;
RA FISCHER M., KUEPPERS R.;
RT "Human Iga and Igm secreting intestinal plasma cells carry heavily mutated VH region genes";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ009525; CAA08732.1; -.
FT NON_TER 1 1
FT NON_TER 77 77
SQ SEQUENCE 77 AA; 8925 MW; EA14CFDF CRC32;

Query Match 71.4%; Score 40; DB 4; Length 77;
Best Local Similarity 66.7%; Pred. No. 1.2;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYYPDTVQG 10
Db 27 TFYPSVKG 35
1:111111

RESULT 2
P78509 PRELIMINARY; PRT; 3460 AA.
ID P78509
AC P78509;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE REELIN.
GN REELN.

Db 58 TTYADSVRG 66

Search completed: May 27, 2000, 20:07:11
Job time: 983 sec

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FT DOMAIN          251 504 PROTEIN KINASE.
FT NP_BIND         257 265 ATP (BY SIMILARITY).
FT BINDING         279 279 ATP (BY SIMILARITY).
FT ACT_SITE        370 370 BY SIMILARITY.
FT MOD_RES         400 400 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
SQ SEQUENCE        517 AA: 58867 MW: F655BDB4510F3076 CRC64;

Query Match          66.1%; Score 37; DB 1; Length 517;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 YYPDVTQVG 10
    |||||
Db 32 YYPDPTQG 39

RESULT 14
POLG_KUNJM STANDARD; PRT; 3433 AA.
AC P14335: Q82983;
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DE GENOME POLYPROTEIN [CONTAINS: CAPSID PROTEIN C (CORE PROTEIN); MATRIX
DE PROTEIN (ENVELOPE PROTEIN M); MAJOR ENVELOPE PROTEIN E; NONSTRUCTURAL
DE PROTEINS NS1, NS2, NS4A AND NS4B; HELICASE (NS3); RNA-DIRECTED RNA
DE POLYMERASE (EC 2.7.7.48) (NS5)].
OS Kunjin virus (strain MR61C).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88089524.
RA Costa G., Parker M.D., Speight G., Byrne M.E., Westaway E.G.;
RT "Nucleotide and complete amino acid sequences of Kunjin virus:
RT definitive gene order and characteristics of the virus-specified
RT proteins.";
RL J. Gen. Virol. 69:1-21(1988).
CC -!- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE
CC HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
CC NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
CC -!- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
CC PROTEIN M AND GLYCOPROTEIN E. THE NUCLEOCAPSID IS A COMPLEX OF
CC PROTEIN C AND MRNA.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL; D00246; BAA00176.1; -.
DR PIR; A28697; GNWVKV.
DR HSSP; P14336; 1SVB.
DR PFAM; PF00869; Flavi_glycoprot; 1.
DR PFAM; PF00948; Flavi_NS1; 1.
DR PFAM; PF00949; Flavi_helicase; 1.
DR PFAM; PF00972; Flavi_NS5; 1.
DR PFAM; PF01002; Flavi_NS2B; 1.
DR PFAM; PF01003; Flavi_Capsid; 1.
DR PFAM; PF01004; Flavi_M; 1.
DR PFAM; PF01005; Flavi_NS2A; 1.
DR PFAM; PF01349; Flavi_NS4B; 1.
DR PFAM; PF01350; Flavi_NS4A; 1.
DR PFAM; PF01570; Flavi_propep; 1.
KW Polyprotein; Glycoprotein; Transferase; RNA-directed RNA polymerase;
KW Core protein; Coat protein; Envelope protein; Helicase; ATP-binding;
KW Transmembrane; Nonstructural protein.
PT INIT_MET 1 1 REMOVED FROM CAPSID PROTEIN C BY THE

```

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FT CHAIN           1 123 CELLULAR AMINOPEPTIDASE.
FT PROPEP          124 215 CAPSID PROTEIN C.
FT CHAIN           216 290 MEMBRANE PROTEIN M.
FT CHAIN           291 791 MAJOR ENVELOPE PROTEIN E.
FT CHAIN           792 1143 NONSTRUCTURAL PROTEIN NS1.
FT CHAIN           1144 1374 NONSTRUCTURAL PROTEIN NS2A.
FT CHAIN           1375 1505 NONSTRUCTURAL PROTEIN NS2B.
FT CHAIN           1506 2124 HELICASE (NS3).
FT CHAIN           2125 2273 NONSTRUCTURAL PROTEIN NS4A.
FT CHAIN           2274 2528 NONSTRUCTURAL PROTEIN NS4B.
FT CHAIN           2529 3433 RNA-DIRECTED RNA POLYMERASE (NS5).
FT NP_BIND         388 401 INVOLVED IN FUSION.
FT SITE            1699 1706 ATP (POTENTIAL).
FT SITE            1790 1793 DEAH BOX.
FT DISULFID        293 320 BY SIMILARITY.
FT DISULFID        350 406 BY SIMILARITY.
FT DISULFID        364 395 BY SIMILARITY.
FT DISULFID        382 411 BY SIMILARITY.
FT DISULFID        480 578 BY SIMILARITY.
FT DISULFID        595 626 BY SIMILARITY.
FT CARBOHYD        138 138 POTENTIAL.
FT CARBOHYD        921 921 POTENTIAL.
FT CARBOHYD        966 966 POTENTIAL.
FT CARBOHYD        998 998 POTENTIAL.
SQ SEQUENCE        3433 AA: 381363 MW: EE4B888A7D040B99 CRC64;

Query Match          66.1%; Score 37; DB 1; Length 3433;
Best Local Similarity 75.0%; Pred. No. 1.le+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YYPDVTQVG 10
    |||||
Db 825 YYPETPGQ 832

RESULT 15
HV3L_HUMAN STANDARD; PRT; 119 AA.
ID HV3L_HUMAN
AC P01773;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION BUR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE (MYELOMA PROTEIN BUR).
RX MEDLINE; 79151016.
RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
RT "Primary structure of a human IgA1 immunoglobulin. IV. Streptococcal
RT IgA1 protease, digestion, Fab and Fc fragments, and the complete
RT amino acid sequence of the alpha 1 heavy chain.";
RL J. Biol. Chem. 254:2865-2874(1979).
DR PIR; A02056; ALHUBR.
DR HSSP; P01772; 2IG2.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Glycoprotein.
FT MOD_RES        1 1 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID        22 96
FT CARBOHYD        28 28
FT NON_TER        119 119
SQ SEQUENCE        119 AA: 12981 MW: 12A709A75344D024 CRC64;

Query Match          64.3%; Score 36; DB 1; Length 119;
Best Local Similarity 66.7%; Pred. No. 4.2;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TYYPDVTQVG 10
    |||||

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RL Mol. Microbiol. 2:159-164(1988).
RN [2]
RP REVISIONS, AND DISULFIDE BOND.
RC STRAIN-3937;
RX MEDLINE; 94203057.
RA Bortoli-German I., Brun E., Py B., Chippaux M., Barras F.;
RT "periplasmic disulphide bond formation is essential for cellulase
secretion by the plant pathogen Erwinia chrysanthemi.";
RL Mol. Microbiol. 11:545-553(1994).
RN [3]
RP MUTAGENESIS, AND DOMAINS.
RX MEDLINE; 91312880.
RA Py B., Bortoli-German I., Hatech J., Chippaux M., Barras F.;
RT "Cellulase EG2 of Erwinia chrysanthemi: structural organization and
importance of His98 and Glu133 residues for catalysis.";
RL Protein Eng. 4:325-333(1991).
RN [4]
RP STEREOCHEMISTRY OF THE REACTION.
RX MEDLINE; 92225124.
RA Barras F., Bortoli-German I., Bauzan M., Rouvier J., Gey C.,
RA Heyraud A., Henrisat B.;
RT "Stereochemistry of the hydrolysis reaction catalyzed by
endoglucanase Z from Erwinia chrysanthemi.";
RL FEBS Lett. 300:145-148(1992).
RN [5]
RP STRUCTURE BY NMR OF 365-426.
RX MEDLINE; 98070232.
RA Brun E., Morlaud F., Gans P., Blackledge M.J., Barras F., Marion D.;
RT "Solution structure of the cellulose-binding domain of the
endoglucanase Z secreted by Erwinia chrysanthemi.";
RL Biochemistry 36:16074-16086(1997).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.30 ANGSTROMS) OF 44-335.
RA Czjzek M., el Hassouni M., Py B., Juy M., Bortoli-German I.,
RA Barras F.;
RT "Protein secretion in Gram-negative pathogenic bacteria: the study of
the structure/function relationships of the Erwinia chrysanthemi
cellulase cel5 (former egz).";
RL Submitted (MAR-1999) to the PDB data bank.
CC -!- FUNCTION: REPRESENTS 97% OF THE GLOBAL CELLULOSE ACTIVITY.
CC -!- CATALYTIC ACTIVITY: ENDOLYOLYSIS OF 1,4-BETA-D-GLUCOSIDIC
LINKAGES IN CELLULOSE.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO CELLULOSE FAMILY A (FAMILY 5 OF GLYCOSYL
HYDROLASES).
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Y00540; CAA58604.1; -.
DR PIR; S03767; S03767.
DR PDB; 1AIW; 06-MAY-98.
DR PDB; 1EGZ; 26-MAR-99.
DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; 1.
DR PFAM; PF00150; cellulase; 1.
KW Cellulose degradation; Hydrolase; Glycosidase; Signal; 3D-structure.
FT SIGNAL 1 43
FT CHAIN 44 426 ENDOGLUCANASE Z.
FT DOMAIN 44 332 CATALYTIC.
FT DOMAIN 333 366 LINKER.
FT ACT_SITE 367 426 CELLULOSE-BINDING.
FT ACT_SITE 176 176 PROTON DONOR.
FT ACT_SITE 263 263 NUCLEOPHILE (BY SIMILARITY).
FT MUTAGEN 141 141 H->A: LOSS OF ACTIVITY.
FT MUTAGEN 176 176 E->A: LOSS OF ACTIVITY.
FT DISULFID 368 425
FT CONFLICT 293 295
FT CONFLICT 350 364 SNA -> QLTK (IN REF. 1).
FT TDTTVDPTTTDTTPA -> MTPPLTNRPQPTHQ (IN

FT CONFLICT 388 426 REF. 1).
FT THNEAGQSIVYKGNLYTANWYTASVPGSDSSWTQVGSNC
FT -> LITTKOANSRSTRATCIPQTGTGTPHFAAIPGRRRLV
FT AVTN (IN REF. 1).
SQ SEQUENCE 426 AA; 46418 MW; E78F2EE021FCA5DA CRC64;

Query Match 66.1%; Score 37; DB 1; Length 426;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDT 7
Db 307 STYYPDS 313
|||||
307 STYYPDS 313

RESULT 13
FGR_MOUSE STANDARD; PRT; 517 AA.
ID FGR_MOUSE
AC P14234;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FGR (EC 2.7.1.112) (P55-FGR)
DE (C-FGR).
GN FGR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DBA/2J;
RX MEDLINE; 89385605.
RA Yi T.L., Willman C.L.;
RT "Cloning of the murine c-fgr proto-oncogene cDNA and induction of
c-fgr expression by proliferation and activation factors in normal
bone marrow-derived monocytic cells.";
RL Oncogene 4:1081-1087(1989).
CC -!- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP +
PROTEIN TYROSINE PHOSPHATE.
CC -!- SIMILARITY: CONTAINS 1 SH2 DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -!- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
DOMAIN. BELONGS TO THE SRC SUBFAMILY.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X16440; CAA34463.1; -.
DR PIR; A33127; A33127.
DR PIR; S10072; S10072.
DR HSSP; P00523; 2PTK.
DR MGD; MGI:95527; FGR.
DR PRINTS; PR00109; TYRKINASE.
DR PRINTS; PR00401; SH2DOMAIN.
DR PRINTS; PR00452; SH3DOMAIN.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS50001; SH2; 1.
DR PROSITE; PS50002; SH3; 1.
DR PFAM; PF00017; SH2; 1.
DR PFAM; PF00018; SH3; 1.
DR PFAM; PF00069; pkinase; 1.
KW Transferase; Tyrosine-protein kinase; Proto-oncogene; ATP-binding;
KW Phosphorylation; SH2 domain; SH3 domain.
FT DOMAIN 65 126
FT DOMAIN 132 229 SH2.

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RX MEDLINE; 81101090.
RA Matthysens G., Rabbitts T.H.;
RT "Structure and multiplicity of genes for the human immunoglobulin
RL heavy chain variable region.";
RL Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; J00236; AAA53516.1; -.
DR EMBL; M35415; AAA58735.1; -.
DR PIR; A02047; H3HU26
DR PFAM; PF00047; I9; 1.
KW Immunoglobulin V region; Signal.
FT CHAIN 1 19 IG HEAVY CHAIN V-III REGION VH26.
FT NON_TER 20 117
FT SEQUENCE 117 117
SQ SEQUENCE 117 AA; 12582 MW; E826733F1A3CB0F1 CRC64;

Query Match 69.6%; Score 39; DB 1; Length 117;
Best Local Similarity 70.0%; Pred. No. 1.1;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
DB 76 STYVGDSVKG 85

RESULT 10
HDAL_YEAST
ID HDAL_YEAST STANDARD; PRT; 706 AA.
AC P53973;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE HISTONE DEACETYLASE HDAL.
GN HDAL OR YNL021W OR N2819.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RA Andre B., Iraqi Housaini I., Urrestarazu L.A., Vissers S.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP CHARACTERIZATION.
RX MEDLINE; 97121415.
RA Rundlett S.E., Carmen A.A., Kobayashi R., Bavykin S., Turner B.M.,
RA Grunstein M.;
RT "HDAL and RPD3 are members of distinct yeast histone deacetylase
RT complexes that regulate silencing and transcription.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:14503-14508(1996).
CC -1- FUNCTION: RESPONSIBLE FOR THE DEACETYLATION OF LYSINE RESIDUES ON
CC THE N-TERMINAL PART OF THE CORE HISTONES (H2A, H2B, H3 AND H4).
CC HISTONE DEACETYLATION PLAYS AN IMPORTANT ROLE IN TRANSCRIPTIONAL
CC REGULATION AND CELL CYCLE PROGRESSION.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: BELONGS TO THE HISTONE DEACETYLASE / ACUC / ALPHA
CC FAMILY.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR SGB; Z71297; CAA95883.1; -.
DR EMBL; L0004088; HDAL.
DR PFAM; PF00850; Hist_deacetyl; 1.
KW Hydrolase; Nuclear protein.
SQ SEQUENCE 706 AA; 80069 MW; 4E7069E66D03264D CRC64;

Query Match 69.6%; Score 39; DB 1; Length 706;
Best Local Similarity 75.0%; Pred. No. 8.1;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 YYPDTVQG 10
DB 275 YYPGTIQG 282

RESULT 11
HV3F_HUMAN
ID HV3F_HUMAN STANDARD; PRT; 115 AA.
AC P01767;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION BUT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE.
RX Torano A., Putnam F.W.;
RT "Complete amino acid sequence of the alpha 2 heavy chain of a human
RT IgA2 immunoglobulin of the A2m (2) allotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
CC -1- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2) ALLOTYPE, C
CC REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
DR PIR; A02050; A2HUBU.
DR PFAM; PF00047; I9; 1.
KW Immunoglobulin V region.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12379 MW; 208876A7DF52DCF4 CRC64;

Query Match 66.1%; Score 37; DB 1; Length 115;
Best Local Similarity 60.0%; Pred. No. 2.6;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
DB 56 TTYADSVKG 65

RESULT 12
GUNZ_ERWCH
ID GUNZ_ERWCH STANDARD; PRT; 426 AA.
AC P07103;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE ENDOGLUCANASE Z PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE Z)
DE (CELLULOSE Z) (EGZ).
GN CELZ OR CEL5.
OS Erwinia chrysanthemi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Erwinia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3937;
RX Guiseppe A., Cami B., Aymeric J.-L., Ball G., Creuzet N.;
RA "Homology between endoglucanase Z of Erwinia chrysanthemi and
RT endoglucanases of Bacillus subtilis and alkalophilic Bacillus.";

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RESULT 6
HV58_MOUSE
ID HV58_MOUSE STANDARD; PRT; 117 AA.
AC P18529;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 5-76 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0506; HVMS57.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-76.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12991 MW; 93A04782B78B8FA0 CRC64;

Query Match 78.6%; Score 44; DB 1; Length 117;
Best Local Similarity 77.8%; Pred. No. 0.13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYYPDTVQG 10
Db 77 TYYPDSVKG 85

RESULT 7
HV59_MOUSE
ID HV59_MOUSE STANDARD; PRT; 117 AA.
AC P18530;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 7-39 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
RL J. Exp. Med. 169:2007-2019(1989).
CC -1- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PIR; JT0507; HVMS39.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 7-39.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.

Query Match 78.6%; Score 44; DB 1; Length 117;
Best Local Similarity 77.8%; Pred. No. 0.13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYYPDTVQG 10
Db 77 TYYPDSVKG 85

RESULT 8
HV05_CARAU
ID HV05_CARAU STANDARD; PRT; 116 AA.
AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 5A PRECURSOR.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinoidae; Cyprinidae; Cyprininae; Carassius.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88144476.
RA Wilson M.R., Middleton D., Warr G.W.;
RT "Immunoglobulin heavy chain variable region gene evolution: structure
RT and family relationships of two genes and a pseudogene in a teleost
RT fish.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
DR PIR; B28966; B28966.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 116 IG HEAVY CHAIN V REGION 5A.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 85 116 FRAMEWORK 3.
FT DISULFID 41 114 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match 71.4%; Score 40; DB 1; Length 116;
Best Local Similarity 70.0%; Pred. No. 0.71;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STIYPTVQG 10
Db 75 STIYADSVKG 84

RESULT 9
HV3C_HUMAN
ID HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION VH26 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.

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FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12972 MW; D5CA4167D0F1774F CRC64;

Query Match 78.6%; Score 44; DB 1; Length 117;
Best Local Similarity 77.8%; Pred. No. 0.13;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 TYYPDTVQG 10
Db 77 TYYPDSVKG 85

RESULT 8
HV05_CARAU
ID HV05_CARAU STANDARD; PRT; 116 AA.
AC P19181;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 5A PRECURSOR.
OS Carassius auratus (Goldfish).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinoidae; Cyprinidae; Cyprininae; Carassius.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88144476.
RA Wilson M.R., Middleton D., Warr G.W.;
RT "Immunoglobulin heavy chain variable region gene evolution: structure
RT and family relationships of two genes and a pseudogene in a teleost
RT fish.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:1566-1570(1988).
DR PIR; B28966; B28966.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 116 IG HEAVY CHAIN V REGION 5A.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 84 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 85 116 FRAMEWORK 3.
FT DISULFID 41 114 BY SIMILARITY.
FT NON_TER 116 116
SQ SEQUENCE 116 AA; 12808 MW; 9C2279E2DF199B12 CRC64;

Query Match 71.4%; Score 40; DB 1; Length 116;
Best Local Similarity 70.0%; Pred. No. 0.71;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 STIYPTVQG 10
Db 75 STIYADSVKG 84

RESULT 9
HV3C_HUMAN
ID HV3C_HUMAN STANDARD; PRT; 117 AA.
AC P01764;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V-III REGION VH26 PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PFAM; PF00047; ig: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 5-84.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12872 MW; 234055CB6A469861 CRC64;

Query Match 92.9%; Score 52; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.0038;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDVTQV 10
Db 76 STYYPDVK 85

RESULT 3
HV55_MOUSE
ID HV55_MOUSE STANDARD; PRT; 117 AA.
AC P18526;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 345 PRECURSOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PFAM; PF00047; ig: 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 345.
FT DOMAIN 20 49 FRAMEWORK 1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 68 FRAMEWORK 2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 86 117 FRAMEWORK 3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12902 MW; 49380E4627ACA99A CRC64;
```

```
Query Match 92.9%; Score 52; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.0038;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDVTQV 10
Db 76 STYYPDVK 85
```

```
RESULT 4
HV56_MOUSE
ID HV56_MOUSE STANDARD; PRT; 97 AA.
AC P18527;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 914.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PFAM; PF00047; ig: 1.
KW Immunoglobulin V region.
FT NON_TER 97 97
SQ SEQUENCE 97 AA; 10661 MW; C23CB33FF55DA893 CRC64;
```

```
Query Match 85.7%; Score 48; DB 1; Length 97;
Best Local Similarity 80.0%; Pred. No. 0.018;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDVTQV 10
Db 56 STYYPDSVK 65
```

```
RESULT 5
HV57_MOUSE
ID HV57_MOUSE STANDARD; PRT; 98 AA.
AC P18528;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG HEAVY CHAIN V REGION 6.96.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RN SEQUENCE FROM N.A.
RC STRAIN=BALB/CJ;
RX MEDLINE; 89279149.
RA Levy N.S., Malipiero U.V., Lebecque S.G., Gearhart P.J.;
RT "Early onset of somatic mutation in immunoglobulin VH genes during
the primary immune response.";
RL J. Exp. Med. 169:2007-2019(1989).
CC -I- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.
DR PFAM; PF00047; ig: 1.
KW Immunoglobulin V region.
FT NON_TER 98 98
SQ SEQUENCE 98 AA; 11007 MW; B8644F7F92FBF95B CRC64;
```

```
Query Match 78.6%; Score 44; DB 1; Length 98;
Best Local Similarity 77.8%; Pred. No. 0.1;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TYYPDVTQV 10
Db 58 TYYPDSVK 66
```

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2000, 20:07:10 ; Search time 69.28 Seconds
(without alignments)
4.396 Million cell updates/sec

Title: US-09-016-061-56
Perfect score: 56
Sequence: 1 STYYPDTVOG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues
Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	92.9	117	1 HV53_MOUSE	P18524 mus musculus
2	52	92.9	117	1 HV54_MOUSE	P18525 mus musculus
3	52	92.9	117	1 HV55_MOUSE	P18526 mus musculus
4	48	85.7	97	1 HV56_MOUSE	P18527 mus musculus
5	44	78.6	98	1 HV57_MOUSE	P18528 mus musculus
6	44	78.6	117	1 HV58_MOUSE	P18529 mus musculus
7	44	78.6	117	1 HV59_MOUSE	P18530 mus musculus
8	40	71.4	116	1 HV05_CARAU	P19181 carassius a
9	39	69.6	117	1 HV3C_HUMAN	P01764 homo sapien
10	39	69.6	706	1 HDAL_YEAST	P03973 saccharomyc
11	37	66.1	115	1 HV3F_HUMAN	P01767 homo sapien
12	37	66.1	426	1 GUNZ_ERWCH	P07103 erwinia chr
13	37	66.1	517	1 FGR_MOUSE	P14234 mus musculus
14	37	66.1	3433	1 POLG_KUNJM	P14335 k genome po
15	36	64.3	119	1 HV3L_HUMAN	P01773 homo sapien
16	36	64.3	329	1 YP22_CABEL	Q09201 caenorhabdi
17	36	64.3	624	1 YE70_METJA	Q58865 methanococc
18	36	64.3	889	1 IREB_CHICK	Q90875 gallus gall
19	35	62.5	117	1 HV02_CANFA	P01785 canis famil
20	35	62.5	121	1 HV3J_HUMAN	P01771 homo sapien
21	35	62.5	519	1 ACHA_DROME	P25162 drosophila
22	34.5	61.6	507	1 VLL_HPV09	Q02480 human papil
23	34	60.7	352	1 GBAL_COPCO	P30675 coprinus co
24	34	60.7	358	1 COQ2_SCHPO	Q10252 schizosacch
25	34	60.7	566	1 Y397_MYCGE	P47637 mycoplasma
26	34	60.7	763	1 DPOL_HPBVP	Q02314 hepatitis b
27	34	60.7	969	1 MSUL_YEAST	P39112 saccharomyc
28	33	58.9	214	1 SC14_SCHCO	P35795 schizophyll
29	33	58.9	477	1 Y006_CABEL	Q09296 caenorhabdi
30	33	58.9	481	1 MEC2_CABEL	Q27433 caenorhabdi
31	33	58.9	532	1 HEXA_DICDI	P13723 dictyosteli
32	33	58.9	608	1 YLP5_CABEL	P34385 caenorhabdi
33	33	58.9	814	1 GUNE_CLOTM	P10477 clostridium
34	33	58.9	870	1 FIMD_SALTY	P37924 salmonella

ALIGNMENTS

RESULT 1									
HV53_MOUSE									
ID	HV53_MOUSE	STANDARD;	PRT;	117 AA.					
AC	P18524;								
DT	01-NOV-1990 (Rel. 16, Created)								
DT	01-NOV-1990 (Rel. 16, Last sequence update)								
DT	15-JUL-1999 (Rel. 38, Last annotation update)								
DE	IG HEAVY CHAIN V REGION RF PRECURSOR.								
OS	Mus musculus (Mouse).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;								
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=BALE/CJ;								
RX	MEDLINE; 89279149.								
RA	Levy N.S., Malpiero U.V., Lebecque S.G., Gearhart P.J.;								
RT	"Early onset of somatic mutation in immunoglobulin VH genes during the primary immune response.";								
RL	J. Exp. Med. 169:2007-2019(1989).								
CC	-!- MISCELLANEOUS: THIS SEQUENCE BELONGS TO THE VH7183 SUBFAMILY.								
DR	PIR: JTO503; HVMSTRF.								
DR	PFAM; PF00047; Ig: 1.								
KW	Immunoglobulin V region; Hybridoma; Signal.								
FT	SIGNAL 1 19								
FT	CHAIN 20 117								
FT	DOMAIN 20 49								
FT	DOMAIN 50 54								
FT	DOMAIN 55 68								
FT	DOMAIN 69 85								
FT	DOMAIN 86 117								
FT	DISULFID 41 115								
FT	NON_TER 117 117								
SQ	SEQUENCE 117 AA; 12866 MW; 2CE3295F390F725B CRC64;								
Query Match					92.9%;	Score 52;	DB 1;	Length 117;	
Best Local Similarity					90.0%;	Pred. No. 0.0038;			
Matches					9;	Conservative 1;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	STYYPDTVOG	10						
Db	76	STYYPDTVRG	85						
RESULT 2									
HV54_MOUSE									
ID	HV54_MOUSE	STANDARD;	PRT;	117 AA.					
AC	P18525;								
DT	01-NOV-1990 (Rel. 16, Created)								
DT	01-NOV-1990 (Rel. 16, Last sequence update)								
DT	15-JUL-1999 (Rel. 38, Last annotation update)								
DE	IG HEAVY CHAIN V REGION 5-84 PRECURSOR.								
OS	Mus musculus (Mouse).								
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;								
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.								
RN	[1]								
RP	SEQUENCE FROM N.A.								

P21399 homo sapien
P28271 mus musculus
Q01059 oryctolagus
Q63270 rattus norv
P54761 mus musculus
P34098 dictyosteli
P06935 w genome po
P27271 tomato yell
P93267 mesembryant
Q05410 bacillus su
P48481 acetabulari

DB 56 NTYYPDTVKG 65
:|||||:|

RESULT 13

PH1550
Ig H chain V region (clone 14E1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999

C:Accession: PH1550

R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.

J. Exp. Med. 177, 1105-1116, 1993

A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans

A:Reference number: PH1528; MUID:93210465

A:Accession: PH1550

A:Molecule type: mRNA

A:Residues: 1-118 <MUK>

A:Note: the stop codon X appears in residue 30

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

Query Match 87.5%; Score 49; DB 2; Length 118;
Best Local Similarity 80.0%; Pred. No. 0.056;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10

:|||||:|

Db 56 NTYYPDTVKG 65

RESULT 14

PH1544

Ig H chain V region (clone 9E11) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999

C:Accession: PH1544

R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.

J. Exp. Med. 177, 1105-1116, 1993

A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans

A:Reference number: PH1528; MUID:93210465

A:Accession: PH1544

A:Molecule type: mRNA

A:Residues: 1-119 <MUK>

A:Note: the stop codons X appear in residues 83, 86 and 107

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

Query Match 87.5%; Score 49; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 0.056;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10

:|||||:|

Db 57 NTYYPDTVKG 66

RESULT 15

PH1551

Ig H chain V region (clone 15E8) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999

C:Accession: PH1551

R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.

J. Exp. Med. 177, 1105-1116, 1993

A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans

A:Reference number: PH1528; MUID:93210465

A:Accession: PH1551

A:Molecule type: mRNA

A:Residues: 1-119 <MUK>

A:Note: the stop codons X appear in residues 88, 100 and 107

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

Query Match 87.5%; Score 49; DB 2; Length 119;
Best Local Similarity 80.0%; Pred. No. 0.056;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10

:|||||:|

Db 57 NTYYPDTVKG 66

Search completed: May 27, 2000, 19:26:38
Job time: 1761 sec

F:34-117/Domain: immunoglobulin homology <IMM>
F:41-115/Disulfide bonds: #status predicted

Query Match 92.9%; Score 52; DB 1; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.016;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
Db 76 STYYPDTVKG 85

RESULT 8
PHI1552
Ig H chain V region (clone 16E4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
C:Accession: PHI1552
R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
J. Exp. Med. 177, 1105-1116, 1993
A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
A:Reference number: PHI1528; MUID:93210465
A:Accession: PHI1552
A:Molecule type: mRNA
A:Residues: 1-117 <MUK>
A:Note: the stop codon X appears in residue 87
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 92.9%; Score 52; DB 2; Length 117;
Best Local Similarity 90.0%; Pred. No. 0.016;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
Db 57 STYYPDTVKG 66

RESULT 9
PHI1548
Ig H chain V region (clone 12F4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
C:Accession: PHI1548
R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
J. Exp. Med. 177, 1105-1116, 1993
A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
A:Reference number: PHI1528; MUID:93210465
A:Accession: PHI1548
A:Molecule type: mRNA
A:Residues: 1-119 <MUK>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.9%; Score 52; DB 2; Length 119;
Best Local Similarity 90.0%; Pred. No. 0.016;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
Db 57 STYYPDTVKG 66

RESULT 10
PHI1549
Ig H chain V region (clone 13F1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
C:Accession: PHI1549

R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
J. Exp. Med. 177, 1105-1116, 1993
A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
A:Reference number: PHI1528; MUID:93210465
A:Accession: PHI1549
A:Molecule type: mRNA
A:Residues: 1-119 <MUK>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.9%; Score 52; DB 2; Length 119;
Best Local Similarity 90.0%; Pred. No. 0.016;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
Db 57 STYYPDTVKG 66

RESULT 11
PHI1006
Ig heavy chain V region (clone 202.33) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PHI1006
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marlon, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective
A:Reference number: PH0971; MUID:92381444
A:Accession: PHI1006
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-108 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:10-93/Domain: immunoglobulin homology <IMM>

Query Match 87.5%; Score 49; DB 2; Length 108;
Best Local Similarity 80.0%; Pred. No. 0.051;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10
Db 52 NTYYPDTVKG 61

RESULT 12
PHI1532
Ig H chain V region (clone 4D4) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
C:Accession: PHI1532
R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
J. Exp. Med. 177, 1105-1116, 1993
A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
A:Reference number: PHI1528; MUID:93210465
A:Accession: PHI1532
A:Molecule type: mRNA
A:Residues: 1-118 <MUK>
A:Note: the stop codons X appear in residues 82 and 85
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 87.5%; Score 49; DB 2; Length 118;
Best Local Similarity 80.0%; Pred. No. 0.056;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 STYYPDTVQG 10

QY 1 STYYPDTVQG 10
 Db 57 STYYPDTVKG 66

RESULT 3

Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S26468

R:Kavaler, J.

submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26468

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <KAV>

A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 92.9%; Score 52; DB 2; Length 113;
 Best Local Similarity 90.0%; Pred. No. 0.015;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
 Db 53 STYYPDTVKG 62

RESULT 4

Ig H chain V region (clone 13G12) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 17-Mar-1999
 C:Accession: PH1538
 R:Mukherjee, J.; Casadevall, A.; Scharff, M.D.
 J. Exp. Med. 177, 1103-1116, 1993
 A:Title: Molecular characterization of the humoral responses to Cryptococcus neoformans
 A:Reference number: PH1528; MUID:93210465
 A:Accession: PH1538
 A:Molecule type: mRNA
 A:Residues: 1-115 <MK>
 A:Note: the stop codons X appear in residues 82, 85 and 106
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: immunoglobulin

Query Match 92.9%; Score 52; DB 2; Length 115;
 Best Local Similarity 90.0%; Pred. No. 0.015;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
 Db 56 STYYPDTVKG 65

RESULT 5

Ig heavy chain precursor V region (RF) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997
 C:Accession: JT0503
 R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.
 J. Exp. Med. 169, 2007-2019, 1989
 A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primary
 A:Reference number: JT0501; MUID:89279149
 A:Accession: JT0503
 A>Status: translation not shown
 A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A:Note: this sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; hybridoma; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (RF) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:41-115/Disulfide bonds: #status predicted

Query Match 92.9%; Score 52; DB 1; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.016;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
 Db 76 STYYPDTVKG 85

RESULT 6

HVMS84

Ig heavy chain precursor V region (5-84) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C:Accession: JT0505

R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primar

A:Reference number: JT0501; MUID:89279149

A:Accession: JT0505

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A:Note: this sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (5-84) #status predicted <MAT>

F:34-117/Domain: immunoglobulin homology <IMM>

F:41-115/Disulfide bonds: #status predicted

Query Match 92.9%; Score 52; DB 1; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.016;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 STYYPDTVQG 10
 Db 76 STYYPDTVKG 85

RESULT 7

HVMS34

Ig heavy chain precursor V region (345) - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1990 #sequence_revision 30-Jun-1990 #text_change 31-Mar-1997

C:Accession: JT0502

R:Levy, N.S.; Malipiero, U.V.; Lebecque, S.G.; Gearhart, P.J.

J. Exp. Med. 169, 2007-2019, 1989

A:Title: Early onset of somatic mutation in immunoglobulin VH genes during the primar

A:Reference number: JT0501; MUID:89279149

A:Accession: JT0502

A>Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-117 <LEV>

A:Experimental source: strain BALB/cJ

A:Note: this sequence belongs to the VH7183 subfamily

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-117/Product: Ig heavy chain V region (345) #status predicted <MAT>

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:26:38 ; Search time 163.56 Seconds
(without alignments)
3.585 Million cell updates/sec

Title: US-09-016-061-56
Perfect score: 56
Sequence: 1 STYYPDVTQVG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_63:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	92.9	111	2 S51211	Ig heavy chain V r
2	52	92.9	113	2 S02717	Ig heavy chain V r
3	52	92.9	113	2 S26468	Ig heavy chain V r
4	52	92.9	115	2 PH1538	Ig H chain V regio
5	52	92.9	117	1 HVMSRF	Ig heavy chain pre
6	52	92.9	117	1 HVMS84	Ig heavy chain pre
7	52	92.9	117	1 HVMS34	Ig heavy chain pre
8	52	92.9	117	2 PH1552	Ig H chain V regio
9	52	92.9	119	2 PH1548	Ig H chain V regio
10	52	92.9	119	2 PH1549	Ig H chain V regio
11	49	87.5	108	2 PH1006	Ig heavy chain V r
12	49	87.5	118	2 PH1532	Ig H chain V regio
13	49	87.5	118	2 PH1550	Ig H chain V regio
14	49	87.5	119	2 PH1544	Ig H chain V regio
15	49	87.5	119	2 PH1551	Ig H chain V regio
16	49	87.5	119	2 PH1547	Ig H chain V regio
17	49	87.5	119	2 PH1555	Ig H chain V regio
18	49	87.5	119	2 PH1531	Ig H chain V regio
19	49	87.5	119	2 PH1533	Ig H chain V regio
20	49	87.5	120	2 PH1534	Ig H chain V regio
21	49	87.5	122	2 PH1537	Ig H chain V regio
22	48	85.7	70	2 PL0250	Ig heavy chain V r
23	48	85.7	97	1 HVMS91	Ig heavy chain V r
24	48	85.7	108	2 PH0248	Ig heavy chain V r
25	48	85.7	111	2 PH1007	Ig heavy chain V r
26	48	85.7	112	2 S26327	Ig heavy chain V r
27	48	85.7	117	2 PH1535	Ig H chain V regio
28	48	85.7	117	2 PH1553	Ig H chain V regio
29	48	85.7	117	2 PH1542	Ig H chain V regio
30	48	85.7	117	2 PL0249	Ig heavy chain V r

ALIGNMENTS

RESULT 1

S51211
Ig heavy chain V region (AC7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 01-Aug-1995 #sequence_revision 01-Dec-1995 #text_change 30-May-1997
C:Accession: S51211; S58929
R:Jarvin, A.; Andrieux, A.; Chapel, A.; Buchou, T.; Marguerie, G.
FEBS Lett. 354, 169-172, 1994
A:Title: A synthetic peptide with anti-platelet activity derived from a CDR of an ant
A:Reference number: S51210; MUID:95046326
A:Accession: S51211
A:Molecule type: mRNA
A:Residues: 9-111 <JAR>
A:Accession: S58929
A:Molecule type: protein
A:Residues: 1-20 <JAR2>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.9%; Score 52; DB 2; Length 111;
Best Local Similarity 90.0%; Pred. No. 0.015;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 STYYPDVTQVG 10
Db 57 STYYPDVTQVG 66
|||||||:|

RESULT 2

S02717
Ig heavy chain V region (clone pH62) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 23-Jul-1999
C:Accession: S02717
R:Sollazzo, M.; Hasemann, C.A.; Meek, K.D.; Glotz, D.; Capra, J.D.; Zanetti, M.
submitted to the EMBL Data Library, February 1989
A:Reference number: S02717
A:Accession: S02717
A:Molecule type: DNA
A:Residues: 1-113 <SOL>
A:Cross-references: EMBL:Y00744; NID:g52472; PIDN:CAA68713.1; PID:e6964; PID:g1334095
A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 92.9%; Score 52; DB 2; Length 113;
Best Local Similarity 90.0%; Pred. No. 0.015;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:26:38 ; Search time 163.56 Seconds
(without alignments)
3.585 Million cell updates/sec

Title: US-09-016-061-60
Perfect score: 58
Sequence: 1 ARNHGSPAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_63:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	67.2	196	2	H64968 acetyl CoA acetyl
2	37	63.8	150	2	D69081 deoxyuridine 5-tri
3	37	63.8	731	1	JC2464 probable copper-tr
4	36	62.1	108	2	S26316 Ig heavy chain v r
5	36	62.1	110	2	S26317 Ig heavy chain v r
6	36	62.1	470	2	H71667 glutamate--trNA li
7	36	62.1	473	2	D70405 glutamine--trNA li
8	35	60.3	272	2	D27819 vitelline B1 precu
9	35	60.3	272	2	S27820 vitelline B2 precu
10	35	60.3	448	1	A60003 nucleocapsid prote
11	35	60.3	480	2	C69438 hypothetical prote
12	35	60.3	538	2	T28874 hypothetical prote
13	35	60.3	628	1	A56707 protein-tyrosine k
14	35	60.3	722	2	S64492 hypothetical prote
15	35	60.3	736	2	T06757 hypothetical prote
16	35	60.3	1797	2	T21889 hypothetical prote
17	35	60.3	1805	2	T21888 hypothetical prote
18	34	58.6	129	2	H70727 hypothetical prote
19	34	58.6	154	2	E72126 ct296 hypothetical
20	34	58.6	170	2	D75554 hypothetical prote
21	34	58.6	219	1	Q0EQA5 hypothetical 23.4K
22	34	58.6	231	1	I5ECP4 L-ribulose-phospha
23	34	58.6	231	2	S47804 L-ribulose-phospha
24	34	58.6	236	2	S16389 sporamin - sweet p
25	34	58.6	243	2	H64108 L-ribulose-phospha
26	34	58.6	248	1	I5EB4T L-ribulose-phospha
27	34	58.6	284	2	S62931 probable membrane
28	34	58.6	284	2	S62955 probable membrane
29	34	58.6	297	2	S37636 hypothetical prote
30	34	58.6	339	1	MUBPCP N-acetylmuramoyl-L

31	34	58.6	339	1	MUBPC9 N-acetylmuramoyl-L
32	34	58.6	349	1	S52763 hypothetical prote
33	34	58.6	379	1	F64633 site-specific DNA-
34	34	58.6	381	2	A71882 type II DNA modifi
35	34	58.6	446	2	T19625 hypothetical prote
36	34	58.6	1446	1	A45344 immediate-early pr
37	34	58.6	1460	1	EBBE1F immediate-early pr
38	34	58.6	2831	2	T31419 cyclic beta 1-2 gl
39	33.5	57.8	164	1	WPSLP lactoylglutathione
40	33	56.9	119	2	E30562 Ig heavy chain v r
41	33	56.9	119	2	C30562 Ig heavy chain v r
42	33	56.9	119	2	D30562 Ig heavy chain v r
43	33	56.9	227	2	D75530 hypothetical prote
44	33	56.9	233	2	S71464 ribonuclease (EC 3
45	33	56.9	259	2	D72425 conserved hypothet

ALIGNMENTS

RESULT 1
H64968
acetyl CoA acetyltransferase - Escherichia coli
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 18-Jun-1999
C:Accession: H64968; I69646; I69656
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: H64968
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-196 <BLAT>
A:Cross-references: GB:AB000294; GB:U00096; NID:q1788338; PIDN:AAC75094.1; PID:gl7883
A:Experimental source: strain K-12, substrain MG1655
R:Yao, Z.; Valvano, M.A.
J. Bacteriol. 176, 4133-4143, 1994
A:Title: Genetic analysis of the O-specific lipopolysaccharide biosynthesis region (r
erotypes Y and 4a.
A:Reference number: I55053; MUID:94292434
A:Accession: I69646
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-167, 'LFRKYCHC', 177-186, 'IMR', 190-196 <RES>
A:Cross-references: EMBL:U03041; NID:g501028; PIDN:AAC31635.1; PID:g510256
R:Stevenson, G.; Neal, B.; Liu, D.; Hobbs, M.; Packer, N.H.; Batley, M.; Redmond, J.W
J. Bacteriol. 176, 4144-4156, 1994
A:Title: Structure of the O antigen of Escherichia coli K-12 and the sequence of its
A:Reference number: I55054; MUID:94292435
A:Accession: I69656
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-167, 'LFRKYCHC', 177-186, 'IMR', 190-196 <RE2>
A:Cross-references: EMBL:U09876; NID:g508236; PID:g508245
C:Genetics:
A:Gene: yefH
A:Map position: 45 min
C:Superfamily: galactoside acetyltransferase

Query Match 67.2%; Score 39; DB 2; Length 196;
Best Local Similarity 75.0%; Pred. No. 4.5;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 3 HNHGSPAY 10
DB 105 HNHGSPFKH 112
RESULT 2
D69081

deoxyuridine 5-triphosphate nucleotidohydrolase related protein - Methanobacterium thermophilum
 C:Species: Methanobacterium thermoautotrophicum
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
 C:Accession: D69081
 R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N.; K., S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
 J. Bacteriol. 179, 7135-7155, 1997
 A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: function
 A:Reference number: A69000; MUID:98037514
 A:Accession: D69081
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-150 <MTH>
 A:Cross-references: GB:AE000920; GB:AE000666; NID:g2622729; PIDN:AAB86078.1; PID:g2622729
 A:Experimental source: strain Delta H
 C:Genetics:
 A:Gene: MTH1605

Query Match 63.8%; Score 37; DB 2; Length 150;
 Best Local Similarity 62.5%; Pred. No. 8;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNHGSEFAY 10
 |||||
 Db 115 HNHGEVEY 122

RESULT 3
 JC2464
 probable copper-transporting ATPase (EC 3.6.1.-) HRA-1 - Enterobacteriaceae spp.
 C:Species: Enterobacteriaceae spp.
 C:Date: 16-Oct-1998 #sequence_revision 16-Oct-1998 #text_change 18-Jun-1999
 C:Accession: JC2464
 R:Trenor III., C.; Lin, W.; Andrews, N.C.
 Biochem. Biophys. Res. Commun. 205, 1644-1650, 1994
 A:Title: Novel bacterial P-type ATPases with histidine-rich heavy-metal-associated sequence
 A:Reference number: JC2464; MUID:95110304
 A:Accession: JC2464
 A:Molecule type: mRNA
 A:Residues: 1-731 <TRE>
 A:Cross-references: GB:U16658; NID:g643612; PIDN:AAA62113.1; PID:g643613
 A:Experimental source: human small intestine cDNA library
 A:Note: the source species is uncertain; the cloned sequence did not hybridize with human
 C:Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding
 C:Keywords: ATP; copper transport; hydrolase; ion transport; phosphoprotein; transmembrane
 F:7-92/Region: His-rich
 F:135-477/Domain: ATPase transduction domain homology <ATT>
 F:544-685/Domain: ATPase nucleotide-binding domain homology <ATN>
 F:287/Active site: Glu #status predicted
 F:431/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 63.8%; Score 37; DB 1; Length 731;
 Best Local Similarity 75.0%; Pred. No. 38;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSEF 8
 |||||
 Db 88 AHNHGSEF 95

RESULT 4
 S26316
 Ig heavy chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S26316
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein
 A:Reference number: S26309; MUID:91341421

A:Accession: S26316
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-108 <STA>
 A:Cross-references: EMBL:X59190; NID:g52066; PIDN:CAA41900.1; PID:e36170; PID:g133403
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:2-85/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 36; DB 2; Length 108;
 Best Local Similarity 60.0%; Pred. No. 8.8;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSEFAY 10
 |||||
 Db 84 ARGNYGNAY 93

RESULT 5
 S26317
 Ig heavy chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 17-Apr-1998
 C:Accession: S26317
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein
 A:Reference number: S26309; MUID:91341421
 A:Accession: S26317
 A:Molecule type: mRNA
 A:Residues: 1-110 <STA>
 A:Cross-references: EMBL:X59186
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin

Query Match 62.1%; Score 36; DB 2; Length 110;
 Best Local Similarity 60.0%; Pred. No. 8.9;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSEFAY 10
 |||||
 Db 86 ARGNYGNAY 95

RESULT 6
 H71667
 glutamate--tRNA ligase (EC 6.1.1.17) (gltx2) RP623 - Rickettsia prowazekii
 C:Species: Rickettsia prowazekii
 C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 08-Oct-1999
 C:Accession: H71667
 R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark
 Nature 396, 133-140, 1998
 A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria
 A:Reference number: A71630; MUID:99039499
 A:Accession: H71667
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-470 <AND>
 A:Cross-references: GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAA15066.1; PID:e134
 A:Experimental source: strain Madrid E
 C:Genetics:
 A:Gene: gltx2; RP623
 C:Superfamily: glutamate--tRNA synthetase; ligase; protein biosynthesis
 C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 62.1%; Score 36; DB 2; Length 470;
 Best Local Similarity 75.0%; Pred. No. 37;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSEF 8

```
||||:| |
Db 31 ARHNGKF 38

RESULT 7
D70405
glutamate--tRNA ligase (EC 6.1.1.17) - Aquifex aeolicus
C:Species: Aquifex aeolicus
C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C:Accession: D70405
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666
A:Accession: D70405
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-473 <AQF>
A:Cross-references: GB:AE000729; NID:g2983659; PIDN:AAC07230.1; PID:g2983664; GB:AE00065
A:Experimental source: strain VF5
C:Genetics:
A:Gene: gltX
C:Superfamily: glutamate--tRNA ligase; glutamine--tRNA ligase homology
C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 62.1%; Score 36; DB 2; Length 473;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNGSF 8
||||:| |
Db 31 ARHNGKF 38

RESULT 8
S27819
vitelline B1 precursor - liver fluke
N:Alternate names: eggshell protein B1
C:Species: Fasciola hepatica (liver fluke)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Oct-1999
C:Accession: A48436; S27819
R:Rice-Ficht, A.C.; Dusek, K.A.; Kochevar, G.J.; Waite, J.H.
Mol. Biochem. Parasitol. 54, 129-141, 1992
A:Title: Eggshell precursor proteins of Fasciola hepatica, I. Structure and expression o
A:Reference number: A48436; MUID:93063029
A:Accession: A48436
A:Molecule type: mRNA; protein
A:Residues: 1-272 <R12>
A:Cross-references: EMBL:M93024; NID:g159065; PID:g159066
A:Note: sequence extracted from NCBI backbone (NCBIN:117208, NCBIP:117210)
C:Keywords: egg shell
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-272/Product: vitelline B1 #status predicted <MAT>

Query Match 60.3%; Score 35; DB 2; Length 272;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNGSF 8
||||:| |
Db 19 ARPHGKF 26

RESULT 9
S27820
vitelline B2 precursor - liver fluke
N:Alternate names: eggshell protein B2
C:Species: Fasciola hepatica (liver fluke)
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Oct-1999
C:Accession: S27820

R:Rice-Ficht, A.C.; Dusek, K.A.; Kochevar, G.J.; Waite, J.H.
submitted to the EMBL Data Library, May 1992
A:Description: Eggshell precursor proteins of Fasciola hepatica: I. structure and exp
A:Reference number: S27819
A:Accession: S27820
A:Molecule type: mRNA
A:Residues: 1-272 <RIC>
A:Cross-references: EMBL:M93025; NID:g159067; PID:g159068
C:Keywords: egg shell
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-272/Product: vitelline B2 #status predicted <MAT>

Query Match 60.3%; Score 35; DB 2; Length 272;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNGSF 8
||||:| |
Db 19 ARPHGKF 26

RESULT 10
A60003
nucleocapsid protein - human coronavirus (strain OC43)
C:Species: human coronavirus
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Feb-1999
C:Accession: A60003
R:Kamahora, T.; Soe, L.H.; Lai, M.M.C.
Virus Res. 12, 1-9, 1989
A:Title: Sequence analysis of nucleocapsid gene and leader RNA of human coronavirus O
A:Reference number: A60003; MUID:89243809
A:Accession: A60003
A:Molecule type: genomic RNA
A:Residues: 1-448 <KAM>
C:Genetics:
A:Gene: N
C:Superfamily: coronavirus nucleocapsid protein
C:Keywords: glycoprotein; nucleocapsid
F:17,221,336,388,408,421/Binding site: carbohydrate (Asn) (covalent) #status predicte

Query Match 60.3%; Score 35; DB 1; Length 448;
Best Local Similarity 85.7%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNHGSF 8
||||:| |
Db 103 RHNHGSF 109

RESULT 11
C69438
hypothetical protein AF1508 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: C69438
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glocke, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A:Reference number: A69250; MUID:98049343
A:Accession: C69438
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-480 <KLE>
A:Cross-references: GB:AE000998; GB:AE000782; NID:g2689321; PIDN:AAB89742.1; PID:g264

Query Match 60.3%; Score 35; DB 2; Length 480;
```

Best Local Similarity 100.0%; Pred. No. 58;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 HGSAFAY 10
| | | | |
Db 429 HGSAFAY 434

RESULT 12
T28874
hypothetical protein R04E5.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T28874
R:Miller, N.
submitted to the EMBL Data Library, December 1995
A:Description: The sequence of C. elegans cosmid R04E5.
A:Reference number: Z20535
A:Accession: T28874
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-538 <MIL>
A:Cross-references: EMBL:U41538; PIDN:AAC48179.1; GSPDB:GN000028; CESP:R04E5.2
A:Experimental source: strain Bristol N2; clone R04E5
C:Genetics:
A:Gene: CESP:R04E5.2
A:Map position: 10
A:Introns: 28/2; 52/3; 91/2; 133/3; 169/1; 199/3; 240/2; 269/3; 302/3; 329/3; 368/3; 450/3

Query Match 60.3%; Score 35; DB 2; Length 538;
Best Local Similarity 62.5%; Pred. No. 65;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNGSFA 9
: | : | : |
Db 434 KHHGKFA 441

RESULT 13
A56707
protein-tyrosine kinase (EC 2.7.1.112) syk, splice form B - rat
N:Contains: protein-tyrosine kinase Syk, splice form A
C:Species: Rattus norvegicus (Norway rat)
C>Date: 19-Oct-1995 #sequence_revision 23-May-1997 #text_change 10-Sep-1999
C:Accession: A56707; B56707; A48875
R:Rowley, R.B.; Bolen, J.B.; Fargnoli, J.
J. Biol. Chem. 270, 12659-12664, 1995
A:Title: Molecular cloning of rodent p72(Syk). Evidence of alternative mRNA splicing.
A:Reference number: A56707; MUID:95279402
A:Accession: A56707
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-628 <ROW>
A:Cross-references: GB:U21684
A:Accession: B56707
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-275,299-628 <RO2>
A:Cross-references: GB:U21683
R:Benhamou, M.; Ryba, N.J.P.; Nishikata, H.; Kihara, H.; Siraganian, R.P.
J. Biol. Chem. 268, 23318-23324, 1993
A:Title: Protein tyrosine kinase p72syk in high affinity IgE receptor signaling: identification of a novel tyrosine phosphorylation site
A:Reference number: A48875; MUID:94043123
A:Accession: A48875
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 15-22-'E', 23-263-'M', 265-269-'S', 271-444-'EL', 447-628 <RES>
A:Cross-references: GB:L20838; NID:g416152; PIDN:AAA42308.1; PID:g416153
C:Superfamily: protein-tyrosine kinase ZAP-70; protein kinase homology; SH2 homology
C:Keywords: alternative splicing; ATP; autophosphorylation; phosphoprotein; phosphotransferase
F:1-628/628; Product: protein-tyrosine kinase syk, splice form B #status predicted <PRB>

F:1-275,299-628/Product: protein-tyrosine kinase syk, splice form A #status predicted <PRB>
F:14-105/Domain: SH2 homology <SH2A>
F:166-257/Domain: SH2 homology <SH2B>
F:362-626/Domain: protein kinase homology <KIN>
F:370-378/Region: protein kinase ATP-binding motif

Query Match 60.3%; Score 35; DB 1; Length 628;
Best Local Similarity 77.8%; Pred. No. 76;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSFA 9
| | : | : | : |
Db 194 ARDNNGSFA 202

RESULT 14
S64492
hypothetical protein YGR178c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein G7139
C:Species: Saccharomyces cerevisiae
C>Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 29-Oct-1999
C:Accession: S64492
R:Hebling, U.; Hofmann, B.; Dalius, H.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64003
A:Accession: S64492
A:Molecule type: DNA
A:Residues: 1-722 <HEB>
A:Cross-references: EMBL:Z72963; NID:gl323314; PIDN:CAA97204.1; PID:e243559; PID:gl32
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:PBPI
A:Cross-references: SGD:S0003410; MIPS:YGR178c
A:Map position: 7R

Query Match 60.3%; Score 35; DB 2; Length 722;
Best Local Similarity 85.7%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNGSF 8
| | | | |
Db 474 RHNGSF 480

RESULT 15
T06757
hypothetical protein F15B8.180 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 22-Oct-1999
C:Accession: T06757
R:Quefiet, F.; Benes, V.; Rechmann, S.; Borkova, D.; Ansoerge, W.; Salanoubat, M.; Mew
submitted to the Protein Sequence Database, April 1999
A:Reference number: Z15794
A:Accession: T06757
A:Molecule type: DNA
A:Residues: 1-736 <QUE>
A:Cross-references: GSPDB:GN00061; ATSP:F15B8.180
A:Experimental source: cultivar Columbia; BAC clone F15B8
C:Genetics:
A:Gene: ATSP:F15B8.180
A:Map position: 3
A:Introns: 114/3; 146/1; 208/2; 293/3; 365/3; 384/3; 429/3; 467/3; 536/2; 563/2; 640/2

Query Match 60.3%; Score 35; DB 2; Length 736;
Best Local Similarity 50.0%; Pred. No. 89;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSFA 10
: | : | : | : |
Db 482 SKHNHSTTAY 491

Search completed: May 27, 2000, 19:26:40
Job time: 1763 sec

GenCore version 4.5
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OK protein - protein search, using sw model

Run on: May 27, 2000, 20:07:12 ; Search time 69.28 Seconds
(without alignments)
4.396 Million cell updates/sec

Title: US-09-016-061-60
Perfect score: 58
Sequence: 1 ARHNHGSFAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	67.2	196	1 WBBJ_ECOLI	P37750 escherichia
2	36	62.1	218	1 Y4VH_RHISN	Q53216 rhizobium s
3	36	62.1	470	1 SYE2_RICPR	Q92ct8 rickettsia
4	36	62.1	473	1 SYE_AQUAE	O67271 aquifex aeo
5	35	60.3	197	1 EGG5_FASHE	P07915 fasciola he
6	35	60.3	448	1 NCAP_CVROC	P33469 human coron
7	35	60.3	567	1 CC45_XENLA	Q9yhz6 xenopus lae
8	35	60.3	629	1 KSK_K_RAT	Q64725 rattus norv
9	35	60.3	722	1 PBP1_YEAST	P53297 saccharomyc
10	34	58.6	129	1 YP56_MYCTU	Q50742 mycobacteri
11	34	58.6	213	1 PNCA_ECOLI	P21369 escherichia
12	34	58.6	231	1 ARAD_ECOLI	P08203 escherichia
13	34	58.6	231	1 ARAD_SALTY	P06190 salmonella
14	34	58.6	231	1 SGBE_ECOLI	P37680 escherichia
15	34	58.6	231	1 SGBE_HAEIN	P44989 haemophilus
16	34	58.6	284	1 YNB9_YEAST	P53975 saccharomyc
17	34	58.6	284	1 YND3_YEAST	P53964 saccharomyc
18	34	58.6	297	1 YC24_ANTSP	Q02857 antithamio
19	34	58.6	339	1 LYCA_BPCP1	P15057 bacterioph
20	34	58.6	339	1 LYCA_BPCP9	P19386 bacterioph
21	34	58.6	349	1 XTY9_YEAST	P41903 saccharomyc
22	34	58.6	538	1 NADB_PSEAE	Q51363 pseudomonas
23	34	58.6	1446	1 IE18_PRVKA	P33479 pseudorabie
24	33.5	57.8	1461	1 IE18_PRVIF	P11675 pseudomonas
25	33.5	57.8	172	1 LGUL_PSEPU	P16635 pseudomonas
26	33	56.9	302	1 YEO6_YEAST	P40049 saccharomyc
27	33	56.9	480	1 SVE_HAEIN	P43818 haemophilus
28	33	56.9	966	1 MI72_HUMAN	Q14596 homo sapien
29	33	56.9	1403	1 YDF3_SCHPO	Q10475 schizosacch
30	32	55.2	190	1 SYLD_HAEIN	P44830 haemophilus
31	32	55.2	235	1 NHAB_RHOSO	Q53117 rhodococcus
32	32	55.2	316	1 YX12_CAEEL	Q11123 caenorhabdi
33	32	55.2	322	1 FATB_VIBAN	P11460 vibrio angu
34	32	55.2	365	1 GAL7_YEAST	P08431 saccharomyc

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35 32 55.2 410 1 TRPB_MYCTU 008376 mycobacteri
36 32 55.2 434 1 TAA7_TREPA P29723 treponema p
37 32 55.2 473 1 SYTM_SCHPO O13969 schizosacch
38 32 55.2 593 1 ARSD_HUMAN P51689 homo sapien
39 32 55.2 635 1 KSYK_HUMAN P43405 homo sapien
40 32 55.2 654 1 BGLA_ERWCH Q46684 e periplasm
41 32 55.2 676 1 HS7C_TRYBB P20030 trypanosoma
42 32 55.2 765 1 AOC3_MOUSE O70423 mus musculu
43 32 55.2 909 1 HEX_ADEM1 P48308 mouse adeno
44 32 55.2 927 1 CC15_SCHPO O09822 schizosacch
45 32 55.2 1112 1 CN3B_HUMAN Q13370 homo sapien

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ALIGNMENTS

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RESULT 1
WBBJ_ECOLI
ID WBBJ_ECOLI STANDARD; PRT; 196 AA.
AC P37750; P76375;
DT 01-OCT-1994 (Rel. 30, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE PUTATIVE LIPOPOLYSACCHARIDE BIOSYNTHESIS O-ACETYL TRANSFERASE WBBJ
  (EC 2.3.1.-).
GN WBBJ
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / W3110;
RX MEDLINE: 94292434.
RA Yao Z., Valvano M.A.;
RT "Genetic analysis of the O-specific lipopolysaccharide biosynthesis
  region (rfb) of Escherichia coli K-12 W3110: identification of genes
  that confer group 6 specificity to Shigella flexneri serotypes Y and
  4a."
RL J. Bacteriol. 176:4133-4143(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / W3110;
RX MEDLINE: 94292435.
RA Stevenson G., Neal B., Liu D., Hobbs M., Packer N.H., Batley M.,
  Redmond J.W., Lindquist L., Reeves P.R.;
RT "Structure of the O antigen of Escherichia coli K-12 and the sequence
  of its rfb gene cluster."
RL J. Bacteriol. 176:4144-4156(1994).
RN [3]
RP REVISIONS TO 168-176 AND 187-189.
RC STRAIN=K12 / W3110;
RX Stevenson G.;
RA Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE: 97426617.
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
  Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,
  Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
  Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
  Science 277:1453-1474(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE: 97251358.
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
  Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
  Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
  Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T.,
  Saito N., Sampei G., Seki Y., Sivasubram S., Tagami H.,
  Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;

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RT  "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RL  corresponding to the 40.1-50.0 min region on the linkage map.";
CC  DNA Res. 3:379-392(1996).
CC  -!- FUNCTION: PUTATIVE O-ACETYLTRANSFERASE THAT TRANSFERS AN O-ACETYL
CC  ON THE O ANTIGEN.
CC  -!- PATHWAY: LIPOLYSACCHARIDE BIOSYNTHESIS.
CC  -!- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDOL FAMILY OF
CC  ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
CC  -----
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CC  -----
DR  EMBL; U03041; AAC31635.1; -.
DR  EMBL; U09876; AAB88406.1; -.
DR  EMBL; AE000294; AAC75094.1; -.
DR  EMBL; D90841; CAB21803.1; -.
DR  EMBL; D90842; CAB21811.1; -.
DR  ECOGENE; EGI1984; WBBJ.
DR  PROSITE; PS00101; HEXAPEP_TRANSFERASES; FALSE_NEG.
DR  PFAM; PF00132; hexapep; 1.
KW  Lipopolysaccharide biosynthesis; Transferase; Acyltransferase; Repeat.
FT  CONFLICT 168 176 SIPENVIA -> LERKYCHC (IN REF. 1).
FT  CONFLICT 187 189 NHE -> IMR (IN REF. 1).
SQ  SEQUENCE 196 AA; 21675 MW; DIC2FA7D3B29A1B1 CRC64;

Query Match 67.2%; Score 39; DB 1; Length 196;
Best Local Similarity 75.0%; Pred. No. 2.1;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  3 HNHGSFAY 10
Db  105 HNHGSFKH 112
|||||:

RESULT 2
Y4VH_RHISN
ID  Y4VH_RHISN STANDARD; PRT; 218 AA.
AC  Q53216;
DT  01-NOV-1997 (Rel. 35, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  01-NOV-1997 (Rel. 35, Last annotation update)
DE  HYPOTHETICAL 24.6 KD PROTEIN Y4VH.
GN  Y4VH.
OS  Rhizobium sp. (strain NGR234).
OG  Plasmid sym pNGR234a.
OC  Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC  Rhizobiaceae; Rhizobium.
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE; 97305956.
RA  Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA  Perret X.;
RT  "Molecular basis of symbiosis between Rhizobium and legumes.";
RL  Nature 387:394-401(1997).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE; 96389014.
RA  Freiberg C., Perret X., Broughton W.J., Rosenthal A.;
RT  "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
RT  NGR234 using dye terminators and a thermostable 'sequenase': a
RT  beginning.";
RL  Genome Res. 6:590-600(1996).
CC  -!- SIMILARITY: NONE OBVIOUS.
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CC  -----
DR  EMBL; Z69203; CAA92423.1; -.
DR  EMBL; AE000101; AAB91896.1; -.
KW  Hypothetical protein; Plasmid.
SQ  SEQUENCE 218 AA; 24594 MW; 501C6CB38A09A2E5 CRC64;

Query Match 62.1%; Score 36; DB 1; Length 218;
Best Local Similarity 66.7%; Pred. No. 8.2;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  1 ARNHGSPA 9
Db  68 ARDNHGSYS 76
|||||:

RESULT 3
SYE2_RICPR
ID  SYE2_RICPR STANDARD; PRT; 470 AA.
AC  Q9ZCT8;
DT  15-FEB-2000 (Rel. 39, Created)
DT  15-FEB-2000 (Rel. 39, Last sequence update)
DT  15-FEB-2000 (Rel. 39, Last annotation update)
DE  GLUTAMYL-TRNA SYNTHETASE 2 (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE 2)
DE  (GLURS 2).
GN  GLUTX2 OR RP623.
OS  Rickettsia prowazekii.
OC  Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC  Rickettsiaceae; Rickettsiae; Rickettsia.
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=MADRID E;
RX  MEDLINE; 99039499.
RA  Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA  Sichertitz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA  Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT  "The genome sequence of Rickettsia prowazekii and the origin of
RT  mitochondria.";
RL  Nature 396:133-140(1998).
CC  -!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) = AMP +
CC  PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC  -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC  -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC  -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC  -----
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CC  -----
DR  EMBL; AJ235272; CAA15066.1; -.
DR  HSP; P27000; IGLN.
DR  PROSITE; PS00178; AA-TRNA_LIGASE_I; FALSE_NEG.
KW  Aminoacyl-TRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT  SIMILAR 10 20 "HIGH" REGION.
FT  SIMILAR 239 243 "KMSK" REGION.
FT  BINDING 242 242 ATP (BY SIMILARITY).
SQ  SEQUENCE 470 AA; 53696 MW; DFICE50A20B8A9FD CRC64;

Query Match 62.1%; Score 36; DB 1; Length 470;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY  1 ARNHGSPF 8
|||||:

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```
Db 31 ARHNGKF 38
RESULT 4
SYE_AQUAE STANDARD; PRT; 473 AA.
AC 067271; 2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE)
DE (GLURS).
GN GLTX OR AQ_1221.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5.
RX MEDLINE; 98196666.
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) = AMP +
CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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CC -----
DR EMBL; AE000729; AAC07230.1; -.
DR PRINTS; PR00987; TRNASYNTHGLU.
DR PROSITE; PS00178; AA-TRNA_LIGASE_I; 1.
DR PFAM; PF00749; tRNA-synt.1c; 1.
DR KW Aminoacyl-TRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
FT SIMILAR 242 246 "KMSKS" REGION.
FT BINDING 245 245 ATP (BY SIMILARITY).
SQ SEQUENCE 473 AA; 55121 MW; 5CB4D1590973E07A CRC64;

Query Match 62.1%; Score 36; DB 1; Length 473;
Best Local Similarity 75.0%; Pred. No. 18;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNGSF 8
| | | | |
Db 31 ARHNGGF 38

RESULT 5
EGGS_FASHE STANDARD; PRT; 197 AA.
AC P07915;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PUTATIVE EGGSHELL PROTEIN PRECURSOR.
OS Fasciola hepatica (Liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Echinostomida; Echinostomatidae; Echinostomata; Fascioloidae;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE; 87175670.
RA Zurita M., Bieber D., Ringold G., Mansour T.E.;
RT "Cloning and characterization of a female genital complex cDNA from
RT the liver fluke Fasciola hepatica";
RL Proc. Natl. Acad. Sci. U.S.A. 84:2340-2344(1987).
CC -----
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CC -----
DR EMBL; M15871; AAA29138.1; -.
KW Eggshell; Signal.
FT SIGNAL 1 17 PUTATIVE EGGSHELL PROTEIN.
FT CHAIN 18 197
SQ SEQUENCE 197 AA; 22470 MW; 72033ED203FC1A3E CRC64;

Query Match 60.3%; Score 35; DB 1; Length 197;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNGSF 8
| | | | |
Db 17 ARHPGKF 24

RESULT 6
NCAP_CVHOC STANDARD; PRT; 448 AA.
ID NCAP_CVHOC
AC P33469;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE NUCLEOCAPSID PROTEIN.
GN N.
OS Human coronavirus (strain OC43).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89243809.
RA Kanahora T., Soe L.H., Lai M.M.C.;
RT "Sequence analysis of nucleocapsid gene and leader RNA of human
RT coronavirus OC43.";
RL Virus Res. 12:1-9(1989).
DR PIR; A60003; A60003.
DR PFAM; PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 448 AA; 49316 MW; 5193AB1AE0D75626 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 448;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNHGSF 8
| | | | |
Db 103 RHNHGSF 109

RESULT 7
CC45_XENLA STANDARD; PRT; 567 AA.
ID CC45_XENLA
AC Q9VHZ6;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE CDC45-RELATED PROTEIN.
GN CDC45.
```


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 CC -----

DR EMBL; Z72963; CAA97204.1; -;
 DR EMBL; U46931; AAB94294.1; -;
 DR SGD; L0003967; BPPI.
 KW Nuclear protein.
 SQ SEQUENCE 722 AA; 78781 MW; 92005F3A2346193E CRC64;

Query Match 60.3%; Score 35; DB 1; Length 722;
 Best Local Similarity 85.7%; Pred. No. 42;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNGSF 8

Db 474 RRHNGSF 480

RESULT 10
 YP56_MYCTU STANDARD; PRT; 129 AA.
 ID YP56_MYCTU
 AC Q50742;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE HYPOTHETICAL 13.9 KD PROTEIN RV2556C.
 GN RV2556C OR MTCY9C4.12.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RX MEDLINE; 98295987.
 RA Cole S.T., Broch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squires R., Sulston J.E.,
 RA Taylor K., Whitehead S., Barrell B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence";
 RL Nature 393:537-544(1998).

CC -1- SIMILARITY: BELONGS TO THE UPF0047 FAMILY.
 CC -----
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 CC -----

DR EMBL; Z77250; CAB01048.1; -;
 DR PROSITE; PS01314; UPF0047; 1.
 DR TUBERCULIST; RV2556C; -;
 KW Hypothetical protein.
 SQ SEQUENCE 129 AA; 13925 MW; AABE57ABEB76B6923 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 129;
 Best Local Similarity 55.6%; Pred. No. 11;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFAY 10

|||||:

Db 69 RHAGSYGH 77
 RESULT 11
 PNCA_ECOLI STANDARD; PRT; 213 AA.
 ID PNCA_ECOLI
 AC P21369; P76229; P76910;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PYRAZINAMIDASE/NICOTINAMIDASE [INCLUDES: PYRAZINAMIDASE (EC 3.5.1.-)
 DE (PZASE); NICOTINAMIDASE (EC 3.5.1.19) (NICOTINE DEAMIDASE)].
 GN PNCA OR NAM.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE; 89357501.
 RA Jernstroem P.G., Bezjak D.A., Jennings M.P., Beacham I.R.;
 RT "Structure and expression in Escherichia coli K-12 of the
 RT L-asparaginase I-encoding ansA gene and its flanking regions.";
 RL Gene 78:37-46(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE; 96338362.
 RA Frothingham R., Meeker-O'Connell W.A., Talbot E.A., George J.W.,
 RA Kreuzer K.N.;
 RT "Identification, cloning, and expression of the Escherichia coli
 RT pyrazinamidase and nicotinamidase gene, pncA";
 RL Antimicrob. Agents Chemother. 40:1426-1431(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE; 97426617.
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RA Aliba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T.,
 RA Ikemoto K., Inada T., Isono K., Itoh T., Kanai K.,
 RA Kasai H., Kashimoto K., Kim S., Kimura S., Kitagawa M.,
 RA Kitakawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H.,
 RA Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
 RA Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C.,
 RA Yamamoto Y., Yano M.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: NICOTINAMIDE + H(2)O = NICOTINATE + NH(3).
 CC -1- PATHWAY: PYRIDINE NUCLEOTIDE CYCLE.
 CC -1- SIMILARITY: TO YEAST YGL037C.
 CC -----
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 CC -----
 DR EMBL; M26934; AAA23447.1; -;
 DR EMBL; AE000271; AAC74838.1; ALT_INIT.
 DR EMBL; D90820; CAB21476.1; -;
 DR EMBL; D90821; CAB21489.1; -;
 DR PIR; JU00048; QOECAS.
 DR ECOGENE; EG1135; PNCA.
 DR PFAM; PF00857; Isochorismatase; 1.
 KW Hydrolase.

```

SQ SEQUENCE 213 AA; 23362 MW; B9F8D946FA18433F CRC64;

Query Match
Best Local Similarity 58.6%; Score 34; DB 1; Length 213;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NHGSFA 9
|||||
Db 57 NHGSFA 62

RESULT 12
ID ARAD_ECOLI STANDARD; PRT; 231 AA.
AC P08203.
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE L-RIBULOSE-5-PHOSPHATE 4-EPIMERASE (EC 5.1.3.4).
GN ARAD.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RC [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B;
RX MEDLINE; 87163495.
RA Lee N., Gielow W., Martin R., Hamilton E., Fowler A.;
RT "The organization of the arabAD operon of Escherichia coli.";
RL Gene 47:231-244(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE; 91083835.
RA Chen H., Sun Y., Stark T., Beattie W., Moses R.E.;
RT "Nucleotide sequence and deletion analysis of the polB gene of
Escherichia coli.";
RL DNA Cell Biol. 9:631-635(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE; 91067495.
RA Mineno J., Fukui H., Ishino Y., Kato I., Shinagawa H.;
RT "Nucleotide sequence of the arad gene of Escherichia coli K12
encoding the L-ribulose 5-phosphate 4-epimerase.";
RL Nucleic Acids Res. 18:6722-6722(1990).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE; 92334977.
RA Yura T., Mori H., Nagai H., Nagata T., Ishihama A., Fujita N.,
RT "Systematic sequencing of the Escherichia coli genome: analysis of
the 0-2.4 min region.";
RL Nucleic Acids Res. 20:3305-3308(1992).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE; 97426617.
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [6]
RP SEQUENCE OF 222-231 FROM N.A.
RC STRAIN-K12;
RX MEDLINE; 91017565.
RA Bonner C.A., Hays S., McEntee K., Goodman M.F.;
RT "DNA polymerase II is encoded by the DNA damage-inducible dna gene
of Escherichia coli.";

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RL Proc. Natl. Acad. Sci. U.S.A. 87:7663-7667(1990).
RN [7]
RP SEQUENCE OF 158-231 FROM N.A.
RC STRAIN-K12 / W3110;
RX MEDLINE; 91238699.
RA Iwasaki H., Ishino Y., Toh H., Nakata A., Shinagawa H.;
RT "Escherichia coli DNA polymerase II is homologous to alpha-like DNA
polymerases.";
RL Mol. Gen. Genet. 226:24-33(1991).
CC -I- CATALYTIC ACTIVITY: L-RIBULOSE 5-PHOSPHATE - D-XULOSE 5-PHOSPHATE.
CC -I- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).
CC -I- PATHWAY: THIRD STEP OF L-ARABINOSE CATABOLISM.
CC -I- SIMILARITY: BELONGS TO THE ARAD / FUCA FAMILY.
CC -----
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CC -----
CC EMBL; M15263; AAA23464.1; -.
DR EMBL; M35371; -. NOT_ANNOTATED_CDS.
DR EMBL; M62646; AAA24405.1; -.
DR EMBL; D10483; CAB20051.1; -.
DR EMBL; A5000116; AAC73172.1; -.
DR EMBL; M37727; AAA23683.1; -.
DR EMBL; M38283; AAA63763.1; -.
DR EMBL; X56048; CAA39519.1; -.
DR PIR; D29022; ISECP4.
DR PIR; S13593; ISECK4.
DR PIR; A36236; A36236.
DR PIR; S40577; S40577.
DR ECO2DBASE; G028.1; 6TH EDITION.
DR ECGENE; EG10055; ARAD.
DR PFAM; PF00596; Aldolase II; 1.
KW Arabinose catabolism; Isomerase; Zinc.
FT METAL 76 76 ZINC (BY SIMILARITY).
FT METAL 95 95 ZINC (BY SIMILARITY).
FT METAL 97 97 ZINC (BY SIMILARITY).
FT METAL 171 171 ZINC (BY SIMILARITY).
FT VARIANT 50 50 V -> I.
FT VARIANT 70 70 T -> A.
FT VARIANT 216 216 D -> N.
SQ SEQUENCE 231 AA; 25519 MW; 1753F75958332163 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 231;
Best Local Similarity 62.5%; Pred. No. 20;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HHNGSFAY 10
|||||
Db 169 HSHGPFAY 176

RESULT 13
ID ARAD_SALTY STANDARD; PRT; 231 AA.
AC P06190;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE L-RIBULOSE-5-PHOSPHATE 4-EPIMERASE (EC 5.1.3.4).
GN ARAD.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-LT2;
RX MEDLINE; 85232046.

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RA Lin H.-C., Lei S.-P., Studnicka G., Wilcox G.;
RT "the arabid operon of Salmonella typhimurium ltr2. ltr. Nucleotide
RT sequence of arab and its flanking regions, and primary structure of
RT its product, L-ribulose-5-phosphate 4-epimerase";
RL Gene 34:129-134(1985).
RN [2]
RP IDENTIFICATION OF PROBABLE FRAMESHIFT.
RA Baloch A.;
RL Unpublished observations (AUG-1995).
CC -1- CATALYTIC ACTIVITY: L-RIBULOSE 5-PHOSPHATE - D-XULOSE 5-PHOSPHATE.
CC -1- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).
CC -1- PATHWAY: THIRD STEP OF L-ARABINOSE CATABOLISM.
CC -1- SIMILARITY: BELONGS TO THE ARAD / FUCA FAMILY.
CC -1- CAUTION: REF.1 SEQUENCE DIFFERS FROM THAT SHOWN FROM POSITION 204
CC ONWARD AND IS LONGER (248 AA) DUE TO A FRAMESHIFT.
CC -----
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CC -----
DR EMBL; M1047; AAA27025.1; ALT_FRAME.
DR PIR; A24986; ISEB4T.
DR SYGENE; SG10015; ARAD.
DR PFAM; PF00596; Aldolase_II; 1.
KW Arabinose catabolism; Isomerase; Zinc.
FT METAL 76 76 ZINC (BY SIMILARITY).
FT METAL 95 95 ZINC (BY SIMILARITY).
FT METAL 97 97 ZINC (BY SIMILARITY).
FT METAL 171 171 ZINC (BY SIMILARITY).
SQ SEQUENCE 231 AA; 25540 MW; DA473505738A1570 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 231;
Best Local Similarity 62.5%; Pred. No. 20;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 3 HNHGSFAY 10
I:| | | |
Db 169 HSHGPFAY 176

RESULT 14
SGBE_ECOLI
ID SGBE_ECOLI STANDARD; PRT; 231 AA.
AC P37680;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PROBABLE SUGAR ISOMERASE SGBE (EC 5.1.1.-).
GN SGBE.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE; 94316500.
RA Sofia H.J., Buriald V., Daniels D.L., Plunkett G. III, Blattner F.R.;
RT "Analysis of the Escherichia coli genome. V. DNA sequence of the
RT region from 76.0 to 81.5 minutes."
RL Nucleic Acids Res. 22:2576-2586(1994).
RN [2]
RP DISCUSSION OF SEQUENCE.
RA Reizer J., Charbit A., Reizer A., Saier M.H. Jr.;
RT "Novel phosphotransferases system genes revealed by bacterial genome
RT analysis: operons encoding homologues of sugar-specific permease
RT domains of the phosphotransferase system and pentose catabolic
RT enzymes";
RL Genome Sci. Technol. 1:53-75(1996).

CC -1- FUNCTION: PROBABLE PENTULOSE-5-PHOSPHATE-4-EPIMERASE.
CC -1- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE ARAD / FUCA FAMILY.
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CC -----
DR EMBL; U00039; AAB18560.1; -.
DR EMBL; AE000435; AAC76607.1; -.
DR ECGENE; EG12287; SGBE.
DR PFAM; PF00596; Aldolase_II; 1.
KW Isomerase; Zinc.
FT METAL 76 76 ZINC (BY SIMILARITY).
FT METAL 95 95 ZINC (BY SIMILARITY).
FT METAL 97 97 ZINC (BY SIMILARITY).
FT METAL 171 171 ZINC (BY SIMILARITY).
SQ SEQUENCE 231 AA; 25561 MW; F4FF4D7EC2A80B3A CRC64;

Query Match 58.6%; Score 34; DB 1; Length 231;
Best Local Similarity 62.5%; Pred. No. 20;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 3 HNHGSFAY 10
I:| | | |
Db 169 HSHGPFAY 176

RESULT 15
SGBE_HAEIN
ID SGBE_HAEIN STANDARD; PRT; 231 AA.
AC P44989;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PROBABLE SUGAR ISOMERASE SGBE (EC 5.1.1.-).
GN SGBE OR H11025.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20;
RX MEDLINE; 95350630.
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrman J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RP "Whole-genome random sequencing and assembly of Haemophilus
RP influenzae Rd.";
RL Science 269:496-512(1995).
CC -1- FUNCTION: PROBABLE PENTULOSE-5-PHOSPHATE-4-EPIMERASE.
CC -1- COFACTOR: BINDS ONE ZINC ION PER MOLECULE (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE ARAD / FUCA FAMILY.
CC -----
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CC -----

DR EMBL; U32783; AAC22685.1; -.
DR TIGR; H11025; -.
DR PFAM; PF00596; Aldolase_II; 1.
KW Isomerase; Zinc.
FT METAL 76 76 ZINC (BY SIMILARITY).
FT METAL 95 95 ZINC (BY SIMILARITY).
FT METAL 97 97 ZINC (BY SIMILARITY).
FT METAL 171 171 ZINC (BY SIMILARITY).
SQ SEQUENCE 231 AA; 25980 MW; 9DE3485E54B10DC7 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 231;
Best Local Similarity 62.5%; Pred. No. 20;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSPAY 10
Db 169 HSHGPFAP 176

Search completed: May 27, 2000, 20:07:13
Job time: 985 sec

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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:38:37 ; Search time 199.56 seconds
(without alignments)
3.474 Million cell updates/sec

Title: US-09-016-061-60

Perfect score: 58

Sequence: 1 ARNHGSPAY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

SPTREMBL12:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	37	63.8	150	1	027642
2	37	63.8	731	2	059369
3	36	62.1	470	2	092CT8
4	36	62.1	1049	12	083611
5	35	60.3	272	5	024950
6	35	60.3	272	5	024951
7	35	60.3	282	2	092A29
8	35	60.3	480	1	028764
9	35	60.3	558	5	021726
10	35	60.3	567	13	09VHZ6
11	35	60.3	615	11	063614
12	35	60.3	651	10	022781
13	35	60.3	1797	5	093692
14	35	60.3	1805	5	093691
15	34	58.6	154	2	0929C6
16	34	58.6	236	10	040088
17	34	58.6	274	2	09XAY5
18	34	58.6	339	9	038009
19	34	58.6	379	2	025568
20	34	58.6	381	2	092KT9

21	34	58.6	385	9	064373
22	34	58.6	446	5	062086
23	34	58.6	463	5	044923
24	34	58.6	489	2	P72495
25	34	58.6	489	2	P72497
26	34	58.6	2831	2	085166
27	33	56.9	79	7	019398
28	33	56.9	89	7	019495
29	33	56.9	191	5	026468
30	33	56.9	233	10	038718
31	33	56.9	259	2	09WXP6
32	33	56.9	268	12	056826
33	33	56.9	275	10	043476
34	33	56.9	283	2	084129
35	33	56.9	353	5	017699
36	33	56.9	624	5	020712
37	33	56.9	1683	12	066034
38	32.5	56.0	110	12	090623
39	32.5	56.0	110	12	09YTS0
40	32	55.2	54	12	08542
41	32	55.2	62	2	049908
42	32	55.2	259	5	093519
43	32	55.2	264	6	028109
44	32	55.2	276	2	084420
45	32	55.2	299	12	084647

ALIGNMENTS

RESULT 1
027642 PRELIMINARY; PRT: 150 AA.
ID 027642;
AC 027642;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
DE DEOXYCYTIDINE-TRIPHOSPHATE DEAMINASE RELATED PROTEIN.
GN MTH1605.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanobacterium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-DELTA H;
RX MEDLINE; 98037514.
RA ALDREDGE T., BASHIRZADEH R., BLAKELY D., COOK R., GILBERT K.,
RA HARRISON D., HOANG L., KEAGLE P., LUMM W., POTHIER B., QIU D.,
RA SPADAFORA R., VICARE R., WANG Y., WIERZBOWSKI J., GIBSON R.,
RA JIWANI N., CARUSO A., BUSH D., SAFER H., PATWELL D., PRABHAKAR S.,
RA MCDUGALL S., SHIMER G., GOYAL A., PIETROVSKI S., CHURCH G.M.,
RA DANIELS C.J., MAO J.-I., RICE P., NOLLING J., REEVE J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
DR EMBL; AE000920; AAB86078.1; -.
DR PFAM; PF00692; dUTPase; 1.
SQ SEQUENCE 150 AA; 16996 MW; B110FE9A CRC32;

Query Match 63.8%; Score 37; DB 1; Length 150;
Best Local Similarity 62.5%; Pred. No. 9;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 HNHGSFAY 10

Db 115 HNHGEY 122

RESULT 2

Q59369 PRELIMINARY; PRT: 731 AA.
ID Q59369

AC Q59369;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE HISTIDINE RICH P TYPE ATPASE.
 GN HRA-1.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95110304.
 RA TRENOR C.C., LIN W., ANDREWS N.C.;
 RT "Novel bacterial p-type ATPases with histidine-rich heavy-metal-
 associated sequences."
 RL Biochem. Biophys. Res. Commun. 205:1644-1650(1994).
 DR EMBL: U16658; AAA62113.1; -.
 DR PROSITE; PS00154; ATPASE_E1_E2; 1.
 DR PFAM; PF00122; E1-E2_ATPase; 1.
 KW Hydrolase; Transmembrane; Phosphorylation; ATP-binding.
 FT MOD_RES 431 431 PHOSPHORYLATION (PROBABLE).
 SQ SEQUENCE 731 AA; 78453 MW; 6765E988 CRC32;

Query Match 63.8%; Score 37; DB 2; Length 731;
 Best Local Similarity 75.0%; Pred. No. 43;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHHGSF 8
 | | | | |
 DB 88 ARHHGSF 95

RESULT 3

Q9ZCT8
 ID Q9ZCT8 PRELIMINARY; PRT; 470 AA.
 AC Q9ZCT8;
 DT 01-MAY-1999 (Tremblrel. 10, Created)
 DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
 DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
 DE GLUTAMYL-TRNA SYNTHETASE (GLTX2).
 GN RP623.
 OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsiae; Rickettsia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 99039499.
 RA ANDERSSON S.G.E., ZOMORODIPOUR A., ANDERSSON J.O.,
 RA SICHERTZ-PONTEN T., ALSMARK U.C.M., PODOWSKI R.M., NAESLUND A.K.,
 RA ERIKSSON A.S., WINKLER H.H., KURLAND C.G.;
 RT "The genome sequence of Rickettsia prowazekii and the origin of
 mitochondria."
 RL Nature 396:133-140(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MADRID E;
 RA ANDERSSON S.G.E.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AJ245272; CAA15066.1; -.
 DR HSSP; P27000; IGLN. 431
 SQ SEQUENCE 470 AA; 53696 MW; A0660D82 CRC32;

Query Match 62.1%; Score 36; DB 2; Length 470;
 Best Local Similarity 75.0%; Pred. No. 43;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHHGSF 8
 | | | | |
 DB 31 ARHHNGKF 38

RESULT 4
 Q83611
 ID Q83611 PRELIMINARY; PRT; 1049 AA.
 AC Q83611;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE A-TYPE INCLUSION PROTEIN.
 GN ATI.
 OS Ectromelia virus.
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MP-1;
 RA OSTERRIEDER N.;
 RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MP-1;
 RA PEDERSEN K., HALLBECK L., ARLINGER J., JAHROMI N., ERLANDSSON A.C.;
 RL FEMS Microbiol. Meth. 0:0-0(0).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-MP-1;
 RX MEDLINE: 94353638.
 RA OSTERRIEDER N., MEYER M., PFEFFER M.;
 RT "Characterization of the gene encoding the A-type inclusion body
 protein of mousepox virus."
 RL Virus Genes 8:125-135(1994).
 DR EMBL: X69325; CAA49168.1; -.
 SQ SEQUENCE 1049 AA; 122466 MW; 0FDD17C6 CRC32;

Query Match 62.1%; Score 36; DB 12; Length 1049;
 Best Local Similarity 66.7%; Pred. No. 95;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFAY 10
 | | | | |
 DB 771 RHNGSGHY 779

RESULT 5

Q24950
 ID Q24950 PRELIMINARY; PRT; 272 AA.
 AC Q24950;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE VITELLINE PROTEIN B1 PRECURSOR.
 OS Fasciola hepatica (liver fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 OC Echinostomida; Echinostomatidae; Echinostomata; Fascioloidae;
 OC Fasciolidae; Fasciola.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 93063029.
 RA RICE-FIGHT A.C., DUSEK K.A., KOCHVAR G.J., WAITE J.H.;
 RT "Eggshell precursor proteins of Fasciola hepatica, I. Structure and
 expression of vitelline protein B."
 RL Mol. Biochem. Parasitol. 54:129-141(1992).
 DR EMBL: M93024; AAA29143.1; -.
 KW Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 272 VITELLINE PROTEIN B1.
 SQ SEQUENCE 272 AA; 31211 MW; 892E4D3A CRC32;

Query Match 60.3%; Score 35; DB 5; Length 272;
 Best Local Similarity 75.0%; Pred. No. 38;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ARNHGSGF 8
Db 19 ARHPHGKF 26

RESULT 6
Q24951 ID Q24951 PRELIMINARY; PRT; 272 AA.
AC Q24951;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE VITELLINE PROTEIN B2 PRECURSOR.
OS Fasciola hepatica (Liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Echinostomida; Echinostomatidae; Echinostomata; Fascioloidae;
OC Fasciolidae; Fasciola.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93063029.
RA RICE-FICHT A.C., DUSEK K.A., KOCHVAR G.J., WAITE J.H.;
RT "Egshell precursor proteins of Fasciola hepatica, I. Structure and
RT expression of vitelline protein B.";
RL Mol. Biochem. Parasitol. 54:129-141(1992).
DR EMBL; M93025; AAA29144.1; -.
KW Signal.
FT SIGNAL.
FT CHAIN 1 19 POTENTIAL.
FT CHAIN 20 272 VITELLINE PROTEIN B2.
SQ SEQUENCE 272 AA; 31418 MW; EBAF123F CRC32;

Query Match 60.3%; Score 35; DB 5; Length 272;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSGF 8
Db 19 ARHPHGKF 26

RESULT 7
Q2429 ID Q2429 PRELIMINARY; PRT; 282 AA.
AC Q2429;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
DE GRA-ORF30 PROTEIN.
GN GRA-ORF30.
OS Streptomyces violaceoruber.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-TU22;
RX MEDLINE; 99051446.
RA ICHINOSE K., BEDFORD D.J., TORNUS D., BECHTHOLD A., BIBB M.J.,
RA REVILL W.P., FLOSS H.G., HOPWOOD D.A.;
RT "The granaticin biosynthetic gene cluster of Streptomyces
RT violaceoruber Tu22: sequence analysis and expression in a heterologous
RT host.";
RL Chem. Biol. 5:647-659(1998).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-TU22;
RX MEDLINE; 90060034.
RA SHERMAN D.H., MALPARTIDA F., BIBB M.J., KIESER H.M., BIBB M.J.,
RA HOPWOOD D.A.;
RT "Structure and deduced function of the granaticin-producing polyketide
RT synthase gene cluster of Streptomyces violaceoruber Tu22.";
RL EMBO J. 8:2717-2725(1998).
RN [3]

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RP SEQUENCE FROM N.A.
RC STRAIN-TU22;
RX MEDLINE; 96027933.
RA BECHTHOLD A., SOHNG J.K., SMITH T.M., CHU X., FLOSS H.G.;
RT "Identification of Streptomyces violaceoruber Tu22 genes involved in
RT the biosynthesis of granaticin.";
RL Mol. Gen. Genet. 248:610-620(1995).
DR EMBL; AJ011500; CAA09657.1; -.
SQ SEQUENCE 282 AA; 29904 MW; FB79BBBA CRC32;

Query Match 60.3%; Score 35; DB 2; Length 282;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 HGSPAY 10
Db 162 HGSPAY 167

RESULT 8
Q28764 ID Q28764 PRELIMINARY; PRT; 480 AA.
AC Q28764;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
DE HYPOTHETICAL 52.2 KD PROTEIN.
GN AFI508.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE; 98049343.
RA KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,
RA KETCHUM K.A., DODSON R.J., GINN M., HICKEY E.K., PETERSON J.D.,
RA RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRIDES N.C.,
RA FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
RA KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
RA PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,
RA OVERBEK R., GOCAYNE J.D., WEIDMAN J.F., McDONALD L., UTTERBACK T.,
RA COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M.,
RA SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
RA MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
RA VENTER J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
RT reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
DR EMBL; AE000998; AAB89742.1; -.
DR TIGR; AFI508; -.
KW Hypothetical protein.
SQ SEQUENCE 480 AA; 52164 MW; 6EA7AAF1 CRC32;

Query Match 60.3%; Score 35; DB 1; Length 480;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 HGSPAY 10
Db 429 HGSPAY 434

RESULT 9
Q21726 ID Q21726 PRELIMINARY; PRT; 538 AA.
AC Q21726;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE COSMID R04E5.

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GN R04E5.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
 OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE; 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMAILDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WAYSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA MILLER N.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U41538; AAC48179.1; -.
 DR PFAM; PF01595; DUF21.1; -.
 SQ SEQUENCE 538 AA; 60480 MW; DE87F3F7 CRC32;

Query Match 60.3%; Score 35; DB 5; Length 538;
 Best Local Similarity 62.5%; Pred. No. 75;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNGSFA 9
 :|:|:|
 Db 434 KHHGKFA 441

RESULT 10
 Q9YH26
 ID Q9YH26 PRELIMINARY; PRT; 567 AA.
 AC Q9YH26;
 DT 01-MAY-1999 (TREMELrel. 10, Created)
 DT 01-MAY-1999 (TREMELrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMELrel. 10, Last annotation update)
 DE CDC45.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
 OC Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae; Xenopodinae;
 OC Xenopus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 98429493.
 RA MIMURA S., TAKISAWA H.;
 RT "Xenopus Cdc45-dependent loading of DNA polymerase alpha onto
 RT chromatin under the control of S-phase Cdk.";
 RL EMBO J. 17:5699-5707(1998).
 DR EMBL; AF062494; AAC67520.1; -.
 SQ SEQUENCE 567 AA; 65444 MW; FFA7D874 CRC32;

Query Match 60.3%; Score 35; DB 13; Length 567;
 Best Local Similarity 71.4%; Pred. No. 79;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNHGS 7
 :|:|:|:|
 Db 251 SRHNHGN 257

RESULT 11

Q63614
 ID Q63614 PRELIMINARY; PRT; 615 AA.
 AC Q63614;
 DT 01-NOV-1996 (TREMELrel. 01, Created)
 DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMELrel. 12, Last annotation update)
 DE TYROSINE KINASE RECEPTOR (FRAGMENT).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SPLEEN;
 RX MEDLINE; 94043123.
 RA BENHAMOU M., RYBA N.J.P., NISHIKATA H., KIHARA H., SIRAGANIAN R.P.;
 RT "Protein-tyrosine kinase p72syk in high affinity Ige receptor
 RT signaling. Identification as a component of pp72 and association with
 RT the receptor gamma chain after receptor aggregation.";
 RL J. Biol. Chem. 268:23318-23324(1993).
 DR EMBL; L20838; AAA42308.1; -.
 DR HSP; P43405; 1A81.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PFAM; PF00069; pkinase; 1.
 DR PFAM; PF00017; SH2; 2.
 FT NON_TER 1 615
 FT NON_TER 615 615
 SQ SEQUENCE 615 AA; 70008 MW; 4BDFD84 CRC32;

Query Match 60.3%; Score 35; DB 11; Length 615;
 Best Local Similarity 77.8%; Pred. No. 85;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNHGSFA 9
 :|:|:|:|
 Db 181 ARDNNGSFA 189

RESULT 12
 O22781
 ID O22781 PRELIMINARY; PRT; 651 AA.
 AC O22781;
 DT 01-JAN-1998 (TREMELrel. 05, Created)
 DT 01-JAN-1998 (TREMELrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMELrel. 08, Last annotation update)
 DE PUTATIVE G9A PROTEIN.
 GN F4P9.6.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 OC Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA ROUNSLEY S.D., LIN X., KETCHUM K.A., CROSBY M.L., BRANDON R.C.,
 RA SYKES S.M., MASON T.M., KERLAVAGE A.R., ADAMS M.D., SOMERVILLE C.R.,
 RA VENTER J.C.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC002332; AAB80647.1; -.
 DR PFAM; PF00856; SET; 1.
 SQ SEQUENCE 651 AA; 72848 MW; C1512869 CRC32;

Query Match 60.3%; Score 35; DB 10; Length 651;
 Best Local Similarity 70.0%; Pred. No. 90;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ARHNHGSFAY 10
 :|:|:|:|
 Db 449 ARKNGGEFAY 458

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RESULT 13
Q93692 PRELIMINARY; PRT; 1797 AA.
AC Q93692;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE F36H2.3B PROTEIN.
GN F36H2.3B.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RA STEWARD C.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RL Nature 368:32-38(1994).
DR EMBL; Z81078; CAB03077.1; -.
DR HSSP; P10998; 1VVC.
DR PFAM; PF00084; sush1; 22.
SQ SEQUENCE 1797 AA; 184147 MW; 114AFD0C CRC32;

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Query Match 60.3%; Score 35; DB 5; Length 1797;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy 4 NHGSPAY 10
Db 1429 NHGTFSY 1435

RESULT 14
Q93691 PRELIMINARY; PRT; 1805 AA.
AC Q93691;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE F36H2.3A PROTEIN.
GN F36H2.3A.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RA STEWARD C.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

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RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RL Nature 368:32-38(1994).
DR EMBL; Z81078; CAB03076.1; -.
DR HSSP; P10998; 1VVC.
DR PFAM; PF00084; sush1; 22.
SQ SEQUENCE 1805 AA; 185044 MW; 8850F8A3 CRC32;

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Query Match 60.3%; Score 35; DB 5; Length 1805;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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```

Qy 4 NHGSPAY 10
Db 1429 NHGTFSY 1435

RESULT 15
Q929C6 PRELIMINARY; PRT; 154 AA.
ID Q929C6;
AC Q929C6;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE CT296 HYPOTHETICAL PROTEIN.
GN CPN0055.
OS Chlamydia pneumoniae.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CWL029;
RA KALMAN S., MITCHELL W., MARATHE R., LAMMEL C., FAN J., OLINGER L.,
RA GRIMWOOD J., DAVIS R.W., STEPHENS R.S.;
RT "Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE001590; AAD18208.1; -.
SQ SEQUENCE 154 AA; 17722 MW; B7E1ED5 CRC32;

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Query Match 58.6%; Score 34; DB 2; Length 154;
Best Local Similarity 62.5%; Pred. No. 33;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy 3 HNHGSFAY 10
Db 14 HNHGSILF 21

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Search completed: May 27, 2000, 19:38:39
Job time: 2372 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:21:33 ; Search time 148.45 seconds
(without alignments)
1.596 Million cell updates/sec

Title: us-09-016-061-60
Perfect score: 58
Sequence: 1 ARNHGsfay 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	10	1 W76020	LM609 grafted anti
2	52	89.7	10	1 W76010	LM609 grafted anti
3	52	89.7	117	1 W76001	Vitaxin antibody h
4	52	89.7	117	1 W76003	LM609 antibody hea
5	51	87.9	10	1 W76037	LM609 grafted anti
6	49	84.5	10	1 W76021	LM609 grafted anti
7	47	81.0	10	1 W76038	LM609 grafted anti
8	46	79.3	10	1 W76022	LM609 grafted anti
9	46	79.3	10	1 W76023	LM609 grafted anti
10	45	77.6	10	1 W76024	LM609 grafted anti
11	45	77.6	10	1 W76025	LM609 grafted anti
12	45	77.6	10	1 W76026	LM609 grafted anti
13	45	77.6	10	1 W76027	LM609 grafted anti
14	45	77.6	10	1 W76028	LM609 grafted anti
15	45	77.6	10	1 W76029	LM609 grafted anti
16	45	77.6	10	1 W76030	LM609 grafted anti
17	44	75.9	110	1 W84099	Vitronectin alpha-
18	44	75.9	117	1 W84093	Murine vitronectin
19	44	75.9	117	1 W84097	Humanised anti- α p
20	41	70.7	10	1 W76039	LM609 grafted anti
21	41	70.7	10	1 W76040	LM609 grafted anti
22	36	62.1	117	1 R79157	Human IgE receptor
23	36	62.1	117	1 R79155	Human IgE receptor
24	36	62.1	117	1 W27357	Heavy chain variab
25	36	62.1	117	1 W27526	Heavy chain variab
26	36	62.1	117	1 W27354	Heavy chain variab
27	36	62.1	239	1 W73874	Human antiFc epsil
28	36	62.1	242	1 W73876	Human antiFc epsil
29	35	60.3	772	1 Y13401	Amino acid sequenc
30	34	58.6	204	1 W59609	DNA-binding/dimeri
31	34	58.6	358	1 W98649	H. pylori GHPO 403
32	34	58.6	489	1 W01556	Acetaminone C-11 hy
33	32	55.2	36	1 W03964	VBJ joint protein,
34	32	55.2	36	1 W41127	VH251 DXP-1 J6 mu

35 32 55.2 123 1 W19888 CEA-specific antib
36 32 55.2 384 1 W14787 FKBP-SYK:SH2 fusio
37 32 55.2 384 1 W96822 A fusion protein o
38 32 55.2 415 1 W33692 Treponema pallidum
39 32 55.2 415 1 W59930 Modified T. pallid
40 32 55.2 415 1 W68498 Treponema pallidum
41 32 55.2 434 1 W59934 Wild type T. palli
42 32 55.2 443 1 R58637 Treponema pallidum
43 32 55.2 443 1 W35744 Treponema pallidum
44 32 55.2 456 1 W33693 Nucleic acid-bound
45 32 55.2 551 1 W59933 Modified T. pallid

ALIGNMENTS

RESULT 1

W76020
ID W76020 standard; Protein; 10 AA.
AC W76020;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #2.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis; primer; V-H region; CDR;
complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998: U01826.
PR 30-JAN-1997: US-791391.
PA (IXSY-) IXSY INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49857.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
integrin - and related grafted antibodies based on murine monoclonal
LM609, also related nucleic acid, used to treat, prevent or diagnose
angiogenesis or restenosis
Claim 62: Page 41: 129pp: English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
LM609 heavy and light chain variable region. LM609 and the antibody
vitaxin bind selectively to integrin alphavbeta3 and can be used to
inhibit binding of alphavbeta3 to a ligand and thus block
integrin-mediated signal transduction. This is useful in the treatment,
prevention and diagnosis of alphavbeta3-mediated disease, specifically,
angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
arthritis, macular degeneration, osteoporosis etc.). The antibodies
contain non-murine framework regions so are suitable for use in humans.
Enhanced types of LM609 have affinity more than 90 times greater than
that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 100.0%; Score 58; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGsfay 10
Db 1 ARNHGsfay 10
|||||||

RESULT 2

W76010
ID W76010 standard; Protein; 10 AA.
AC W76010;
DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #1.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49847.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Disclosure; Page 40; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region; LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 CC Sequence 10 AA;

Query Match 89.7%; Score 52; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0016;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARNHGSEFAY 10
 ||||:||||
 Db 1 ARHNYGSFAY 10

RESULT 3
 W76001
 ID W76001 standard; Protein; 117 AA.
 AC W76001;
 DT 02-NOV-1998 (first entry)
 DE Vitaxin antibody heavy chain variable region protein fragment.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49820.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 1; Fig 1a; 129pp; English.
 CC This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated

CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 SQ Sequence 117 AA;

Query Match 89.7%; Score 52; DB 1; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.02;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSEFAY 10
 ||||:||||
 Db 97 ARHNYGSFAY 106

RESULT 4
 W76003
 ID W76003 standard; Protein; 117 AA.
 AC W76003;
 DT 02-NOV-1998 (first entry)
 DE LM609 antibody heavy chain variable region protein fragment.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49822.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 43; Fig 2a; 129pp; English.
 CC This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 SQ Sequence 117 AA;

Query Match 89.7%; Score 52; DB 1; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.02;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSEFAY 10
 ||||:||||
 Db 97 ARHNYGSFAY 106

RESULT 5
 W76037
 ID W76037 standard; Protein; 10 AA.
 AC W76037;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #13.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49874.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT Integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 43; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 87.9%; Score 51; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0024;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSFA 9
 |||||
 Db 1 ARNHGSFA 9

RESULT 6
 ID W76021
 AC W76021 standard; Protein; 10 AA.

DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #3.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

OS Mus sp.
 PN W09833919-A2.

PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.

PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

DR WPI; 98-437472/37.

DR N-PSDB; V49858.

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT Integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

PS Claim 62; Page 41; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 84.5%; Score 49; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.0054;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSFAY 10
 |||||
 Db 1 ARHNYGSYAY 10

RESULT 7

ID W76038 standard; Protein; 10 AA.

AC W76038;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #14.

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis; primer; V-H region; CDR;

KW complementarity determining region.

OS Mus sp.

PN W09833919-A2.

PD 06-AUG-1998.

PF 30-JAN-1998; U01826.

PR 30-JAN-1997; US-791391.

PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

DR WPI; 98-437472/37.

DR N-PSDB; V49875.

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT Integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

PS Claim 62; Page 43; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody

CC vitaxin bind selectively to integrin alphavbeta3 and can be used to

CC inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies

CC contain non-murine framework regions so are suitable for use in humans.

CC Enhanced types of LM609 have affinity more than 90 times greater than

CC that of parent the parent antibody.

SQ Sequence 10 AA;

Query Match 81.0%; Score 47; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.012;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSF 8
 |||||
 Db 1 ARHNGSF 8

RESULT 8

ID W76022 standard; Protein; 10 AA.

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AC W76022;
DE 02-NOV-1998 (first entry)
KW LM609 grafted antibody V-H region CDR3 protein fragment #4.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer: V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB; V49859.
DR Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB; V49860.
DR Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.

Query Match 79.3%; Score 46; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.018;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNHGSFAY 10
    ||||:||||
DB 1 ARHNYSFDY 10

RESULT 9
W76023
ID W76023 standard; Protein; 10 AA.
AC W76023;
DE 02-NOV-1998 (first entry)
KW LM609 grafted antibody V-H region CDR3 protein fragment #5.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer: V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB; V49861.
DR Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 79.3%; Score 46; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.018;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNHGSFAY 10
    ||||:||||
DB 1 ARHNYSFDY 10

RESULT 10
W76024
ID W76024 standard; Protein; 10 AA.
AC W76024;
DE 02-NOV-1998 (first entry)
KW LM609 grafted antibody V-H region CDR3 protein fragment #6.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer: V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB; V49861.
DR Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 77.6%; Score 45; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.027;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSFA 9
    ||||:||||
DB 1 ARHNYSGFA 9

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RESULT 11
W76025
ID W76025 standard; Protein; 10 AA.
AC W76025;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #7.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49862.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related nucleic acid, used to treat, prevent or diagnose
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 77.6%; Score 45; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.027;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSFA 9
Db 1 ARHNHGSFA 9
||||:||||

RESULT 13
W76027
ID W76027 standard; Protein; 10 AA.
AC W76027;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #9.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49864.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related nucleic acid, used to treat, prevent or diagnose
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 77.6%; Score 45; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.027;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSFA 9
Db 1 ARHNHGSFA 9
||||:||||

RESULT 12
W76026
ID W76026 standard; Protein; 10 AA.
AC W76026;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #8.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49863.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

```



```

QY 1 ARNHGSFA 9
    ||||:||||
Db 1 ARHNYGSFA 9

RESULT 14
W76028
ID W76028 standard; Protein: 10 AA.
AC W76028;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #10.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB; V49865.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related nucleic acid, used to treat, prevent or diagnose
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angio genesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 77.6%; Score 45; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.027;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSFA 9
    ||||:||||
Db 1 ARHNYGSFA 9

Search completed: May 27, 2000, 19:21:34
Job time: 1588 sec

QY 1 ARNHGSFA 9
    ||||:||||
Db 1 ARHNYGSFA 9

Query Match 77.6%; Score 45; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.027;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSFA 9
    ||||:||||
Db 1 ARHNYGSFA 9

RESULT 15
W76029
ID W76029 standard; Protein: 10 AA.
AC W76029;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #11.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.

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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:26:40 ; Search time 163.56 Seconds
(without alignments)
3.585 Million cell updates/sec

Title: US-09-016-061-62
Perfect score: 58
Sequence: 1 ARHNYGSYAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues
Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_63:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	45	77.6	108	2 S26316	Ig heavy chain V r
2	45	77.6	110	2 S26317	Ig heavy chain V r
3	42	72.4	446	2 T19625	hypothetical prote
4	40	69.0	316	2 T15395	hypothetical prote
5	38	65.5	236	2 T27233	hypothetical prote
6	38	65.5	428	2 T03934	DNA binding protei
7	38	65.5	482	2 T01932	RNA binding protei
8	37	63.8	289	2 T34688	probable lipoprote
9	37	63.8	420	2 I51088	L-SF precursor - J
10	37	63.8	1144	2 A36968	Pl-like adhesin pr
11	36	62.1	9	2 S36850	Ig heavy chain V r
12	36	62.1	113	2 S26468	Ig heavy chain V r
13	36	62.1	143	1 HSURB2	histone H2B.2, spe
14	36	62.1	301	2 JW0079	heterogeneous nucl
15	36	62.1	349	1 S52763	hypothetical prote
16	36	62.1	349	2 T33263	hypothetical prote
17	36	62.1	626	2 T18733	hypothetical prote
18	35	60.3	119	2 E30562	Ig heavy chain V r
19	35	60.3	119	2 C30562	Ig heavy chain V r
20	35	60.3	119	2 D30562	Ig heavy chain V r
21	35	60.3	150	2 D69081	deoxyuridine 5-tri
22	35	60.3	155	2 T03042	hypothetical prote
23	35	60.3	241	2 T16802	hypothetical prote
24	35	60.3	246	1 C64705	gerC2 protein - He
25	35	60.3	246	2 C71815	ubiquinone/menaqui
26	35	60.3	281	2 S71251	C-5 sterol desatur
27	35	60.3	293	2 F64969	glucose-1-phosphat
28	35	60.3	326	2 S47248	site-specific DNA-
29	35	60.3	377	2 T12042	cysteine proteinas
30	35	60.3	417	2 T20199	hypothetical prote

31	35	60.3	521	2 F64522	conserved hypothet
32	35	60.3	544	2 S75388	probable phenylala
33	35	60.3	808	2 JQ2205	UL47h protein - Ma
34	34	58.6	45	2 PC2006	amelogenin TRAP -
35	34	58.6	150	2 G71477	hypothetical prote
36	34	58.6	195	2 S62519	hypothetical prote
37	34	58.6	195	2 T39125	hypothetical prote
38	34	58.6	205	2 T05713	dehydrin - barley
39	34	58.6	213	1 JMBO	amelogenin I precu
40	34	58.6	225	2 S05546	dehydrin 18 - barl
41	34	58.6	456	2 T37662	choline kinase - f
42	34	58.6	456	2 S67441	hypothetical prote
43	34	58.6	576	2 A40688	peroxisomal protei
44	34	58.6	1011	2 T13669	neuromusculin - fr
45	34	58.6	1154	2 S39536	parasporal crystal

ALIGNMENTS

RESULT 1
S26316
Ig heavy chain V region - mouse
C/Species: Mus musculus (house mouse)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C/Accession: S26316
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A/Title: Antibodies that are specific for a single amino acid interchange in a protei
A/Reference number: S26309; MUID:91341421
A/Accession: S26316
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-108 <STA>
A/Cross-references: EMBL:X59190; NID:G52066; PIDN:CAA41900.1; PID:e36170; PID:gl33403
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F;2-85/Domain: immunoglobulin homology <IMM>

Query Match 77.6%; Score 45; DB 2; Length 108;
Best Local Similarity 80.0%; Pred. No. 0.31;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ARHNYGSYAY 10
DB 84 ARGNYGNVAY 93
|||:|||||

RESULT 2
S26317
Ig heavy chain V region - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 17-Apr-1998
C/Accession: S26317
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A/Title: Antibodies that are specific for a single amino acid interchange in a protei
A/Reference number: S26309; MUID:91341421
A/Accession: S26317
A/Molecule type: mRNA
A/Residues: 1-110 <STA>
A/Cross-references: EMBL:X59186
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 77.6%; Score 45; DB 2; Length 110;
Best Local Similarity 80.0%; Pred. No. 0.32;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ARHNYGSYAY 10
|||:|||||

Db 86 ARGNYGNAY 95

RESULT 3
T19625
hypothetical protein C31H5.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19625
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19625
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-446 <WIL>
A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6
A:Experimental source: clone C31H5
C:Genetics:
A:Gene: CESP:C31H5.6
A:Map position: 1
A:Introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3

Query Match 72.4%; Score 42; DB 2; Length 446;
Best Local Similarity 87.5%; Pred. No. 4.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSA 9
|||||:|
Db 51 RHNYGSHA 58

RESULT 4
T15395
hypothetical protein C03F11.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15395
R:Bentley, D.
submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid C03F11.
A:Reference number: Z18342
A:Accession: T15395
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-316 <BEN>
A:Cross-references: EMBL:U39744; NID:g1049465; PID:g1049467; PIDN:AAA80440.1; CESP:C03F11.2
A:Gene: CESP:C03F11.2
A:Introns: 90/3; 133/2; 171/1; 227/1; 262/1; 309/2

Query Match 69.0%; Score 40; DB 2; Length 316;
Best Local Similarity 70.0%; Pred. No. 6.9;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
|||:||||
Db 69 ARHFFGSVEY 78

RESULT 5
T27233
hypothetical protein Y57G11C.21 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27233
R:McMurray, A.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z20330
A:Accession: T27233
A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA
A:Residues: 1-236 <WIL>
A:Cross-references: EMBL:Z99281; PIDN:CAB16522.1; GSPDB:GN00022; CESP:Y57G11C.21
A:Experimental source: clone Y57G11C
C:Genetics:
A:Gene: CESP:Y57G11C.21
A:Map position: 4

Query Match 65.5%; Score 38; DB 2; Length 236;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
| |||: |||
Db 118 AYHFNFSYAY 127

RESULT 6
T03934
DNA binding protein ACBF - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C:Accession: T03934
R:Seguin, A.; Laible, G.; Leyva, A.; Dixon, R.A.; Lamb, C.J.
Plant Mol. Biol. 35, 281-291, 1997
A:Title: Characterization of a gene encoding a DNA-binding protein that interacts in
A:Reference number: Z15144
A:Accession: T03934
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-428 <SEG>
A:Cross-references: EMBL:U90212; NID:g1899187; PIDN:AAC49850.1; PID:g1899188
A:Experimental source: tissue-type stem
A:Note: interacts in vitro with vascular-specific cis-elements of the phenylalanine a

Query Match 65.5%; Score 38; DB 2; Length 428;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10
| ||| | |
Db 387 RQNYGGYGY 395

RESULT 7
T01932
RNA binding protein homolog - common tobacco (fragment)
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 26-Feb-1999 #sequence_revision 26-Feb-1999 #text_change 26-Feb-1999
C:Accession: T01932
R:Deslandes, L.; Manevski, A.; Lescure, B.; Marco, Y.; Tremousaygue, D.
submitted to the EMBL Data Library, October 1997
A:Reference number: Z14459
A:Accession: T01932
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-482 <DES>
A:Cross-references: EMBL:AF029351; NID:g2708531; PID:g2708532
C:Genetics:
A:Gene: QRRBP-1

Query Match 65.5%; Score 38; DB 2; Length 482;
Best Local Similarity 66.7%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10
| ||| | |
Db 442 RQNYGGYGY 450

RESULT 8

T34688
probable lipoprotein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C:Accession: T34688
R:Harris, D.; Taylor, K.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, May 1998
A:Reference number: Z21553
A:Accession: T34688
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-289 <HAR>
A:Cross-references: EMBL:AL023517; PIDN:CAAL1894.1; GSPDB:GN00070; SCOEDB:SC1B5.10C
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC1B5.10C

Query Match 63.8%; Score 37; DB 2; Length 289;
Best Local Similarity 60.0%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
|:|:|:|:|
Db 144 ANHSYSHYAY 153

RESULT 9

I51088
L-SF precursor - Japanese medaka
C:Species: Oryzias latipes (Japanese medaka)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 20-Aug-1999
C:Accession: I51088
R:Murata, K.; Sasaki, T.; Yasumasu, S.; Iuchi, I.; Enami, J.; Yasumasu, I.; Yamagami, K.
Dev. Biol. 167, 9-17, 1995
A:Title: Cloning of cDNAs for the precursor protein of a low-molecular-weight subunit of
A:Reference number: I51088; MUID:95154588
A:Accession: I51088
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-420 <MUR>
A:Cross-references: GB:D38630; NID:gi060937; PIDN:BAA07610.1; PID:gl060938
C:Genetics:
A:Gene: l-sf
C:Superfamily: sperm-binding glycoprotein 2P3; 2P domain homology
F:84-338/Domain: 2P domain homology <ZPH>

Query Match 63.8%; Score 37; DB 2; Length 420;
Best Local Similarity 60.0%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
|:|:|:|:|
Db 21 AQHNYGKPSY 30

RESULT 10

A36968
P1-like adhesin precursor - Mycoplasma pirum
C:Species: Mycoplasma pirum
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-Dec-1999
C:Accession: A36968
R:Tham, T.N.; Ferris, S.; Bahraoui, E.; Canarelli, S.; Montagnier, L.; Blanchard, A.
J. Bacteriol. 176, 781-788, 1994
A:Title: Molecular characterization of the P1-like adhesin gene from Mycoplasma pirum.
A:Reference number: A36968; MUID:94131957
A:Accession: A36968
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1144 <THA>
A:Cross-references: GB:L19685; NID:g404770; PIDN:AAC36866.1; PID:g404771

C:Genetics:

A:Genetic code: SGC3

Query Match 63.8%; Score 37; DB 2; Length 1144;
Best Local Similarity 66.7%; Pred. No. 83;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10
|:|:|:|:|
Db 885 KONYGSYFY 893

RESULT 11

S36850
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1994 #sequence_revision 01-Dec-1995 #text_change 05-Nov-1999
C:Accession: S36850
R:Jacob, J.; Kelsoe, G.
submitted to the EMBL Data Library, July 1992
A:Description: In situ studies on the primary immune response to (4-hydroxy-3-nitroph
A:Reference number: S25024
A:Accession: S36850
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-9 <JAC>
A:Cross-references: EMBL:X67387; NID:g50113; PIDN:CAA47799.1; PID:e51594; PID:gl33387
C:Keywords: heterotrimer; immunoglobulin

Query Match 62.1%; Score 36; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+05;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSY 8
|:|:|:|:|
Db 1 ARYDYGSI 8

RESULT 12

S26468
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26468
R:Kavaler, J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S26468
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <KAV>
A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 62.1%; Score 36; DB 2; Length 113;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSY 8
|:|:|:|:|
Db 93 ARHPYGYNI 100

RESULT 13

HSURB2
histone H2B.2, sperm - sea urchin (Lytechinus pictus)
C:Species: Lytechinus pictus (painted urchin)
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 22-Jun-1999

C:Accession: A24329; B25381
 R:Lai, Z.C.; Childs, G.
 Nucleic Acids Res. 14, 6845-6856, 1986
 A:Title: Isolation and characterization of the gene encoding the testis specific histone H2B
 A:Reference number: A93637; MUID:87016329
 A:Accession: A24329
 A:Molecule type: DNA
 A:Residues: 1-143 <LAI>
 A:Cross-references: GB:X04384; NID:g9618; PIDN:CAA27971.1; PID:g9619
 A:Experimental source: testis
 R:Lieber, T.; Weisser, K.; Childs, G.
 Mol. Cell. Biol. 6, 2602-2612, 1986
 A:Title: Analysis of histone gene expression in adult tissues of the sea urchins Strongylocentrotus purpuratus
 A:Reference number: A93078; MUID:87064560
 A:Accession: B25381
 A:Molecule type: mRNA
 A:Residues: 59-75, 'A', 77-137, 'N', 139-143 <LIE>
 A:Cross-references: GB:M13635; NID:g161315; PIDN:AAA30001.1; PID:g161316
 A:Experimental source: testis
 A:Note: This sequence most likely represents an alternative allele of the same gene
 C:Superfamily: histone H2B
 C:Keywords: Chromosomal protein; DNA binding; nucleosome core
 F:2-143/Product: histone H2B.2, sperm #status predicted <MAT>

Query Match 62.1%; Score 36; DB 1; Length 143;
 Best Local Similarity 66.7%; Pred. No. 17;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10
 | : |||||
 DB 52 RESYGSYIY 60

RESULT 14
 JW0079
 heterogenous nuclear ribonucleoprotein-like protein JKTBP - human
 N:Alternate names: JKTBP
 C:Species: Homo sapiens (man)
 C:Date: 17-Jun-1998 #sequence_revision 10-Jul-1998 #text_change 24-Sep-1999
 C:Accession: JW0079
 R:Tsuchiya, N.; Kamei, D.; Takano, A.; Matsui, T.; Yamada, M.
 J. Biochem. 123, 499-507, 1998
 A:Title: Cloning and characterization of a cDNA encoding a novel heterogeneous nuclear ribonucleoprotein
 A:Reference number: JW0079; MUID:98207031
 A:Accession: JW0079
 A:Molecule type: mRNA
 A:Residues: 1-301 <TSU>
 A:Cross-references: DBJ:D89092; NID:g2780747; PIDN:BAA24361.1; PID:d1025273; PID:g2780747
 C:Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoproteins
 F:28-101,113-187/Domain: RNA-binding #status predicted <RNA>
 F:30-96/Domain: ribonucleoprotein repeat homology <RRM1>

Query Match 62.1%; Score 36; DB 2; Length 301;
 Best Local Similarity 62.5%; Pred. No. 34;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSYAY 10
 : |||||
 DB 263 YNYGNYGY 270

RESULT 15
 S52763
 hypothetical protein YJR019c - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein J1456
 C:Species: Saccharomyces cerevisiae
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 12-Nov-1999
 C:Accession: S52763; S55209; S57034; S65928
 R:Hani, J.; Stumpf, G.; Domdey, H.
 submitted to the EMBL Data Library, March 1995
 A:Description: PFT1 encodes an essential protein in Saccharomyces cerevisiae, which shows

A:Reference number: S52762
 A:Accession: S52763
 A:Molecule type: DNA
 A:Residues: 1-349 <HAN>
 A:Cross-references: EMBL:X85972; NID:g758283; PID:g758285
 R:de Haan, M.; Smits, P.H.M.; Grivell, L.A.
 submitted to the EMBL Data Library, May 1995
 A:Reference number: S55183
 A:Accession: S55209
 A:Molecule type: DNA
 A:Residues: 1-349 <DEH>
 A:Cross-references: EMBL:X87611; NID:g854567; PID:g854594
 R:de Haan, M.; Grivell, L.A.; Smits, P.H.M.
 submitted to the Protein Sequence Database, September 1995
 A:Reference number: S56771
 A:Accession: S57034
 A:Molecule type: DNA
 A:Residues: 1-349 <ZAG>
 A:Cross-references: EMBL:Z49519; NID:g1015654; PID:g1015655; GSPDB:GN00010; MIPS:YJRO
 R:Hani, J.; Stumpf, G.; Domdey, H.
 FEBS Lett. 365, 198-202, 1995
 A:Title: PFT1 encodes an essential protein in Saccharomyces cerevisiae, which shows s
 A:Reference number: S65927; MUID:95300974
 A:Accession: S65928
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-349 <HAN>
 A:Cross-references: EMBL:X85972; NID:g758283; PID:g758285
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1995
 C:Genetics:
 A:Gene: SGD:TES1; MIPS:YJR019c
 A:Cross-references: SGD:S0003780; MIPS:YJR019c
 A:Map position: 10R
 C:Superfamily: acyl-CoA thioesterase II

Query Match 62.1%; Score 36; DB 1; Length 349;
 Best Local Similarity 60.0%; Pred. No. 39;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
 | : |||||
 DB 247 ARYNYVAFAY 256

Search completed: May 27, 2000, 19:26:41
 Job time: 1764 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 20:07:13 ; Search time 69.28 Seconds
(without alignments)
4.396 Million cell updates/sec

Title: US-09-016-061-62
Perfect score: 58
Sequence: 1 ARHNYGSYAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	41	70.7	909	1 HEX_ADEM1	P48308 mouse adeno
2	40	69.0	316	1 YX12_CAEEL	Q11123 caenorhabdi
3	36	62.1	142	1 H2B2_LYTP1	P06146 lytechinus
4	36	62.1	202	1 AMEL_MONDO	Q28462 monodelphis
5	36	62.1	349	1 YJY9_YEAST	P41903 saccharomyc
6	35	60.3	293	1 RBAL_ECOLI	P37744 escherichia
7	34	58.6	150	1 Y736_CHLTR	O84741 chlamydia t
8	34	58.6	189	1 AMEL_PIG	P45561 sus scrofa
9	34	58.6	213	1 AMEX_BOVIN	P02817 bos taurus
10	34	58.6	218	1 Y4VH_RHISN	O53216 rhizobium s
11	34	58.6	225	1 DH4_HORVU	P12949 hordeum vul
12	34	58.6	448	1 ASTB_PSEAE	O50175 pseudomonas
13	34	58.6	456	1 KICH_SCHPO	Q10276 schizosacch
14	34	58.6	576	1 PEX5_PICPA	P33292 pichia past
15	33	56.9	180	1 CH19_DROSU	P13428 drosophila
16	33	56.9	405	1 VGLM_EBV	P03215 epstein-bar
17	33	56.9	419	1 YMD2_CAEEL	P34456 caenorhabdi
18	33	56.9	425	1 PURA_FUSNU	O68581 fusobacteri
19	33	56.9	467	1 PAX7_HUMAN	P23759 homo sapien
20	33	56.9	629	1 KSKY_MOUSE	P48025 mus musculu
21	33	56.9	635	1 KSKY_HUMAN	P43405 homo sapien
22	33	56.9	649	1 GPDM_SCHPO	Q14400 schizosacch
23	33	56.9	786	1 EXOP_RHIME	P33698 rhizobium m
24	33	56.9	809	1 UBPL_YEAST	P25037 saccharomyc
25	33	56.9	1569	1 GLI3_XENLA	Q91660 xenopus lae
26	33	56.9	1596	1 GLI3_HUMAN	P10071 homo sapien
27	33	56.9	1596	1 GLI3_MOUSE	Q61602 mus musculu
28	32	55.2	79	1 CYB_DIFCA	P16359 dipodomys c
29	32	55.2	79	1 CYB_DIPHE	P16358 dipodomys h
30	32	55.2	79	1 CYB_DIPPA	P16357 dipodomys p
31	32	55.2	129	1 YP56_MYCTU	O50742 mycobacteri
32	32	55.2	134	1 CYB_DRYNI	O03713 dryomys nit
33	32	55.2	198	1 HB2C_HUMAN	P01911 homo sapien
34	32	55.2	202	1 DHSC_BACSU	P08064 bacillus su

RESULT 1

HEX_ADEM1
ID AC P48308; O11839; STANDARD; PRT; 909 AA.
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HEXON PROTEIN (LATE PROTEIN 2).
GN PII.
OS Mouse adenovirus type 1 (MAV-1).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FL;
RX MEDLINE; 94157453.
RA Weber J.M., Cai F., Murali R., Burnett R.M.:
RT "Sequence and structural analysis of murine adenovirus type 1 hexon.";
RL J. Gen. Virol. 75:141-147(1994).
RN [2]
RP REVISIONS TO 443.
RA Weber J.M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE STRUCTURAL PROTEINS IN THE
CC -1- VIRAL COAT AND IS SYNTHESIZED DURING LATE INFECTION.
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -----
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CC -----
CC EMBL; M81889; AAB48187.1; -.
DR HSSP; P03277; 1DHX.
DR PFAM; PF01065; Adeno_hexon; 1.
KW Coat protein; Hexon protein; Late protein.
SQ SEQUENCE 909 AA; 102368 MW; 7E1C17DF7F0E95A0 CRC64;

Query Match 70.7%; Score 41; DB 1; Length 909;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 NYGSYAY 10
| | | | |
Db 210 NYGSYAY 216

RESULT 2

YX12_CAEEL
ID YX12_CAEEL STANDARD; PRT; 316 AA.
AC Q11123;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)


```
DE HYPOTHETICAL 35.1 KD PROTEIN C03F11.2 IN CHROMOSOME X.
GN C03F11.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2.
RA Bentley D.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: WEAK, IN THE N-TERMINUS, TO C.ELEGANS F53B1.5.
CC
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CC
DR EMBL: U39744; AAA80440.1; -
DR WORMPEP: C03F11.2; CE03914.
KW Hypothetical protein.
SQ SEQUENCE 316 AA; 35107 MW; 6A725FCAC21CF676 CRC64;

Query Match 69.0%; Score 40; DB 1; Length 316;
Best Local Similarity 70.0%; Pred. No. 5.6;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
| | | | |
DB 69 ARHFGSYEY 78

RESULT 3
H2B2_LYTP1
ID H2B2_LYTP1 STANDARD; PRT; 142 AA.
AC P06146;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE HISTONE H2B.2, SPERM.
OS Lytechinus pictus (Painted sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Echinozoa; Echinoidea;
OC Euechinoidea; Echinacea; Temnopleuroidea; Toxopneustidae; Lytechinus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE; 87016329.
RA Lai Z.-C., Childs G.J.;
RT "Isolation and characterization of the gene encoding the testis
RT specific histone protein H2B-2 from the sea urchin Lytechinus
RT pictus."
RL Nucleic Acids Res. 14:6845-6856(1986).
RN [2]
RP SEQUENCE OF 58-142 FROM N.A.
RC TISSUE=TESTIS;
RX MEDLINE; 87064560.
RA Lieber T., Weissner K., Childs G.;
RT "Analysis of histone gene expression in adult tissues of the sea
RT urchins Strongylocentrotus purpuratus and Lytechinus pictus:
RT tissue-specific expression of sperm histone genes."
RL Mol. Cell. Biol. 6:2602-2612(1986).
CC -1- SUBUNIT: THE NUCLEOSOME IS AN OCTAMER CONTAINING TWO MOLECULES OF
CC H2A, H2B, H3, AND H4: WHICH WRAP APPROXIMATELY 146 BP OF DNA.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC
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CC
DR EMBL: X04384; CAA27971.1; -
DR EMBL: M13635; AAA30001.1; -
DR PIR; A24329; HSURB2.
DR PRINTS; PR00621; HISTONEH2B.
DR PROSITE; PS00357; HISTONE_H2B; 1.
DR PFAM; PF00125; histone; 1.
KW Chromosomal protein; Nucleosome core; Nuclear protein; DNA-binding;
KW Multigene family.
FT INIT_MET 0
FT VARIANT 75 75 G -> A.
FT VARIANT 137 137 K -> N.
SQ SEQUENCE 142 AA; 15805 MW; 8BF47E2C5EB878D5 CRC64;

Query Match 62.1%; Score 36; DB 1; Length 142;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10
| | | | |
DB 51 RESYGSYIY 59

RESULT 4
AMEL_MONDO
ID AMEL_MONDO STANDARD; PRT; 202 AA.
AC Q28462;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE AMELOGENIN.
GN AMEL.
OS Monodelphis domestica (Short-tailed grey opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-42.
RX MEDLINE; 97113826.
RA Hu C.-C., Zhang C., Qian Q., Ryu O.H., Moradian-Oldak J., Fincham A.G.,
RA Simmer J.P.;
RT "Cloning, DNA sequence, and alternative splicing of opossum
RT amelogenin mRNAs."
RL J. Dent. Res. 75:1728-1734(1996).
CC -1- FUNCTION: PLAYS A ROLE IN THE BIOMINERALIZATION OF TOOTH. SEEMS
CC TO REGULATE THE FORMATION OF CRYSTALLITES DURING THE SECRETORY
CC STAGE OF TOOTH ENAMEL DEVELOPMENT. THOUGHT TO PLAY A MAJOR ROLE IN
CC THE STRUCTURAL ORGANIZATION AND MINERALIZATION OF DEVELOPING
CC ENAMEL.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
CC -1- ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING.
CC -1- SIMILARITY: BELONGS TO THE AMELOGENIN FAMILY.
CC
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CC
DR EMBL: U43407; AAB41109.1; -
KW Extracellular matrix; Phosphorylation; Enamel; Repeat;
KW Alternative splicing.
FT MOD_RES 16 16 PHOSPHORYLATION (BY SIMILARITY).
FT CONFLICT 32 33 HE -> QQ (IN AA SEQUENCE).
SQ SEQUENCE 202 AA; 22996 MW; 277FD2935211A6C6 CRC64;

Query Match 62.1%; Score 36; DB 1; Length 202;
```

```
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSVAY 10
Db 31 RHEYPSTGY 39
||| |||
RESULT 5
YJY9_YEAST STANDARD; PRT; 349 AA.
AC P41903;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE HYPOTHETICAL 40.3 KD PROTEIN IN ESSI-MER2 INTERGENIC REGION.
GN YJY019C OR J1456.
OS Saccharomycetes cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN-DH484;
RA Hani J., Stumpf G., Domdey H.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
[2]
RN RP SEQUENCE FROM N.A.
RC STRAIN-S288C / FY1679;
RA de Haan M., Smits P.H.M., Grivell L.A.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; X85972; CAA59960.1; -
DR EMBL; X87611; CAA60943.1; -
DR EMBL; Z49519; CAA89543.1; -
KW Hypothetical protein.
SQ SEQUENCE 349 AA; 40259 MW; F1B5A51C9A46783E CRC64;

Query Match 62.1%; Score 36; DB 1; Length 349;
Best Local Similarity 60.0%; Pred. No. 29;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSVAY 10
Db 247 ARYNYVAFAY 256
||| ||| |||
RESULT 6
RBAL_ECOLI STANDARD; PRT; 293 AA.
AC P37744; P78081;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE GLUCOSE-1-PHOSPHATE THYMIDYLTRANSFERASE (EC 2.7.7.24) (DTDP-GLUCOSE
DE SYNTHASE) (DTDP-GLUCOSE PYROPHOSPHORYLASE).
GN RFEA OR RMLA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN-K12 / WGI.
RX MEDLINE; 94292435.
RA Stevenson G., Neal B., Liu D., Hobbs M., Packer N.H., Batley M.,
```

```
RA Redmond J.W., Lindquist L., Reeves P.R.;
RT "Structure of the O antigen of Escherichia coli K-12 and the sequence
RT of its rfb gene cluster.";
RL J. Bacteriol. 176:4144-4156(1994).
RN [2]
RN RP REVISION TO 288.
RC STRAIN-K12 / WGI;
RA Stevenson G.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
[3]
RN RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE; 97426617.
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Rilett M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [4]
RN RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE; 97251358.
RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sampei G., Seki Y., Sivasubramanian S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [5]
RN RP SEQUENCE OF 247-293 FROM N.A.
RC STRAIN-K12 / W3110;
RX MEDLINE; 94292434.
RA Yao Z., Valvano M.A.;
RT "Genetic analysis of the O-specific lipopolysaccharide biosynthesis
RT region (rfb) of Escherichia coli K-12 W3110: identification of genes
RT that confer group 6 specificity to Shigella flexneri serotypes Y and
RT 4a.";
RL J. Bacteriol. 176:4133-4143(1994).
CC -1- CATALYTIC ACTIVITY: DTPP + ALPHA-D-GLUCOSE 1-PHOSPHATE -
CC -1- PYROPHOSPHATE + DTDP-GLUCOSE.
CC -1- PATHWAY: DTDP-L-RHAMNOSE BIOSYNTHESIS WITHIN THE O ANTIGEN
CC BIOSYNTHESIS PATHWAY OF LIPOPOLYSACCHARIDE BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE GLUCOSE-1-PHOSPHATE
CC THYMIDYLTRANSFERASE FAMILY.
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CC -----
DR EMBL; U09876; AAB88400.1; -
DR EMBL; AE000294; AAC75100.1; -
DR EMBL; D90841; CAB21785.1; -
DR EMBL; D90842; CAB21817.1; -
DR EMBL; U03041; AAC31629.1; -
DR EMBL; U03041; AAC31629.1; -
DR EMBL; E011978; RFEA.
DR PFAM; PF00483; NTP transferase; 1.
KW Lipopolysaccharide biosynthesis; Transferase; Kinase;
KW Nucleotidyltransferase.
FT CONFLICT 247 247
SQ SEQUENCE 293 AA; 32693 MW; BA895362D1C5CA55 CRC64;
```

```
Query Match 60.3%; Score 35; DB 1; Length 293;
Best Local Similarity 55.6%; Pred. No. 37;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
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QY 2 RHNYGSYAY 10
Db 278 KNNYGQYLY 286

RESULT 7
Y736.CHLTR
ID Y736.CHLTR STANDARD; PRT; 150 AA.
AC O84741;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE HYPOTHETICAL PROTEIN CT736.
GN CT736.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-D/UW-3/CX;
RX MEDLINE; 9900809.
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis."
RL Science 282:754-759(1998).
CC -1- SIMILARITY: BELONGS TO THE UPF0098 FAMILY.
CC -----
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CC -----
DR EMBL; U43405; AAB41110.1; -
DR EMBL; U43406; AAB41111.1; -
DR PIR; PC2006; PC2006.
DR PIR; PC2008; PC2008.
KW Extracellular matrix; Phosphorylation; Enamel; Repeat; Signal;
FT SIGNAL 1 16
FT CHAIN 17 189 AMELOGENIN.
FT MOD_RES 32 32 PHOSPHORYLATION.
FT VARSPPLIC 34 45 MISSING (IN LRAP).
FT VARSPPLIC 6 6 L -> F (IN ISOFORM 173B).
FT VARSPPLIC 14 16 AFS -> SLA (IN ISOFORM 173B).
SQ SEQUENCE 189 AA; 21387 MW; 6392212E0A31D00C CRC64;

Query Match 58.6%; Score 34; DB 1; Length 189;
Best Local Similarity 60.0%; Pred. No. 29;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
Db 103 AKHRYFYAY 112

RESULT 8
AMEL_PIG
ID AMEL_PIG STANDARD; PRT; 189 AA.
AC P45561;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE AMELOGENIN PRECURSOR (AMELOGENIN 173A/173B) [CONTAINS: LEUCINE-RICH
DE AMELOGENIN PEPTIDE (LRAP)].
GN AMEL.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97113827.
RA Hu C.C., Bartlett J.D., Zhang C.H., Qian Q., Ryu O.H., Simmer J.P.;
RT "Cloning, cDNA sequence, and alternative splicing of porcine
RT amelogenin mRNAs."
RL J. Dent. Res. 75:1735-1741(1996).
RN [2]
RP SEQUENCE OF 17-61 AND 78-181.

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RC MEDLINE; 94071951.
RX Fincham A.G., Moradian-Oldak J.;
RT "Amelogenin post-translational modifications: carboxy-terminal
RT processing and the phosphorylation of bovine and porcine 'LRAP' and
RT 'LRAP' amelogenins."
RL Biochem. Biophys. Res. Commun. 197:248-255(1993).
CC -1- FUNCTION: PLAYS A ROLE IN THE BIOMINERALIZATION OF TOOTH. SEEMS
CC TO REGULATE THE FORMATION OF CRYSTALLITES DURING THE SECRETORY
CC STAGE OF TOOTH ENAMEL DEVELOPMENT. THOUGHT TO PLAY A MAJOR ROLE IN
CC THE STRUCTURAL ORGANIZATION AND MINERALIZATION OF DEVELOPING
CC ENAMEL.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
CC -1- ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING. ONE OF THESE FORMS, LRAP, LACKS THE CENTRAL SECTION OF
CC AMELOGENIN.
CC -1- SIMILARITY: BELONGS TO THE AMALOGENIN FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U43405; AAB41110.1; -
DR EMBL; U43406; AAB41111.1; -
DR PIR; PC2006; PC2006.
DR PIR; PC2008; PC2008.
KW Extracellular matrix; Phosphorylation; Enamel; Repeat; Signal;
FT SIGNAL 1 16
FT CHAIN 17 189 AMELOGENIN.
FT MOD_RES 32 32 PHOSPHORYLATION.
FT VARSPPLIC 34 45 MISSING (IN LRAP).
FT VARSPPLIC 6 6 L -> F (IN ISOFORM 173B).
FT VARSPPLIC 14 16 AFS -> SLA (IN ISOFORM 173B).
SQ SEQUENCE 189 AA; 21387 MW; 6392212E0A31D00C CRC64;

Query Match 58.6%; Score 34; DB 1; Length 189;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10
Db 47 RHPYTSYGY 55

RESULT 9
AMEX_BOVIN
ID AMEX_BOVIN STANDARD; PRT; 213 AA.
AC P02817;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE AMELOGENIN, CLASS I PRECURSOR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91113686.
RA Gibson C., Golub E., Herold R., Risser M., Ding W., Shimokawa H.,
RA Young M., Termini J., Rosenbloom J.;
RT "Structure and expression of the bovine amelogenin gene."
RL Biochemistry 30:1075-1079(1991).
RN [2]
RP PRELIMINARY SEQUENCE OF 17-201.
RX MEDLINE; 84231410.
RA Takagi T., Suzuki M., Baba T., Minegishi K., Sasaki S.;

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RT "Complete amino acid sequence of amelogenin in developing bovine
RL enamel.";
RN [3]
RN ALTERNATIVE SPLICING (LRAP).
RP TISSUE-TOOTH;
RC MEDLINE; 91144612.
RX Gibson C.W., Golub E., Ding W., Shimokawa H., Young M., Termine J.,
RA Rosenbloom J.;
RT "Identification of the leucine-rich amelogenin peptide (LRAP) as the
RT translation product of an alternatively spliced transcript.";
RL Blochem. Biophys. Res. Commun. 174:1306-1312(1991).
RN [4]
RP SEQUENCE OF 17-49 AND 188-213.
RX MEDLINE; 94071951.
RA Fincham A.G., Moradian-Oldak J.;
RT "Amelogenin post-translational modifications: carboxy-terminal
RT processing and the phosphorylation of bovine and porcine 'TRAP' and
RT 'LRAP' amelogenins.";
RL Blochem. Biophys. Res. Commun. 197:248-255(1993).
RN [5]
RP STRUCTURE BY NMR.
RX MEDLINE; 90091473.
RA Renuopalakrishnan V., Prabhakaran M., Huang S.G., Balasubramaniam A.,
RA Strawich E., Glimcher M.J.;
RT "Secondary structure and limited three-dimensional structure of
RT bovine amelogenin.";
RL Connect. Tissue Res. 22:131-138(1989).
CC -1- FUNCTION: PLAYS A ROLE IN THE BIOMINERALIZATION OF TOOTHES. SEEMS
CC TO REGULATE THE FORMATION OF CRYSTALLITES DURING THE SECRETORY
CC STAGE OF TOOTH ENAMEL DEVELOPMENT. THOUGHT TO PLAY A MAJOR ROLE IN
CC THE STRUCTURAL ORGANIZATION AND MINERALIZATION OF DEVELOPING
CC ENAMEL.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
CC -1- ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING. ONE OF THESE FORMS, LRAP, LACKS THE CENTRAL SECTION OF
CC AMELOGENIN.
CC -1- MISCELLANEOUS: AMELOGENIN IS THE PREDOMINANT PROTEIN IN DEVELOPING
CC DENTAL ENAMEL.
CC -1- MISCELLANEOUS: CLASS I AMELOGENINS LOCATED ON X CHROMOSOME.
CC -1- SIMILARITY: BELONGS TO THE AMALOGENIN FAMILY.
CC -----
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CC -----
DR EMBL; M63499; AAA30372.1; -.
DR EMBL; M63631; AAA30625.1; -.
DR PIR; A03300; JMBO.
DR PIR; JN0123; JN0123.
DR PIR; PC2007; PC2007.
KW Extracellular matrix; Phosphorylation; Enamel; Repeat; Signal;
KW Alternative splicing.
FT SIGNAL 1 16
FT CHAIN 17 213 AMELOGENIN, CLASS I.
FT VARSPLIC 50 187 MISSING (IN LRAP).
FT MOD_RES 32 32 PHOSPHORYLATION.
SQ SEQUENCE 213 AA; 24119 MW; 163BD538806366DF CRC64;

Query Match 58.6%; Score 34; DB 1; Length 213;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10
DB 47 RHPYPSYGY 55

RT "Complete amino acid sequence of amelogenin in developing bovine
RL enamel.";
RN [3]
RN ALTERNATIVE SPLICING (LRAP).
RP TISSUE-TOOTH;
RC MEDLINE; 91144612.
RX Gibson C.W., Golub E., Ding W., Shimokawa H., Young M., Termine J.,
RA Rosenbloom J.;
RT "Identification of the leucine-rich amelogenin peptide (LRAP) as the
RT translation product of an alternatively spliced transcript.";
RL Blochem. Biophys. Res. Commun. 174:1306-1312(1991).
RN [4]
RP SEQUENCE OF 17-49 AND 188-213.
RX MEDLINE; 94071951.
RA Fincham A.G., Moradian-Oldak J.;
RT "Amelogenin post-translational modifications: carboxy-terminal
RT processing and the phosphorylation of bovine and porcine 'TRAP' and
RT 'LRAP' amelogenins.";
RL Blochem. Biophys. Res. Commun. 197:248-255(1993).
RN [5]
RP STRUCTURE BY NMR.
RX MEDLINE; 90091473.
RA Renuopalakrishnan V., Prabhakaran M., Huang S.G., Balasubramaniam A.,
RA Strawich E., Glimcher M.J.;
RT "Secondary structure and limited three-dimensional structure of
RT bovine amelogenin.";
RL Connect. Tissue Res. 22:131-138(1989).
CC -1- FUNCTION: PLAYS A ROLE IN THE BIOMINERALIZATION OF TOOTHES. SEEMS
CC TO REGULATE THE FORMATION OF CRYSTALLITES DURING THE SECRETORY
CC STAGE OF TOOTH ENAMEL DEVELOPMENT. THOUGHT TO PLAY A MAJOR ROLE IN
CC THE STRUCTURAL ORGANIZATION AND MINERALIZATION OF DEVELOPING
CC ENAMEL.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
CC -1- ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE
CC SPLICING. ONE OF THESE FORMS, LRAP, LACKS THE CENTRAL SECTION OF
CC AMELOGENIN.
CC -1- MISCELLANEOUS: AMELOGENIN IS THE PREDOMINANT PROTEIN IN DEVELOPING
CC DENTAL ENAMEL.
CC -1- MISCELLANEOUS: CLASS I AMELOGENINS LOCATED ON X CHROMOSOME.
CC -1- SIMILARITY: BELONGS TO THE AMALOGENIN FAMILY.
CC -----
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CC -----
DR EMBL; M63499; AAA30372.1; -.
DR EMBL; M63631; AAA30625.1; -.
DR PIR; A03300; JMBO.
DR PIR; JN0123; JN0123.
DR PIR; PC2007; PC2007.
KW Extracellular matrix; Phosphorylation; Enamel; Repeat; Signal;
KW Alternative splicing.
FT SIGNAL 1 16
FT CHAIN 17 213 AMELOGENIN, CLASS I.
FT VARSPLIC 50 187 MISSING (IN LRAP).
FT MOD_RES 32 32 PHOSPHORYLATION.
SQ SEQUENCE 213 AA; 24119 MW; 163BD538806366DF CRC64;

Query Match 58.6%; Score 34; DB 1; Length 213;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10
DB 47 RHPYPSYGY 55

RESULT 10
Y4VH_RHISN
ID Y4VH_RHISN STANDARD; PRT; 218 AA.
AC Q53216;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 24.6 KD PROTEIN Y4VH.
GN Y4VH.
OS Rhizobium sp. (strain NGR234).
OC Plasmid sym pNGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97305956.
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96389014.
RA Freiberg C., Perret X., Broughton W.J., Rosenthal A.;
RT "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
RT NGR234 using dye terminators and a thermostable 'sequenase' a
RT beginning.";
RL Genome Res. 6:590-600(1996).
CC -1- SIMILARITY: NONE OBVIOUS.
CC -----
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CC -----
DR EMBL; 268203; CAA92423.1; -.
DR EMBL; AE000101; AAB91896.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 218 AA; 24594 MW; 501C6CB38A09A2E5 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 218;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSYA 9
DB 68 ARDNHGSYS 76

RESULT 11
DH4_HORVU
ID DH4_HORVU STANDARD; PRT; 225 AA.
AC P12949;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-AUG-1991 (Rel. 19, Last annotation update)
DE DEHYDRIN DHN4 (B18).
GN DHN4.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
OC Poaceae; Hordeum.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV. HIMALAYA; TISSUE-SEEDLING;
RX MEDLINE; 93357436.
RA Close T.J., Kortt A.A., Chandler P.M.;
RT "A cDNA-based comparison of dehydration-induced proteins (dehydrins)
RT in barley and corn.";

```
RL Plant Mol. Biol. 13:95-108(1989).
CC -|- INDUCTION: BY ABCISIC ACID AND WATER-STRESS.
CC -|- SIMILARITY: STRONG TO BARLEY DHN1 AND DHN2, MAIZE DHN1, AND
CC ESPECIALLY TO BARLEY DHN3. TWO EXTREMELY CONSERVED BLOCKS WERE
CC IDENTIFIED, WITH A LESS CONSERVED REPEATING UNIT POSITIONED
CC BETWEEN THEM. DEHYDRIN DHN4 HAS FIVE SUCH SEMI-CONSERVED TANDEM
CC REPEATING UNITS.
CC -|- SIMILARITY: BELONGS TO THE PLANT DEHYDRIN FAMILY.
CC -----
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CC -----
DR EMBL; X15287; CAA33361.1; -.
DR PIR; S05546; S05546.
DR PROSITE; PS00315; DEHYDRIN_1; 1.
DR PROSITE; PS00823; DEHYDRIN_2; 2.
DR PFAM; PF00257; dehydrin; 3.
KW Dehydrin; Repeat.
FT DOMAIN 60 68 POLY-SER.
FT DOMAIN 105 199 5 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 105 118 1.
FT REPEAT 119 136 2.
FT REPEAT 137 159 3.
FT REPEAT 160 178 4.
FT REPEAT 179 199 5.
FT REPEAT 225 AA; 22574 MW; F0636B368CE5FF1C CRC64;
SQ SEQUENCE 225 AA; 22574 MW; 22574 MW; F0636B368CE5FF1C CRC64;

Query Match 58.6%; Score 34; DB 1; Length 225;
Best Local Similarity 55.8%; Pred. No. 42;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10
Db 97 OHNAGTYGY 105
::|::|:|
|::|::|:|

RESULT 12
ASTB_PSEAE STANDARD; PRT; 448 AA.
AC Q50175;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE SUCCINYLARGININE DIHYDROLASE (EC 3.-.-.-).
GN ASTB OR ARUB.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
OC Pseudomonas.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 15692 / PAO1;
RX MEDLINE; 98053840.
RA Itoh Y.;
RT "Cloning and characterization of the aru genes encoding enzymes of
RT the catabolic arginine succinyltransferase pathway in Pseudomonas
RT aeruginosa.";
RL J. Bacteriol. 179:7280-7290(1997).
CC -|- FUNCTION: CATALYZES THE HYDROLYSIS OF N(2)-SUCCINYLARGININE INTO
CC N(2)-SUCCINYLORNITHINE, AMMONIA AND CO(2).
CC -|- PATHWAY: SECOND STEP IN ARGININE CATABOLISM BY THE ARGININE
CC SUCCINYLTRANSFERASE PATHWAY.
CC -----
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CC -----
DR EMBL; AF011922; AAC46013.1; -.
KW Arginine metabolism; Hydrolase.
SQ SEQUENCE 448 AA; 48875 MW; 39F9F379CCCC16196 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 448;
Best Local Similarity 62.5%; Pred. No. 80;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSYAY 10
Db 16 HNYGGLSY 23
||||:|

RESULT 13
KICH_SCHPO STANDARD; PRT; 456 AA.
AC Q10276;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-FEB-2000 (Rel. 39, Last annotation update)
DE PUTATIVE CHOLINE KINASE (EC 2.7.1.32).
GN SPAC1367.12C.
OS Schizosaccharomyces pombe (Fission Yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
OC Schizosaccharomycetaceae; Schizosaccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-972;
RA Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -|- CATALYTIC ACTIVITY: ATP + CHOLINE = ADP + O-PHOSPHOCHOLINE.
CC -|- PATHWAY: CDP-CHOLINE AND CDP-ETHANOLAMINE PATHWAYS IN THE
CC SYNTHESIS OF PHOSPHOLIPIDS (BY SIMILARITY).
CC -|- SUBUNIT: MONOMER (BY SIMILARITY).
CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -|- SIMILARITY: BELONGS TO THE CHOLINE/ETHANOLAMINE KINASES FAMILY.
CC -----
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CC -----
DR EMBL; Z69729; CAA93600.1; -.
DR PFAM; PF01633; Choline_kinase; 1.
KW Hypothetical protein; Transferase; Kinase.
FT ACT_SITE 242 242 BY SIMILARITY.
SQ SEQUENCE 456 AA; 52536 MW; 08284FF1FC5FA089 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 456;
Best Local Similarity 75.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSY 8
Db 116 ARHNIGPY 123
|||||:|

RESULT 14
PEX5_PICPA STANDARD; PRT; 576 AA.
AC P33292; Q01967;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PEROXISOMAL TARGETING SIGNAL RECEPTOR (PEROXISOMAL PROTEIN PAS8)
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DE (PEROXIN-5) (PTS1 RECEPTOR).
GN PEX5 OR PAS8.
OS Pichia pastoris (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Pichia.
RN [1]
RC SEQUENCE FROM N.A.
RP STRAIN-NRRL 11430;
RX MEDLINE; 93260010.
RA McCollum D., Monosov E., Subramani S.;
RT "The pas8 mutant of Pichia pastoris exhibits the peroxisomal protein
RT import deficiencies of Zellweger syndrome cells -- the PAS8 protein
RT binds to the COOH-terminal tripeptide peroxisomal targeting signal,
RT and is a member of the TPR protein family.";
RL J. Cell Biol. 121:761-774(1993).
RN [2]
RC SEQUENCE FROM N.A.
RP Gould S.J., Kalish J.E., Morrel J.C., Bjorkman J., Urquhart A.J.,
RA Crane D.I.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RC FUNCTION.
RX MEDLINE; 95369234.
RA Terlecky S.R., Nuttley W.M., McCollum D., Sock E., Subramani S.;
RT "The Pichia pastoris peroxisomal protein PAS8p is the receptor for
RT the C-terminal tripeptide peroxisomal targeting signal.";
RL EMBO J. 14:3627-3634(1995).
CC -1- FUNCTION: BINDS TO THE C-TERMINAL PTS1-TYPE TRIPPEPTIDE PEROXISOMAL
CC TARGETING SIGNAL (SKL-TYPE) AND PLAYS AN ESSENTIAL ROLE IN
CC PEROXISOMAL PROTEIN IMPORT.
CC -1- SUBCELLULAR LOCATION: ITS DISTRIBUTION APPEARS TO BE DYNAMIC. IT
CC IS PROBABLY A CYCLING RECEPTOR FOUND MAINLY IN THE CYTOPLASM AND
CC AS WELL ASSOCIATED TO THE PEROXISOMAL MEMBRANE THROUGH A DOCKING
CC FACTOR (PEX13).
CC -1- SIMILARITY: CONTAINS 7 TPR DOMAINS.
CC -1- SIMILARITY: STRONG, TO OTHER PEROXISOMAL TARGETING SIGNAL
CC RECEPTORS.
CC -----
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CC -----
DR EMBL; Z19592; CAA79640.1; -.
DR EMBL; U59222; AAB40613.1; -.
DR PIR; A40688; A40688.
DR PFAM; PF00515; TPR; 4.
KW Peroxisome; Repeat; TPR domain; Transport; Protein transport.
FT DOMAIN 19 232 GLN-RICH.
FT REPEAT 278 311 TPR 1.
FT REPEAT 312 345 TPR 2.
FT REPEAT 346 383 TPR 3.
FT REPEAT 384 421 TPR 4.
FT REPEAT 422 455 TPR 5.
FT REPEAT 456 489 TPR 6.
FT REPEAT 490 523 TPR 7.
FT CONFLICT 243 259 DOFOAOHEKDFAOYAEG -> RPYVSGSMGERFCPIRRR
FT (IN REF. 1).
SQ SEQUENCE 576 AA; 65083 MW; C249FBES0FDE5247 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 576;
Best Local Similarity 66.7%; Pred. No. 1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 6; Conservative 0;

Oy 2 RHNYGSYAY 10
Db 260 RLNYGEYKY 268
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RESULT 15
CH19_DROSU STANDARD; PRT; 180 AA.
AC P13428;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE CHORION PROTEIN S19.
GN CP19 OR S19.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88297142.
RA Martinez-Cruzado J.C., Swimmer C., Fenerjian M.G., Kafatos F.C.;
RT "Evolution of the autosomal chorion locus in Drosophila. I. General
RT organization of the locus and sequence comparisons of genes s15 and
RT s19 in evolutionary distant species.";
RL Genetics 119:663-677(1988).
CC -----
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CC -----
DR EMBL; X53423; CAA37510.1; -.
DR PIR; S06616; S06616.
DR FLIBASE; FBgn0012936; Dsub\Cp19.
KW Chorion.
SQ SEQUENCE 180 AA; 19029 MW; 7AB643E8D4312C75 CRC64;

Query Match 56.9%; Score 33; DB 1; Length 180;
Best Local Similarity 55.6%; Pred. No. 51;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 1 ARHNYGSYA 9
Db 160 SQQNYGTGA 168
```

Search completed: May 27, 2000, 20:07:15
Job time: 987 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:38:39 ; Search time 199.56 Seconds
(without alignments)
3.474 Million cell updates/sec

Title: US-09-016-061-62

Perfect score: 58

Sequence: 1 ARHNYGSYAY 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL12.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	42	72.4	446	5	O62086
2	39	67.2	576	9	O64311
3	38	65.5	236	5	O18245
4	38	65.5	271	10	Q92T29
5	38	65.5	271	10	Q9XE12
6	38	65.5	428	10	P93843
7	38	65.5	482	10	O48955
8	37	63.8	289	2	O69838
9	37	63.8	420	13	Q91184
10	37	63.8	1144	2	Q50371
11	36	62.1	301	11	Q92130
12	36	62.1	349	5	O76436
13	36	62.1	420	4	O14979
14	36	62.1	626	5	O62017
15	36	62.1	1049	12	Q83611
16	35	60.3	89	7	O19495
17	35	60.3	120	7	O98183
18	35	60.3	120	7	O98186
19	35	60.3	150	1	O27642
20	35	60.3	155	12	O55705

21	35	60.3	241	5	Q22205
22	35	60.3	246	2	O26017
23	35	60.3	246	2	Q92JD6
24	35	60.3	281	10	Q39208
25	35	60.3	326	9	Q38652
26	35	60.3	377	10	O24324
27	35	60.3	378	8	O21173
28	35	60.3	417	5	O17705
29	35	60.3	521	2	O24867
30	35	60.3	544	1	P95960
31	35	60.3	808	12	Q69320
32	34	58.6	71	12	Q89635
33	34	58.6	118	4	O15155
34	34	58.6	150	2	O84741
35	34	58.6	205	10	O43477
36	34	58.6	247	10	Q92TR6
37	34	58.6	279	2	Q925Q4
38	34	58.6	588	9	O64304
39	34	58.6	1011	5	O24273
40	34	58.6	1144	2	O45745
41	34	58.6	1150	2	Q92NL9
42	34	58.6	1151	2	Q83747
43	34	58.6	1156	2	Q99031
44	34	58.6	1157	2	O45733
45	34	58.6	1169	2	O06014

ALIGNMENTS

RESULT 1

O62086

ID O62086 PRELIMINARY; PRT; 446 AA.

AC O62086;

DT 01-AUG-1998 (TREMBlrel. 07, Created)

DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)

DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)

DE C31H5.6 PROTEIN.

GN C31H5.6.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;

OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

RN [1]

RP SEQUENCE FROM N.A.

RA KERSHAW J.;

RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

EX MEDLINE: 94150718.

RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M.,

RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

RA JONES M., KERSHAW J., KIRSTEN J., LAYSTER N., LATREILLE P.,

RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RT elegans.";

RL Nature 368:32-38(1994).

DR EMBL: 293778; CAB07846.1; .

SQ SEQUENCE 446 AA; 50763 MW; B347C0C8 CRC32;

Query Match 72.4%; Score 42; DB 5; Length 446;

Best Local Similarity 87.5%; Pred. No. 6.4;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNYGSA 9

|||||:|

Db 51 RHNYGSA 58

*2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

RT elegans.;
RL Nature 368:32-38(1994).
DR EMBL: Z99281; CAB16522.1; -.
SQ SEQUENCE 236 AA; 26579 MW; 393A98F5 CRC32;

Query Match 65.5%; Score 38; DB 5; Length 236;
Best Local Similarity 60.0%; Pred. No. 17;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNGSYAY 10
| | | : | | |
DB 118 AYHNFNAY 127

RESULT 4

Q92T29 PRELIMINARY; PRT; 271 AA.

AC Q92T29;
DT 01-MAY-1999 (TREMREL. 10, Created)
DT 01-MAY-1999 (TREMREL. 10, Last sequence update)
DT 01-NOV-1999 (TREMREL. 12, Last annotation update)

DE STEROL-C5(6)-DESATURASE.

OS Nicotiana tabacum (Common tobacco).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eukaryotes; Spermatophyta; Magnoliophyta; eudicotyledons;

OC core eudicots; Asteridae; euasterids I; Solanales; Solanaceae;

OC Nicotiana.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-CV. XANTHI SH6; TISSUE-CALLI DERIVED FROM LEAF PROTOPLASTS;

RA HUSSELSTEIN T., SCHALLER H., GACHOTTE D., BENVENISTE P.;

RT "sterol-C5(6)-desaturase: molecular characterization and functional expression of wild-type and mutant alleles.";

RL Submitted (JUL1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF081794; AAD04034.1; -.

DR MENDEL: 36287; Nicta: 1710; 36287.

SQ SEQUENCE 271 AA; 31842 MW; A447E09C CRC32;

Query Match 65.5%; Score 38; DB 10; Length 271;

Best Local Similarity 85.7%; Pred. No. 19;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNGSY 8

| | | | |

DB 243 RHNGHY 249

RESULT 5

Q9XEI2 PRELIMINARY; PRT; 271 AA.

AC Q9XEI2;

DT 01-NOV-1999 (TREMREL. 12, Created)

DT 01-NOV-1999 (TREMREL. 12, Last sequence update)

DT 01-NOV-1999 (TREMREL. 12, Last annotation update)

DE STEROL-C5(6)-DESATURASE HOMOLOG.

OS Nicotiana tabacum (Common tobacco).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eukaryotes; Spermatophyta; Magnoliophyta; eudicotyledons;

OC core eudicots; Asteridae; euasterids I; Solanales; Solanaceae;

OC Nicotiana.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-CV. XANTHI SH6; TISSUE-LEAF;

RX MEDLINE: 99273992.

RA HUSSELSTEIN T., SCHALLER H., GACHOTTE D., BENVENISTE P.;

RT "delta7-sterol-C5-desaturase: molecular characterization and functional expression of wild-type and mutant alleles.";

RL Plant Mol. Biol. 39:891-906(1999).

DR EMBL: AF099969; AAD20458.1; -.

SQ SEQUENCE 271 AA; 32036 MW; 1F78D116 CRC32;

RT "Secondary structure model for the last two domains of single-stranded RNA phase Q beta.";

RL J. Mol. Biol. 247:903-917(1995).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE: 96190948.

RA BEEKWILDER J., NIEUWENHUIZEN R., POOT R., VAN DUIN J.;

RT "Secondary structure model for the first three domains of Q beta RNA.

RT Control of A-protein synthesis.";

RL J. Mol. Biol. 256:8-19(1996).

RN [3]

RP SEQUENCE FROM N.A.

RA BEEKWILDER M.J., NIEUWENHUIZEN R., VAN DUIN J.;

RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF059243; AAC14705.1; -.

SQ SEQUENCE 576 AA; 65012 MW; 696B4C49 CRC32;

Query Match 67.2%; Score 39; DB 9; Length 576;

Best Local Similarity 66.7%; Pred. No. 29;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSYAY 10

| | : | | | |

DB 503 RHEFGSYLY 511

RESULT 3

O18245 PRELIMINARY; PRT; 236 AA.

AC O18245;

DT 01-JAN-1998 (TREMREL. 05, Created)

DT 01-JAN-1998 (TREMREL. 05, Last sequence update)

DT 01-JAN-1999 (TREMREL. 09, Last annotation update)

DE Y57G11C.21 PROTEIN.

GN Y57G11C.21.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;

OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

RN [1]

RP SEQUENCE FROM N.A.

RA MCMURRAY A.;

RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE: 94150718.

RA WILSON R., AINSKOUGH R., ANDERSON K., BAYNES C., BERKS M.,

RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

RA JONES M., KERSHAW J., KRISTEN J., LAISTER N., LATREILLE P.,

RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

RA SMAILDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;

Query Match 65.5%; Score 38; DB 10; Length 271;
 Best Local Similarity 85.7%; Pred. No. 19;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSY 8
 | | | | |
 Db 243 RHNYGHY 249

RESULT 6
 P93843 PRELIMINARY; PRT; 428 AA.
 AC P93843;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE DNA BINDING PROTEIN ACBF.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Asteridae; euasterids I; Solanales; Solanaceae;
 OC Nicotiana.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-STEM;
 RX MEDLINE; 98009965.
 RA SEGUN A., LAIBLE G., LEYVA A., DIXON R.A., LAMB C.J.;
 RT "Characterization of a gene encoding a DNA-binding protein that
 RT interacts in vitro with vascular specific cis elements of the
 RT phenylalanine ammonia-lyase promoter.";
 RL Plant Mol. Biol. 35:281-291(1997).
 DR EMBL; U90212; AAC49850.1; -.
 DR HSSP; P09651; 1UP1.
 DR MENDEL; 15238; Nicta;2406;15238.
 DR PFAM; PF00076; rrm; 3.
 SQ SEQUENCE 428 AA; 46981 MW; BF3F671B CRC32;

Query Match 65.5%; Score 38; DB 10; Length 428;
 Best Local Similarity 66.7%; Pred. No. 31;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RHNYGSY 10
 | | | | |
 Db 387 RQNYGGY 395

RESULT 7
 O48955 PRELIMINARY; PRT; 482 AA.
 AC O48955;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE PUTATIVE RNA BINDING PROTEIN (FRAGMENT).
 GN QRRBP-1.
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Asteridae; euasterids I; Solanales; Solanaceae;
 OC Nicotiana.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA DESLANDES L., MANEWSKI A., LESCURE B., MARCO Y., TREMOUSAYGUE D.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AR029351; AAB92518.1; -.
 DR HSSP; P09651; 1UP1.
 DR MENDEL; 28002; Nicta;2406;28002.
 DR PFAM; PF00076; rrm; 3.
 FT NON_TER 1
 SQ SEQUENCE 482 AA; 53582 MW; EE0728DB CRC32;

Query Match 65.5%; Score 38; DB 10; Length 482;
 Best Local Similarity 66.7%; Pred. No. 36;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 RHNYGSY 10
 | | | | |
 Db 442 RQNYGGY 450

RESULT 8
 O69838 PRELIMINARY; PRT; 289 AA.
 AC O69838;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE PUTATIVE LIPOPROTEIN.
 GN SC1B5.10C.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomycetes.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA HARRIS D., TAYLOR K.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RX MEDLINE; 97000351.
 RA REDENBACH M., KIESER H.M., DENAPATTE D., EICHNER A., CULLUM J.,
 RA KINASHI H., HOPWOOD D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 DR EMBL; AL023517; CAA18984.1; -.
 DR PFAM; PF01522; Polysac_deacet; 1.
 KW Lipoprotein.
 SQ SEQUENCE 289 AA; 30748 MW; DB9D6633 CRC32;

Query Match 63.8%; Score 37; DB 2; Length 289;
 Best Local Similarity 60.0%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ARHNYGSY 10
 | | | | |
 Db 144 ANHSYSHY 153

RESULT 9
 Q91184 PRELIMINARY; PRT; 420 AA.
 AC Q91184;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
 DE L-SF PRECURSOR.
 GN L-SF.
 OS Oryzias latipes (Medaka fish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
 OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Atherinomorpha;
 OC Cyprinodontiformes; Adrianichthyoidae; Adrianichthyidae; Oryziinae;
 OC Oryzias.
 RN [1]
 RP SEQUENCE FROM N.A.

```

RC TISSUE=LIVER;
RX MEDLINE; 95154588.
RA MURATA K., SASAKI T., YASUMASU S., IUCHI I., ENAMI J., YASUMASU I.,
RA YAMAGAMI K.;
RT "Cloning of cDNAs for the precursor protein of a low-molecular-weight
RT subunit of the inner layer of the egg envelope (chorion) of the fish
RT Oryzias latipes.";
RL Dev. Biol. 167:9-17(1995).
DR EMBL; D38630; BAA07610.1; -.
DR PFAM; PF00100; zona_pellucida; 1.
KW Signal; Chorion.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 420 L-SF.
SQ SEQUENCE 420 AA; 46168 MW; CFAED79F CRC32;

Query Match 63.8%; Score 37; DB 13; Length 420;
Best Local Similarity 60.0%; Pred. No. 46;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
Db 21 AQHNYGKPSY 30

RESULT 10
Q50371 PRELIMINARY; PRT; 1144 AA.
AC Q50371;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE P1-LIKE ADHESIN.
OS Mycoplasma pirum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
RN [1]
RC STRAIN=BER;
RX MEDLINE; 94131957.
RA THAM T.N., FERRIS S., BAHRAOUI E., CANARELLI S., MONTAGNIER L.,
RA BLANCHARD A.;
RT "Molecular characterization of the P1-like adhesin gene from
RT Mycoplasma pirum.";
RL J. Bacteriol. 176:781-788(1994).
DR EMBL; I19685; AAC36866.1; -.
SQ SEQUENCE 1144 AA; 126732 MW; 081F55F1 CRC32;

Query Match 63.8%; Score 37; DB 2; Length 1144;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10
Db 885 KONYGSIFY 893

RESULT 11
Q92130 PRELIMINARY; PRT; 301 AA.
AC Q92130;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE JKTEP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE; 98207031.
RA TSUCHIYA N., KAMEI D., TAKANO A., MATSUI T., YAMADA M.;

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RT "Cloning and characterization of a cDNA encoding a novel heterogeneous
RT nuclear ribonucleoprotein-like protein and its expression in myeloid
RT leukemia cells.";
RL J. Biochem. 123:499-507(1998).
DR EMBL; AB017020; BAA75479.1; -.
DR HSP; P09651; I0P1.
SQ SEQUENCE 301 AA; 33559 MW; 9922B1FB CRC32;

Query Match 62.1%; Score 36; DB 11; Length 301;
Best Local Similarity 62.5%; Pred. No. 49;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSYAY 10
Db 263 YNYGNYGY 270

RESULT 12
O76436 PRELIMINARY; PRT; 349 AA.
AC O76436;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE C24B9.8 PROTEIN.
GN C24B9.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=BRISTOL N2;
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA MURRAY J., WOHLDMANN P., LANGSTON Y., O'NEAL D.;
RT "The sequence of C. elegans cosmid C24B9.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RC SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA WATERSTON R.;
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF068709; AAC19248.1; -.
DR PFAM; PF01461; 7tm_4; 1.
SQ SEQUENCE 349 AA; 40196 MW; 3951B4CB CRC32;

Query Match 62.1%; Score 36; DB 5; Length 349;
Best Local Similarity 60.0%; Pred. No. 57;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
Db 38 AQKNFGSYKY 47

RESULT 13

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014979
ID O14979 PRELIMINARY; PRT; 420 AA.
AC O14979;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE JKTBP2 (HNRNP JKTBP) (A+U-RICH ELEMENT RNA BINDING FACTOR).
GN JKTBP OR HNRNP JKTBP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RA KAMEI D., TSUCHIYA N., YAMAZAKI M., MEGURO H., YAMADA M.;
RT "Two forms of expression and genomic structure of the human
RT heterogeneous nuclear ribonucleoprotein D-like JKTBP gene (HNRPD1).";
RL Gene 0:0-0(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98207031.
RA TSUCHIYA N., KAMEI D., TAKANO A., MATSUI T., YAMADA M.;
RT "Cloning and characterization of a cDNA encoding a novel heterogeneous
RT nuclear ribonucleoprotein-like protein and its expression in myeloid
RT leukemia cells.";
RL J. Biochem. 123:499-507(1998).
RN [3]
RP SEQUENCE OF 120-420 FROM N.A.
RA TSUCHIYA N., KAMEI D., TAKANO A., MATSUI T., YAMADA M.;
RL J. Biochem. 0:0-0(1998).
RN [4]
RP SEQUENCE OF 150-420 FROM N.A.
RA DOI A., TAKAOKA Y., YANAGISAWA K., SHIOSAKA T., FUJITA S.;
RL Blochim. Biophys. Acta 0:0-0(1997).
DR EMBL; AB017019; BAA75241.1; -.
DR EMBL; AB017018; BAA75239.1; -.
DR EMBL; D89092; BAA24361.1; -.
DR EMBL; D89678; BAA22860.1; -.
DR EMBL; AB017018; BAA75240.1; -.
DR HSSP; P09651; IUP1.
DR PFAM; PF00076; Irm. 2.
SQ SEQUENCE 420 AA; 46437 MW; 39F9419E CRC32;

Query Match 62.1%; Score 36; DB 4; Length 420;
Best Local Similarity 62.5%; Pred. No. 69;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSYAY 10
Db 382 YNYGNGY 389
:|:|:|

RESULT 14
O62017 PRELIMINARY; PRT; 626 AA.
AC O62017;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE B0391.4 PROTEIN.
GN B0391.4
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidae; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RA GARDNER A.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

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RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WAYSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
DR EMBL; 281454; CAB03804.1; -.
DR PFAM; PF01461; 7tm_4; 2.
SQ SEQUENCE 626 AA; 72339 MW; E1340CF8 CRC32;

Query Match 62.1%; Score 36; DB 5; Length 626;
Best Local Similarity 60.0%; Pred. No. 11e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
Db 38 AQRNFGSYKI 47
|:|:|:|

RESULT 15
Q83611 PRELIMINARY; PRT; 1049 AA.
ID Q83611;
AC Q83611;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE A-TYPE INCLUSION PROTEIN.
GN ATI.
OS Ectromelia virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MP-1;
RA OSTERRIEDER N.;
RL Submitted (NOV-1992) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-MP-1;
RA PEDERSEN K., HALLBECK L., ARLINGER J., JAHROMI N., ERLANDSSON A.C.;
RL FEMS Microbiol. Meth. 0:0-0(0).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-MP-1;
RX MEDLINE; 94353638.
RA OSTERRIEDE N., MEYER M., PFEFFER M.;
RT "Characterization of the gene encoding the A-type inclusion body
RT protein of mousepox virus.";
RL Virus Genes 8:125-135(1994).
DR EMBL; X69325; CAA49168.1; -.
SQ SEQUENCE 1049 AA; 122466 MW; 0FDD17C6 CRC32;

Query Match 62.1%; Score 36; DB 12; Length 1049;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSYAY 10
Db 771 RHNGSHGY 779
|:|:|:|

Search completed: May 27, 2000, 19:38:40
Job time: 2373 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:21:34 ; Search time 148.45 Seconds
(without alignments)
1.596 Million cell updates/sec

Title: US-09-016-061-62
Perfect score: 58
Sequence: 1 ARHNYGSYAY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	10	W76021	LM609 grafted anti
2	54	93.1	10	W76010	LM609 grafted anti
3	54	93.1	117	W76001	Vitaxin antibody h
4	54	93.1	117	W76003	LM609 antibody hea
5	49	84.5	10	W76020	LM609 grafted anti
6	48	82.8	10	W76022	LM609 grafted anti
7	48	82.8	10	W76023	LM609 grafted anti
8	47	81.0	10	W76024	LM609 grafted anti
9	47	81.0	10	W76025	LM609 grafted anti
10	47	81.0	10	W76026	LM609 grafted anti
11	47	81.0	10	W76027	LM609 grafted anti
12	47	81.0	10	W76028	LM609 grafted anti
13	47	81.0	10	W76029	LM609 grafted anti
14	47	81.0	10	W76030	LM609 grafted anti
15	46	79.3	110	W84099	Vitronectin alpha-
16	46	79.3	117	W84093	Murine vitronectin
17	46	79.3	117	W84097	Humanised anti- α p
18	43	74.1	10	W76039	LM609 grafted anti
19	43	74.1	10	W76040	LM609 grafted anti
20	42	72.4	10	W76037	LM609 grafted anti
21	40	69.0	117	W79157	Human IGE receptor
22	40	69.0	117	R79155	Human IGE receptor
23	40	69.0	117	W27357	Heavy chain variab
24	40	69.0	117	W27526	Heavy chain variab
25	40	69.0	117	W27354	Heavy chain variab
26	40	69.0	119	W01578	Lead binding MAB 8
27	40	69.0	239	W73874	Human antiFc epsil
28	40	69.0	242	W73876	Human antiFc epsil
29	39	67.2	172	W46819	Endo-beta-1,4-gluc
30	38	65.5	10	W76038	LM609 grafted anti
31	37	63.8	36	W03964	VDJ joint protein,
32	37	63.8	36	W41127	WH251 DXp'1 J6 mu
33	37	63.8	1144	R76059	Mycoplasma pirum a
34	35	60.3	246	W98752	H. pylori GHPO 105

35	35	60.3	328	1	W98781	H. pylori GHPO 119
36	35	60.3	806	1	R65495	Marek's disease vi
37	34	58.6	120	1	W73192	Human vesicle traf
38	34	58.6	279	1	W88425	Chlamydia pneumoni
39	34	58.6	1134	1	W46859	Bacillus thuringie
40	34	58.6	1150	1	W46858	Bacillus thuringie
41	34	58.6	1150	1	W62541	Bacillus thuringie
42	34	58.6	1156	1	W46856	Bacillus thuringie
43	34	58.6	1156	1	W46857	Bacillus thuringie
44	34	58.6	1157	1	R48678	Insecticidal proto
45	34	58.6	1157	1	W84582	Amino acid sequenc

ALIGNMENTS

RESULT 1

W76021
ID W76021 standard; Protein; 10 AA.
AC W76021;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #3.
KW Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;
KW LM609; inhibitor; Integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (XSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49858.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to Integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 100.0%; Score 58; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00049;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSYAY 10
| | | | | | | | | |
Db 1 ARHNYGSYAY 10

RESULT 2

W76010
ID W76010 standard; Protein; 10 AA.
AC W76010;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #1.
KW Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB: V49847.
 DR Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Disclosure; Page 40; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 CC Sequence 10 AA;

Query Match 93.1%; Score 54; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0022;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
 |||||:|
 DB 1 ARHNYGSFAY 10

RESULT 3
 W76001
 ID W76001 standard; Protein; 117 AA.

AC W76001:
 DT 02-NOV-1998 (first entry)
 DE Vitaxin antibody heavy chain variable region protein fragment.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB: V49820.
 DR Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 1; Fig 1a; 129pp; English.
 CC This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated

CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 CC Sequence 117 AA;

Query Match 93.1%; Score 54; DB 1; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.028;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
 |||||:|
 DB 97 ARHNYGSFAY 106

RESULT 4
 W76003
 ID W76003 standard; Protein; 117 AA.

AC W76003:
 DT 02-NOV-1998 (first entry)
 DE LM609 antibody heavy chain variable region protein fragment.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB: V49822.
 DR Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 43; Fig 2a; 129pp; English.
 CC This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 CC Sequence 117 AA;

Query Match 93.1%; Score 54; DB 1; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.028;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
 |||||:|
 DB 97 ARHNYGSFAY 106

RESULT 5
 W76020
 ID W76020 standard; Protein; 10 AA.

AC W76020:
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #2.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49859.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 CC Sequence 10 AA;
 SQ

Query Match 84.5%; Score 49; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.015;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
 |||||:|:|
 Db 1 ARHNGSFAY 10

RESULT 6
 W76022 ID W76022 standard; Protein; 10 AA.

AC W76022;
 DE 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #4.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49859.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 82.8%; Score 48; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.021;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
 |||||:|
 Db 1 ARHNGSFY 10

RESULT 7
 W76023 ID W76023 standard; Protein; 10 AA.

AC W76023;
 DE 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #5.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49860.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 82.8%; Score 48; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.021;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
 |||||:|
 Db 1 ARHNGSFY 10

RESULT 8
 W76024 ID W76024 standard; Protein; 10 AA.

AC W76024;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #6.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; 001826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49861.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;
 Query Match 81.0%; Score 47; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 0.031;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSA 9
 | | | | | | | |
 Db 1 ARHNYGSFA 9
 | | | | | | | |
 RESULT 9
 W76025 standard; Protein; 10 AA.
 AC W76025;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #7.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; 001826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49862.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;
 Query Match 81.0%; Score 47; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 0.031;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSA 9
 | | | | | | | |
 Db 1 ARHNYGSFA 9
 | | | | | | | |
 RESULT 10
 W76026 standard; Protein; 10 AA.
 AC W76026;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #8.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; 001826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49863.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;
 Query Match 81.0%; Score 47; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 0.031;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSA 9
 | | | | | | | |
 Db 1 ARHNYGSFA 9
 | | | | | | | |

```

RESULT 11
W76027
ID W76027 standard; Protein; 10 AA.
AC W76027;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #9.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49864.
PT Humanised antibody, vitaxin, that binds selectively to alphavbeta3
PT integrin - and related nucleic acid, used to treat, prevent or diagnose
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62: Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 81.0%; Score 47; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.031;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYA 9
Db 1 ARHNYGSFA 9
|||||:|

RESULT 12
W76029
ID W76029 standard; Protein; 10 AA.
AC W76029;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #11.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49866.
PT Humanised antibody, vitaxin, that binds selectively to alphavbeta3
PT integrin - and related nucleic acid, used to treat, prevent or diagnose
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62: Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 81.0%; Score 47; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.031;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYA 9
Db 1 ARHNYGSFA 9
|||||:|

RESULT 12
W76028
ID W76028 standard; Protein; 10 AA.
AC W76028;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #10.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49865.
PT Humanised antibody, vitaxin, that binds selectively to alphavbeta3

```

QY 1 ARHNYGSYA 9
| | | | | | | |
DB 1 ARHNYGSFA 9

RESULT 14

W76030
ID W76030 standard; Protein; 10 AA.

AC W76030;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #12.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49867.
DR Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CS W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 81.0%; Score 47; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.031;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSYA 9
| | | | | | | |
DB 1 ARHNYGSFA 9

RESULT 15

W84099
ID W84099 standard; Protein; 110 AA.

AC W84099;
DT 15-MAR-1999 (first entry)
DE Vitronectin alpha-v beta-3 Mab VH.
KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;
KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
KW angiogenesis; diabetic retinopathy; inflammation;
KW macular degeneration; osteoporosis; Paget's disease;
KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.
OS Mus sp.
PN WO9840488-A1.
PD 17-SEP-1998.
PF 12-MAR-1998; U04987.
PR 12-MAR-1997; US-039609.
PA (SMIK) SMITHKLINE BEECHAM CORP.

PI Johanson KO, Jonak ZL, Taylor AH;
DR WPI; 99-034590/03.
DR N-PSDB; V71801.

PT New anti alpha_v beta_3 vitronectin receptor antibodies - used for
PT immunotherapeutic treatment of e.g. diabetic retinopathy.
PT inflammatory disorders, atherosclerosis, restenosis, cancers or
PT osteoporosis

PS Example 13; Page 63; 97pp; English.

CC This is the amino acid sequence of the region of the murine
CC monoclonal antibody (MAB) D12 heavy chain variable region (VH)
CC that is altered in humanised D12 VH (see also W84097). A
CC synthetic gene (see V81901) encoding the protein was prepared
CC from synthetic oligonucleotides and used to prepare an expression
CC vector for humanised D12 VH. D12 is an anti-human alpha-v beta-3
CC vitronectin receptor MAB. Humanised D12 MABs can be used for
CC passive immunotherapy of disorders mediated by the alpha-v beta-3
CC vitronectin receptor, e.g. restenosis and angiogenic associated
CC diseases.
SQ Sequence 110 AA;

Query Match 79.3%; Score 46; DB 1; Length 110;
Best Local Similarity 80.0%; Pred. No. 0.54;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSYAY 10
| | . | | | | | | | |
DB 95 ARQNYGSFAY 104

Search completed: May 27, 2000, 19:21:35
Job time: 1589 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2000, 19:26:41 ; Search time 163.56 Seconds
(without alignments)
3.585 Million cell updates/sec

Title: US-09-016-061-64
Perfect score: 59
Sequence: 1 ARHNYGSFDY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_63:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	39.5	66.9	137	2 H32513	Ig heavy chain pre
2	39	66.1	316	2 T15395	hypothetical prote
3	39	66.1	544	2 S75388	probable phenylala
4	38	64.4	82	2 I51106	Major Histocompati
5	38	64.4	89	2 S38688	MHC class II histo
6	38	64.4	89	2 S38683	MHC class II histo
7	38	64.4	89	2 S38684	MHC class II histo
8	38	64.4	117	2 S17386	Ig heavy chain v r
9	38	64.4	225	2 I47095	MHC class II OVAR-
10	38	64.4	605	2 E71314	probable GTP-bindi
11	37.5	63.6	369	2 T04947	hypothetical prote
12	37	62.7	377	2 D64888	outer membrane por
13	36.5	61.9	139	2 S01158	Ig heavy chain pre
14	36	61.0	86	2 D33989	Ig heavy chain v-4
15	36	61.0	369	2 S70847	outer membrane por
16	36	61.0	394	2 S34263	outer membrane por
17	36	61.0	446	2 T19625	hypothetical prote
18	36	61.0	602	2 B71561	probable GTPase -
19	36	61.0	602	2 B72088	GTPase - Chlamydia
20	36	61.0	783	1 S02755	outer membrane ush
21	36	61.0	922	2 T03854	hypothetical prote
22	36	61.0	1116	2 S43778	gene X104 protein
23	35	59.3	32	2 PH1735	Ig heavy chain v r
24	35	59.3	108	2 S26316	Ig heavy chain v r
25	35	59.3	110	2 S26317	Ig heavy chain v r
26	35	59.3	371	2 T24853	hypothetical prote
27	35	59.3	420	2 T51088	L-SF precursor - J
28	35	59.3	458	2 T34574	hypothetical prote
29	35	59.3	536	2 T24218	hypothetical prote
30	35	59.3	587	2 E69171	conserved hypothet

ALIGNMENTS

RESULT 1

H32513
Ig heavy chain precursor V region (BXW16) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 23-Jul-1999
C:Accession: H32513
R:Kotler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A
J. Clin. Invest. 82, 852-860, 1988
A:Title: Immunoglobulin kappa light chain variable region gene complex organization a
A:Reference number: A94689; MUID:88331394
A:Accession: H32513
A:Molecule type: DNA
A:Residues: 1-137 <KOF>
A:Cross-references: GB:M20831; NID:gl96949; PTDN:AAA38848.1; PTD:gl96950
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 66.9%; Score 39.5; DB 2; Length 137;
Best Local Similarity 81.8%; Pred. No. 3.4;
Matches 9; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 ARHNYG-SFDY 10
Db 116 ARKNGSSFDY 126

RESULT 2

T15395
hypothetical protein C03F11.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15395
R:Bentley, D.
submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid C03F11.
A:Reference number: Z18342
A:Accession: T15395
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-316 <BEN>
A:Cross-references: EMBL:U039744; NID:gl049465; PTD:gl049467; PTDN:AAA80440.1; CESP:CO
C:Genetics:
A:Gene: CESP:C03F11.2
A:Introns: 90/3; 133/2; 171/1; 227/1; 262/1; 309/2

Query Match 66.1%; Score 39; DB 2; Length 316;
Best Local Similarity 60.0%; Pred. No. 9.6;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFDY 10
||| :||::|

Db 69 ARHFFGSY 78

RESULT 3

S75388

probable phenylalanine--tRNA ligase (EC 6.1.1.20) beta chain - Sulfolobus solfataricus

N:Alternate names: phenylalanyl-tRNA synthetase beta chain; protein c04021

C:Species: Sulfolobus solfataricus

C>Date: 09-Oct-1997 #sequence_revision 24-Oct-1997 #text_change 16-Jul-1999

C:Accession: S75388

R:Sensen, C.W.; Klenk, H.P.; Singh, R.K.; Allard, G.; Chan, C.C.Y.; Liu, Q.Y.; Penny, S.

Mol. Microbiol. 22, 175-191, 1996

A:Title: Organizational characteristics and information content of an archaeal genome: I

A:Reference number: S73076; MUID:97055432

A:Accession: S75388

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-544 <SEN>

A:Cross-references: EMBL:V08257; NID:g1707772; PIDN:CAA69550.1; PID:e283832; PID:g170779

A:Experimental source: strain P2

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1996

C:Superfamily: yeast cytosolic phenylalanine--tRNA ligase alpha chain

C:Keywords: aminoacyl-tRNA synthetase; ATP; ligase; protein biosynthesis

Query Match 66.1%; Score 39; DB 2; Length 544;

Best Local Similarity 85.7%; Pred. No. 17;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10

Db 350 NYGSYDY 356

RESULT 4

I51106

Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)

C:Species: Phasianus colchicus (ring-necked pheasant)

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999

C:Accession: I51106

R:Witzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.

Immunogenetics 39, 395-403, 1994

A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-necked

A:Reference number: I51103; MUID:94245280

A:Accession: I51106

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-82 <WIT>

A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.4%; Score 38; DB 2; Length 82;

Best Local Similarity 75.0%; Pred. No. 3.8;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9

Db 75 RHNYGVFE 82

RESULT 5

S38688

MHC class II histocompatibility antigen HLA-DR-08 beta chain - Galago senegalensis (frag

C:Species: Galago senegalensis

C>Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997

C:Accession: S38688

R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.

submitted to the EMBL Data Library, November 1993

A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced f

A:Reference number: S38676

A:Accession: S38688

A:Molecule type: DNA

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:Z27154

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.4%; Score 38; DB 2; Length 89;

Best Local Similarity 75.0%; Pred. No. 4.1;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9

Db 75 RHNYGVFE 82

RESULT 6

S38683

MHC class II histocompatibility antigen HLA-DR-03 beta chain - Galago senegalensis (f

C:Species: Galago senegalensis

C>Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997

C:Accession: S38683

R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.

submitted to the EMBL Data Library, November 1993

A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduce

A:Reference number: S38676

A:Accession: S38683

A:Molecule type: DNA

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:Z27153

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.4%; Score 38; DB 2; Length 89;

Best Local Similarity 75.0%; Pred. No. 4.1;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9

Db 75 RHNYGVFE 82

RESULT 7

S38684

MHC class II histocompatibility antigen HLA-DR-04 beta chain - Galago senegalensis (f

C:Species: Galago senegalensis

C>Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997

C:Accession: S38684

R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.

submitted to the EMBL Data Library, November 1993

A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduce

A:Reference number: S38676

A:Accession: S38684

A:Molecule type: DNA

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:Z27154

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.4%; Score 38; DB 2; Length 89;

Best Local Similarity 75.0%; Pred. No. 4.1;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9

Db 75 RHNYGVFE 82

RESULT 8

S17586

Ig heavy chain V region (E8) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 23-Jul-1999

C:Accession: S17586

R:Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:Z27158

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.4%; Score 38; DB 2; Length 89;

Best Local Similarity 75.0%; Pred. No. 4.1;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9

Db 75 RHNYGVFE 82

RESULT 6

S38683

MHC class II histocompatibility antigen HLA-DR-03 beta chain - Galago senegalensis (f

C:Species: Galago senegalensis

C>Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997

C:Accession: S38683

R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.

submitted to the EMBL Data Library, November 1993

A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduce

A:Reference number: S38676

A:Accession: S38683

A:Molecule type: DNA

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:Z27153

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.4%; Score 38; DB 2; Length 89;

Best Local Similarity 75.0%; Pred. No. 4.1;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9

Db 75 RHNYGVFE 82

RESULT 7

S38684

MHC class II histocompatibility antigen HLA-DR-04 beta chain - Galago senegalensis (f

C:Species: Galago senegalensis

C>Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997

C:Accession: S38684

R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.

submitted to the EMBL Data Library, November 1993

A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduce

A:Reference number: S38676

A:Accession: S38684

A:Molecule type: DNA

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:Z27154

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.4%; Score 38; DB 2; Length 89;

Best Local Similarity 75.0%; Pred. No. 4.1;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9

Db 75 RHNYGVFE 82

RESULT 8

S17586

Ig heavy chain V region (E8) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 23-Jul-1999

C:Accession: S17586

R:Mylvaganam, S.E.; Paterson, Y.; Kaiser, K.; Bowdish, K.; Getzoff, E.D.

J. Mol. Biol. 221, 455-462, 1991
A:Title: Biochemical implications from the variable gene sequences of an anti-cytochrome forms.

A:Reference number: S17586; MUID:92015240

A:Accession: S17586

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-117 <MYL>

A:Cross-references: EMBL:X60683; NID:g51820; PIDN:CAA43095.1; PID:g51821

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 64.4%; Score 38; DB 2; Length 117;
Best Local Similarity 60.0%; Pred. No. 5.4;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10

Db 97 AGYDGNFDY 106

RESULT 9

I47095

MHC class II OVAR-DR-beta-3 - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 23-Jul-1999

C:Accession: I47095

R:FabB, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.

AnIm. Genet. 24, 249-255, 1993

A:Title: Isolation, characterization and evolution of ovine major histocompatibility com

A:Reference number: I47075; MUID:94057592

A:Accession: I47095

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-225 <FAB>

A:Cross-references: GB:L04790; NID:g458880; PIDN:AAA16562.1; PID:g458881

C:Genetics:

A:Gene: OVAR-DRB3

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.4%; Score 38; DB 2; Length 225;
Best Local Similarity 75.0%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9

Db 68 RHNYGVFE 75

RESULT 10

E71314

probable GTP-binding membrane protein (lepA) - syphilis spirochete

C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 26-Aug-1999

C:Accession: E71314

R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin

rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD

they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A:Reference number: A71250; MUID:98332770

A:Accession: E71314

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-605 <COL>

A:Cross-references: GB:AE001227; GB:AE000520; NID:g3322797; PIDN:AAC65498.1; PID:g332280

A:Experimental source: strain Nichols

C:Genetics:

A:Gene: TP0510

C:Superfamily: GTP-binding membrane protein lepA; translation elongation factor Tu homol

C:Keywords: GTP binding; P-loop

F:11-140/Domain: translation elongation factor Tu homology <ETU>
F:17-24/Region: nucleotide-binding motif A (P-loop)

F:137-140/Region: GTP-binding NKXD motif

F:168-170/Region: GTP-binding SAK/L motif

F:23,24,59,137,138,140,168/Binding site: Mg-GTP (Lys, Ser, Thr, Asn, Lys, Asp, Ser) #

Query Match 64.4%; Score 38; DB 2; Length 605;
Best Local Similarity 75.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFDY 10

Db 470 HGYASFDY 477

RESULT 11

T04947

hypothetical protein F7J7.100 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 11-Jun-1999

C:Accession: T04947

R:Bevan, M.; Murphy, G.; Ridley, P.; Hudson, S.; Bancroft, I.; Mewes, H.W.; Mayer, K.

submitted to the Protein Sequence Database, July 1998

A:Reference number: Z15391

A:Accession: T04947

A:Molecule type: DNA

A:Residues: 1-369 <BEV>

A:Cross-references: EMBL:AL021960

A:Experimental source: cultivar Columbia; BAC clone F7J7

C:Genetics:

A:Map position: 4

A:Introns: 14/1; 41/2; 98/3; 153/2; 203/3; 244/3; 276/3

A:Note: F7J7.100

Query Match 63.6%; Score 37.5; DB 2; Length 369;
Best Local Similarity 61.5%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 5; Gaps 1;

QY 3 HNYGS-----FDY 10

Db 269 HNYGSVKLQVFDY 281

RESULT 12

D64888

outer membrane porin bl377 precursor - Escherichia coli

C:Species: Escherichia coli

C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 20-Aug-1999

C:Accession: D64888

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;

.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617

A:Accession: D64888

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-377 <BLAT>

A:Cross-references: GB:AE000234; GB:U00096; NID:g1787633; PIDN:AAC74459.1; PID:g17876

A:Experimental source: strain K-12, substrain MG1655

C:Superfamily: outer membrane protein porin

C:Keywords: membrane protein; porin; trimer

F:1-21/Domain: signal sequence #status predicted <SIG>

F:22-377/Product: probable outer membrane porin bl377 #status predicted <OPP>

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

Db 106 DYGSFDY 112
:|||||

RESULT 13

S01158

Ig heavy chain precursor (clone c40) - African clawed frog (fragment)

C:Species: Xenopus laevis (African clawed frog)

C>Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 16-Feb-1997

C:Accession: S01158

R:Schwager, J.; Grossberger, D.; du Pasquier, L.

EMBO J. 7, 2409-2415, 1988

A:Title: Organization and rearrangement of immunoglobulin M genes in the amphibian Xenopus

A:Reference number: S01158; MUID:89052653

A:Accession: S01158

A:Molecule type: mRNA

A:Residues: 1-139 <SCH>

A:Cross-references: EMBL:X14919

A:Note: the sequence of residues 1-18 is not shown

C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:1-18/Domain: signal sequence (fragment) #status predicted <SIG>

F:19-139/Product: Ig heavy chain (fragment) #status predicted <MAT>

F:19-134/Domain: V-D-J region #status predicted <VRE>

F:135-139/Domain: C region (mu chain) (fragment) #status predicted <CRE>

Query Match 61.0%; Score 36.5; DB 2; Length 139;
Best Local Similarity 72.7%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 1 ARHN-YGSFDY 10

||| ||||

Db 113 ARHPYGGFDY 123

RESULT 14

D33989

Ig heavy chain V-4-D-J region - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C>Date: 23-Mar-1990 #sequence_revision 23-Mar-1990 #text_change 09-May-1997

C:Accession: D33989

R:Hsu, E.; Schwager, J.; Alt, F.W.

Proc. Natl. Acad. Sci. U.S.A. 86, 8010-8014, 1989

A:Title: Evolution of immunoglobulin genes: V-H families in the amphibian Xenopus.

A:Reference number: A33989; MUID:90046727

A:Accession: D33989

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 1-86 <HSU>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 61.0%; Score 36; DB 2; Length 86;
Best Local Similarity 60.0%; Pred. No. 9.2;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10

||: ||||

Db 66 ARYGVGAFDY 75

RESULT 15

S70847

outer membrane porin opnp precursor - Xenorhabdus nematophilus

N:Alternate names: ompF-like protein

C:Species: Xenorhabdus nematophilus

C>Date: 11-Mar-1998 #sequence_revision 11-Mar-1998 #text_change 20-Aug-1999

C:Accession: S70847

R:Forst, S.; Waukau, J.; Leisman, G.; Exner, M.; Hancock, R.

Mol. Microbiol. 18, 779-789, 1995

A:Title: Functional and regulatory analysis of the OmpF-like porin, OpnP, of the symbiont

A:Reference number: S70779; MUID:96414477

A:Reference

A:Accession: S70847
A:Molecule type: DNA
A:Residues: 1-369 <FOR>
A:Cross-references: EMBL:L40919; NID:g1129070; PIDN:AAB41114.1; PID:g1129071
A:Experimental source: strain AN6/1
C:Genetics:
A:Gene: opnp
C:Superfamily: outer membrane protein phoE
C:Keywords: membrane protein; porin; trimer
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-369/Product: outer membrane porin opnp #status predicted <MAT>

Query Match 61.0%; Score 36; DB 2; Length 369;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NYGSFDY 10

|||||

Db 107 NYGSLDY 113

Search completed: May 27, 2000, 19:26:42
Job time: 1765 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 20:07:15 ; Search time 69.28 Seconds
(without alignments)
4.396 Million cell updates/sec

Title: US-09-016-061-64
Perfect score: 59
Sequence: 1 ARHNYGSFDY 10

Scoring table: BLOSUM62
Gap 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	42	71.2	349	1 PHOE_KLEOX	Q01606 klebsiella
2	42	71.2	351	1 PHOE_KLEPN	P30704 klebsiella
3	39	66.1	316	1 YX12_CAEEL	Q11123 caenorhabdi
4	38	64.4	605	1 LEPA_TREPA	O83523 treponema p
5	37	62.7	282	1 OMPD_SALTY	P37592 salmonella
6	37	62.7	374	1 OMPD_SERMA	Q33980 serratia ma
7	37	62.7	376	1 OMPN_SERMA	Q54471 serratia ma
8	37	62.7	377	1 OMPN_ECOLI	P77747 escherichia
9	37	62.7	383	1 OMS2_SALTI	Q56111 salmonella
10	37	62.7	789	1 LP1B_DROME	P11996 drosophila
11	36	61.0	369	1 OMPF_XENNE	Q56828 xenorhabdus
12	36	61.0	394	1 OMS1_SALTI	Q56110 salmonella
13	36	61.0	602	1 LEPA_CHLPN	Q92814 chlamydia p
14	36	61.0	602	1 LEPA_CHLTR	O84067 chlamydia t
15	36	61.0	783	1 FAND_ECOLI	P12050 escherichia
16	35	59.3	536	1 YNR2_CAEEL	Q21988 caenorhabdi
17	35	59.3	1166	1 RPA2_EUPOC	P28365 euplotes oc
18	34.5	58.5	131	1 YRAN_ECOLI	P45465 escherichia
19	34	57.6	102	1 RNBP_PENBR	P07446 penicillium
20	34	57.6	105	1 RNF2_GIBBA	P16412 gibberella
21	34	57.6	146	1 LYC2_PIG	P12068 sus scrofa
22	34	57.6	264	1 HB24_MOUSE	P20040 mus musculus
23	34	57.6	264	1 HB21_MOUSE	P18468 mus musculus
24	34	57.6	264	1 HB22_MOUSE	P18469 mus musculus
25	34	57.6	275	1 IF2A_PYRHO	O58655 pyrococcus
26	34	57.6	284	1 IPYR_PICPA	O13505 pichia past
27	34	57.6	286	1 IPYR_KLULA	P13998 kluyveromyc
28	34	57.6	286	1 IPYR_YEAST	P00817 saccharomyc
29	34	57.6	351	1 PHOE_CITFR	Q01605 citrobacter
30	34	57.6	360	1 MANB_BACSU	P55278 bacillus su
31	34	57.6	448	1 ASTB_PSEAE	O50175 pseudomonas
32	34	57.6	798	1 YLFN_CAEEL	Q20296 caenorhabdi
33	34	57.6	1323	1 RRPO_SMYEA	P28897 strawberry
34	33.5	56.8	274	1 PK1_NPVOP	O10269 orgyia pseu

35	33	55.9	65	1 CCSA_OENBE	P31565 oenothera b
36	33	55.9	196	1 WBJJ_ECOLI	P37750 escherichia
37	33	55.9	250	1 Y028_RICPR	Q05972 rickettsia
38	33	55.9	349	1 YJY9_YEAST	P41903 saccharomyc
39	33	55.9	426	1 TWIN_DROME	Q03019 drosophila
40	33	55.9	432	1 PURA_YEAST	P80210 saccharomyc
41	33	55.9	448	1 NCAP_CVHOC	P33469 human coron
42	33	55.9	470	1 SYE2_RICPR	Q92ct8 rickettsia
43	33	55.9	473	1 SYE_AQUAE	O67271 aquifex aeo
44	33	55.9	700	1 BIB_DROME	P23645 drosophila
45	33	55.9	759	1 ARYL_CALVI	P28513 calliphora

ALIGNMENTS

```
RESULT 1
PHOE_KLEOX
ID PHOE_KLEOX STANDARD; PRT; 349 AA.
AC Q01606;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE OUTER MEMBRANE PORE PROTEIN E PRECURSOR.
GN PHOE.
OS Klebsiella oxytoca.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K26;
RC MEDLINE; 93146376.
RA Sierlings G., Ochulsen C., Hofstra H., Tommassen J.;
RT "Characterization of the Citrobacter freundii phoE gene and
development of C. freundii-specific oligonucleotides.";
RL FEMS Microbiol. Lett. 78:199-204(1992).
CC -!- FUNCTION: THIS IS ONE OF THE PROTEINS INDUCED WHEN CELLS ARE
GROWN UNDER PHOSPHATE LIMITATION. ITS PROTEIN PORE IS
PARTICULARLY EFFICIENT IN THE UPTAKE OF INORGANIC PHOSPHATE,
CC PHOSPHORYLATED COMPOUNDS, AND SOME OTHER NEGATIVELY CHARGED
SOLUTIONS.
CC -!- SUBUNIT: HOMOTRIMER.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
CC -----
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CC -----
CC EMBL; X68022; CAA48163.1; -.
CC HSSP; P02932; 1PHO.
CC PRINTS; PR00182; ECOLNEIPORIN.
CC PROSITE; PR00183; ECOLIPORIN.
CC PROSITE; PS00576; GRAM_NEG_PORIN; 1.
CC PFAM; PF00267; Gram-ve_porins; 1.
CC Outer membrane; Transmembrane; Porin; Signal.
FT SIGNAL 1 21
FT CHAIN 22 349
FT SEQUENCE 349 AA; 38550 MW; D0B0A5427542B3F5 CRC64;
SQ SEQUENCE 349 AA; 38550 MW; D0B0A5427542B3F5 CRC64;
```

Query Match 71.2%; Score 42; DB 1; Length 349;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 NYGSFDY 10
DB 105 NYGSFDY 111

```
RESULT 2
PHOE_KLEPN
ID PHOE_KLEPN STANDARD; PRT; 351 AA.
AC P30704;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE OUTER MEMBRANE PORE PROTEIN E PRECURSOR.
GN PHOE.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87190417.
RA van der Ley P., Bekkers A., van Meersbergen J., Tommassen J.;
RT "A comparative study on the phoE genes of three enterobacterial
RT species. Implications for structure-function relationships in a
RT pore-forming protein of the outer membrane.";
RL Eur. J. Biochem. 164:469-475(1987).
CC -!- FUNCTION: THIS IS ONE OF THE PROTEINS INDUCED WHEN CELLS ARE
CC GROWN UNDER PHOSPHATE LIMITATION. ITS PROTEIN PORE IS
CC PARTICULARLY EFFICIENT IN THE UPTAKE OF INORGANIC PHOSPHATE,
CC PHOSPHORYLATED COMPOUNDS, AND SOME OTHER NEGATIVELY CHARGED
CC SOLUTES.
CC -!- SUBUNIT: HOMOTRIMER.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
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CC EMBL; M28295; AAA25121.1; -.
DR HSP; P02932; 1PHO.
DR PRINTS; PRO0182; ECOLNEIPORIN.
DR PROSITE; PRO0183; ECOLIPORIN.
DR PROSITE; PS00576; GRAM_NEG_PORIN; 1.
DR PFAM; PF00267; Gram-ve porins; 1.
KW Outer membrane; Transmembrane; Porin; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 351 OUTER MEMBRANE PORE PROTEIN E.
SQ SEQUENCE 351 AA; 38894 MW; 86A5286C12502EC7 CRC64;

Query Match 71.2%; Score 42; DB 1; Length 351;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10
Db 106 NYGSFDY 112
|||||

RESULT 3
YX12_CAEEL
ID YX12_CAEEL STANDARD; PRT; 316 AA.
AC Q11123;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 35.1 KD PROTEIN C03F11.2 IN CHROMOSOME X.
GN C03F11.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.

STRAIN-BRISTOL N2;
RA Bentley D.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: WEAK, IN THE N-TERMINUS, TO C.ELEGANS F53B1.5.
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CC
CC EMBL; U39744; AAA80440.1; -.
DR WORMPEP; C03F11.2; CE03914.
KW Hypothetical protein.
SQ SEQUENCE 316 AA; 35107 MW; 6A725FCA21CF676 CRC64;

Query Match 66.1%; Score 39; DB 1; Length 316;
Best Local Similarity 60.0%; Pred. No. 5.2;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
Db 69 ARHFGGSVEY 78
|||||

RESULT 4
LEPA_TREPA
ID LEPA_TREPA STANDARD; PRT; 605 AA.
AC O83523;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE GTP-BINDING PROTEIN LEPA.
GN LEPA OR TP0510.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NICHOLS;
RX MEDLINE; 98332770.
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RA "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete.";
RL Science 281:375-388(1998).
CC -!- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC LEPA SUBFAMILY.
CC
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CC EMBL; AE001227; AAC65498.1; -.
DR TIGR; TP0510; -.
DR PROSITE; PS00301; EFACITOR_GTP; FALSE_NEG.
DR PFAM; PF00009; GTP_EFTU; 1.
KW GTP-binding.
FT NP_BIND 17 24 GTP (BY SIMILARITY).
FT NP_BIND 83 87 GTP (BY SIMILARITY).
FT NP_BIND 137 140 GTP (BY SIMILARITY).
SQ SEQUENCE 605 AA; 67622 MW; BA537DEC26FD3349 CRC64;
```

```
Query Match      64.4%; Score 38; DB 1; Length 605;
Best Local Similarity 75.0%; Pred. No. 15;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFDY 10
   | | | | |
Db 470 HGYASFDY 477

RESULT 5
OMPD_SALTY
ID  OMPD_SALTY  STANDARD; PRT; 282 AA.
AC  P37592;
DT  01-OCT-1994 (Rel. 30, Created)
DT  01-OCT-1994 (Rel. 30, Last sequence update)
DT  15-DEC-1998 (Rel. 37, Last annotation update)
DE  OUTER MEMBRANE PORIN PROTEIN OMPD (FRAGMENT).
GN  OMPD OR NMPC.
OS  Salmonella typhimurium.
OC  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC  Salmonella.
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=SL1303;
RX  MEDLINE; 95011654.
RA  Hongo E., Morimyo M., Mita K., Machida I., Hama-Inaba H., Tsuji H.,
RA  Ichimura S., Noda Y.;
RT  "The methyl viologen-resistance-encoding gene smva of Salmonella
RT  typhimurium."
RL  Gene 148:173-174(1994).
RN  [2]
RP  IDENTIFICATION AS OMPD.
RA  Singh S.P., Miller S., Williams Y.U., Rudd K.E., Nikaido H.;
RL  Unpublished observations (FEB-1996).
CC  -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC  -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; D26057; BAA05056.1; -.
DR  HSSP; P02931; 1GFN.
DR  STYGENE; SG10249; OMPD.
DR  PROSITE; PS00576; GRAM_NEG_PORIN; 1.
DR  PFAM; PF00267; Gram-ve_porins; 1.
KW  Outer membrane; Transmembrane; Porin.
FT  NON_TER 1
FT  NON_TER 1
SQ  SEQUENCE 282 AA; 30954 MW; BE137053E7F6C6A7 CRC64;

Query Match      62.7%; Score 37; DB 1; Length 282;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10
   | | | | |
Db 28 DYGSFDY 34

RESULT 6
OMPF_SERMA
ID  OMPF_SERMA  STANDARD; PRT; 374 AA.
AC  O33980;
DT  15-DEC-1998 (Rel. 37, Created)
DT  15-DEC-1998 (Rel. 37, Last sequence update)
DE  OUTER MEMBRANE PORIN C PRECURSOR (PORIN OMPF).
GN  OMPF.
OS  Serratia marcescens.
OC  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC  Serratia.
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=UOC-51;
RX  MEDLINE; 94236242.
RA  Hutsul J.A.M., Worobec E.A.;
RT  "Molecular characterization of a 40 kDa OmpC-like porin from Serratia
RT  marcescens."
RL  Microbiology 140:379-387(1994).
CC  -1- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR
CC  WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE.
CC  -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC  -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC  -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
CC  -----
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```
DE  OUTER MEMBRANE PROTEIN F PRECURSOR (PORIN OMPF).
GN  OMPF.
OS  Serratia marcescens.
OC  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC  Serratia.
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=UOC-51;
RX  MEDLINE; 97419518.
RA  Hutsul J.A.M., Worobec E.A.;
RT  "Molecular characterization of the Serratia marcescens OmpF porin,
RT  and analysis of S. marcescens OmpF and OmpC osmoregulation."
RL  Microbiology 143:2797-2806(1997).
CC  -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC  -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC  -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; U81967; AAB69103.1; ALT_INIT.
DR  PRINTS; PR00182; ECOLNEIPORIN.
DR  PRINTS; PR00183; ECOLIPORIN.
DR  PROSITE; PS00576; GRAM_NEG_PORIN; 1.
DR  PFAM; PF00267; Gram-Ve_Porins; 1.
KW  Outer membrane; Transmembrane; Porin; Signal.
FT  SIGNAL 1 21 POTENTIAL.
FT  CHAIN 22 374 OUTER MEMBRANE PROTEIN F.
SQ  SEQUENCE 374 AA; 41184 MW; BF821D385E441049 CRC64;

Query Match      62.7%; Score 37; DB 1; Length 374;
Best Local Similarity 85.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10
   | | | | |
Db 108 DYGSFDY 114

RESULT 7
OMPC_SERMA
ID  OMPC_SERMA  STANDARD; PRT; 376 AA.
AC  Q54471;
DT  15-DEC-1998 (Rel. 37, Created)
DT  15-DEC-1998 (Rel. 37, Last sequence update)
DT  15-DEC-1998 (Rel. 37, Last annotation update)
DE  OUTER MEMBRANE PROTEIN C PRECURSOR (PORIN OMPF).
GN  OMPF.
OS  Serratia marcescens.
OC  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC  Serratia.
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=UOC-51;
RX  MEDLINE; 94236242.
RA  Hutsul J.A.M., Worobec E.A.;
RT  "Molecular characterization of a 40 kDa OmpC-like porin from Serratia
RT  marcescens."
RL  Microbiology 140:379-387(1994).
CC  -1- FUNCTION: FORM PASSIVE DIFFUSION PORES WHICH ALLOW SMALL MOLECULAR
CC  WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER MEMBRANE.
CC  -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC  -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC  -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
CC  -----
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CC EMBL; L24960; AAA26562.1; -
 DR PRINTS; PR00182; ECOLNEIPORIN.
 DR PROSITE; PS00576; GRAM_NEG_PORIN; 1.
 DR PFAM; PF00267; Gram-ve_porins; 1.
 KW Outer membrane; Transmembrane; Porin; Phage recognition; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT CHAIN 22 376 OUTER MEMBRANE PROTEIN C.
 SQ SEQUENCE 376 AA; 41440 MW; 81227FB8515B568E CRC64;

Query Match 62.7%; Score 37; DB 1; Length 376;
 Best Local Similarity 85.7%; Pred. No. 14;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10 :|||||
 Db 106 DYGSFDY 112

RESULT 8
 OMPN_ECOLI STANDARD; PRT; 377 AA.
 AC P77747; P76854;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE OUTER MEMBRANE PROTEIN N PRECURSOR (PORIN OMPN).
 GN OMPN.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE; 97426617.
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE; 97251357.
 RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Itoh T.,
 RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
 RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
 RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
 RA Sampei G., Seki Y., Sivasubramanian S., Tagami H., Takeda J.,
 RA Takekoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
 RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
 RT corresponding to the 28.0-40.1 min region on the linkage map.";
 RL DNA Res. 3:363-377(1996).
 RN [3]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 22-33.
 RX MEDLINE; 98317278.
 RA Prilipov A., Phale P.S., Koebnik R., Widmer C., Rosenbusch J.P.;
 RT "Identification and characterization of two quiescent porin genes,
 RT nmpC and ompN, in Escherichia coli BE.";
 RL J. Bacteriol. 180:3388-3392(1998).
 CC -!- FUNCTION: NON-SPECIFIC PORIN.
 CC -!- SUBUNIT: HOMOTRIMER.
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
 CC -!- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.

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CC EMBL; AE000234; AAC74459.1; -
 DR EMBL; D90775; CAB20897.1; -
 DR EMBL; D90776; CAB20905.1; -
 DR ECOGENE; EGI3375; OMPN.
 DR PFAM; PF00267; Gram-ve_porins; 1.
 DR PRINTS; PR00182; ECOLNEIPORIN.
 DR PRINTS; PR00183; ECOLIPORIN.
 KW Outer membrane; Transmembrane; Porin; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 377 OUTER MEMBRANE PROTEIN N.
 SQ SEQUENCE 377 AA; 41220 MW; 4420D2CB9BC10F95 CRC64;

Query Match 62.7%; Score 37; DB 1; Length 377;
 Best Local Similarity 85.7%; Pred. No. 14;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFDY 10 :|||||
 Db 106 DYGSFDY 112

RESULT 9
 OMS2_SALTI STANDARD; PRT; 383 AA.
 AC Q56111;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE OUTER MEMBRANE PROTEIN S2 PRECURSOR.
 GN OMS2.
 OS Salmonella typhi.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Salmonella.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-IMSS-1;
 RA Fernandez-Mora M., Calva E.;
 RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
 CC (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.

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CC EMBL; X89756; CAA61903.1; -
 DR PFAM; PF00267; Gram-ve_porins; 1.
 DR PRINTS; PR00182; ECOLNEIPORIN.
 DR PRINTS; PR00183; ECOLIPORIN.
 KW Outer membrane; Transmembrane; Porin; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 383 OUTER MEMBRANE PROTEIN S2.
 SQ SEQUENCE 383 AA; 42183 MW; 47CFB6B5F6A2370F CRC64;

Query Match 62.7%; Score 37; DB 1; Length 383;
 Best Local Similarity 85.7%; Pred. No. 14;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy 4 NYGSFDY 10
Db 106 DYGSFDY 112

RESULT 10
LP1B_DROME STANDARD; PRT; 789 AA.
AC P1196;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE LARVAL SERUM PROTEIN 1 BETA CHAIN PRECURSOR (HEXAMERIN 1 BETA).
GN LSP1-B.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RC STRAIN=CANTON-S.
RX MEDLINE; 97274657.
RA Massey H.C. Jr., Kejzlarova-Lepesant J., Willis R.L.,
RA Castleberry A.B., Benes H.;
RT "The Drosophila Lsp-1 beta gene. A structural and phylogenetic
RT analysis";
RL Eur. J. Biochem. 245:199-207(1997).
RN [2]
RP SEQUENCE OF 1-100 FROM N.A.
RX MEDLINE; 87060914.
RA Delaney S.J., Smith D.F., McClelland A., Sunkel C., Glover D.M.;
RT "Sequence conservation around the 5' ends of the larval serum protein
RT 1 genes of Drosophila melanogaster.";
RL J. Mol. Biol. 189:1-11(1986).
CC -1- FUNCTION: LARVAL STORAGE PROTEIN (LSP) WHICH MAY SERVE AS A STORE
CC OF AMINO ACIDS FOR SYNTHESIS OF ADULT PROTEINS (BY SIMILARITY).
CC -1- SUBUNIT: HETEROHEXAMER, COMPOSED OF THREE SUBUNITS, ALPHA, BETA
CC AND GAMMA.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- TISSUE SPECIFICITY: LARVAL HEMOLYMPH.
CC -1- SIMILARITY: TO ARYLPHORINS AND TO ARTHROPOD HEMOCYANINS.
CC
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CC -----
CC EMBL; U63556; AAB58821.1; -.
CC DR EMBL; X03873; CAA27507.1; -.
CC DR PIR; B27144; B27144.
CC DR HSP; P04253; LOXY.
CC DR FLYBASE; FBgn0002563; Lsp1-beta.
CC DR PRINTS; PR00187; HAEMOCYANIN.
CC DR PROSITE; PS00209; HEMOCYANIN_1; FALSE_NEG.
CC DR PROSITE; PS00210; HEMOCYANIN_2; 1.
CC DR PFAM; PF00372; hemocyanin; 1.
CC Signal; Hemolymph; Storage protein; Glycoprotein; Multigene family.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 789 LARVAL SERUM PROTEIN 1 BETA CHAIN.
SQ SEQUENCE 789 AA; 95995 MW; AFA3EF4855D06A5B CRC64;

Query Match 62.7%; Score 37; DB 1; Length 789;
Best Local Similarity 85.7%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NYGSFDY 10
Db 770 NYGHFDY 776

RESULT 11
OMPF_XENNE STANDARD; PRT; 369 AA.
AC Q56828;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE OUTER MEMBRANE PROTEIN F PRECURSOR (PORIN OMPF) (OUTER MEMBRANE
DE PROTEIN OMPF).
OS Xenorhabdus nematophilus.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Xenorhabdus.
RN [1]
RC STRAIN=AN6/1;
RX MEDLINE; 96414477.
RA Forst S., Waukau J., Leisman G., Exner M., Hancock R.;
RT "Functional and regulatory analysis of the OmpF-like porin, OmpP, of
RT the symbiotic bacterium Xenorhabdus nematophilus.";
RL Mol. Microbiol. 18:779-789(1995).
CC -1- FUNCTION: OMPF IS A PORIN THAT PASSIVE DIFFUSION PORES WHICH ALLOW
CC SMALL MOLECULAR WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER
CC MEMBRANE (BY SIMILARITY).
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
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CC -----
CC EMBL; L40919; AAB41114.1; -.
CC DR PRINTS; PR00182; ECOLNEIPORIN.
CC DR PRINTS; PR00183; ECOTIPORIN.
CC DR PROSITE; PS00576; GRAM_NEG_PORIN; 1.
CC DR PFAM; PF00267; Gram-ve_porins; 1.
CC KW Outer membrane; Transmembrane; Porin; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 369 OUTER MEMBRANE PROTEIN F.
SQ SEQUENCE 369 AA; 40851 MW; 20E30CA680F8557A CRC64;

Query Match 61.0%; Score 36; DB 1; Length 369;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NYGSFDY 10
Db 107 NYGSLDY 113

RESULT 12
OMSL_SALTI STANDARD; PRT; 394 AA.
AC Q56110;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE OUTER MEMBRANE PROTEIN SI PRECURSOR.
GN OMP51.
OS Salmonella typhi.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
RN [1]
RC STRAIN=IMSS-1;
RP SEQUENCE FROM N.A.
RX MEDLINE; 96414477.
RA Forst S., Waukau J., Leisman G., Exner M., Hancock R.;
RT "Functional and regulatory analysis of the OmpF-like porin, OmpP, of
RT the symbiotic bacterium Xenorhabdus nematophilus.";
RL Mol. Microbiol. 18:779-789(1995).
CC -1- FUNCTION: OMPF IS A PORIN THAT PASSIVE DIFFUSION PORES WHICH ALLOW
CC SMALL MOLECULAR WEIGHT HYDROPHILIC MATERIALS ACROSS THE OUTER
CC MEMBRANE (BY SIMILARITY).
CC -1- SUBUNIT: HOMOTRIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE.
CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
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CC -----
CC EMBL; L40919; AAB41114.1; -.
CC DR PRINTS; PR00182; ECOLNEIPORIN.
CC DR PRINTS; PR00183; ECOTIPORIN.
CC DR PROSITE; PS00576; GRAM_NEG_PORIN; 1.
CC DR PFAM; PF00267; Gram-ve_porins; 1.
CC KW Outer membrane; Transmembrane; Porin; Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 369 OUTER MEMBRANE PROTEIN F.
SQ SEQUENCE 369 AA; 40851 MW; 20E30CA680F8557A CRC64;

Query Match 61.0%; Score 36; DB 1; Length 369;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
RX MEDLINE; 95309727.
RA Fernandez-Mora M., Oropeza R., Puente J.L., Calva E.;
RT "Isolation and characterization of ompS1, a novel Salmonella typhi
RL outer membrane protein-encoding gene.";
RL Gene 158:67-72(1995).
CC -1- SUBUNIT: HOMOPOLYMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE OMPC/PHOE FAMILY OF PORINS.
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CC -----
CC EMBL; X73237; CAAS1710.1; -.
DR PRINTS; PR00182; ECOLNEIPORIN.
DR PRINTS; PR00183; ECOLIPORIN.
DR PROSITE; PS00576; GRAM_NEG_PORIN; 1.
DR PFAM; PF00267; Gram-ve_porins; 1.
KW Signal; Outer membrane; transmembrane; Porin.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 394 OUTER MEMBRANE PROTEIN S1.
FT SEQUENCE 394 AA; 43253 MW; E7C8FEED424931D1 CRC64;
SQ
Query Match 61.0%; Score 36; DB 1; Length 394;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 YGSFDY 10
DB 107 YGSFDY 112
RESULT 13
LEPA_CHLPN STANDARD; PRT; 602 AA.
AC Q9Z814;
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE GTP-BINDING PROTEIN LEPA.
LEPA OR CPN0359.
GN Chlamydia pneumoniae (Chlamydophila pneumoniae).
OS Chlamydia; Chlamydiales; Chlamydiaceae; Chlamydophila.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CWL029;
RX MEDLINE; 99206606.
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RT Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RA "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC LEPA SUBFAMILY.
CC -----
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CC -----
CC EMBL; AE001620; AAD18503.1; -.
DR PROSITE; PS00301; EFACOR_GTP; FALSE_NEG.
KW GTP-binding.
FT NP_BIND 16 23 GTP (BY SIMILARITY).
FT NP_BIND 81 85 GTP (BY SIMILARITY).
FT NP_BIND 81 85 GTP (BY SIMILARITY).
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FT NP_BIND 135 138 GTP (BY SIMILARITY).
SQ SEQUENCE 602 AA; 67285 MW; A4C110B1A10578E2 CRC64;
Query Match 61.0%; Score 36; DB 1; Length 602;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 YGSFDY 10
DB 472 YGSFDY 477
RESULT 14
LEPA_CHLTR STANDARD; PRT; 602 AA.
AC O84067;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE GTP-BINDING PROTEIN LEPA.
GN LEPA OR CT064.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/UW-3/CX;
RX MEDLINE; 99000809.
RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis.";
RL Science 282:754-759(1998).
CC -1- SIMILARITY: BELONGS TO THE GTP-BINDING ELONGATION FACTOR FAMILY.
CC LEPA SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AE001281; AAC67655.1; -.
DR PROSITE; PS00301; EFACOR_GTP; FALSE_NEG.
DR PFAM; PF00009; GTP_EFTU; 1.
KW GTP-binding.
FT NP_BIND 16 23 GTP (BY SIMILARITY).
FT NP_BIND 81 85 GTP (BY SIMILARITY).
FT NP_BIND 135 138 GTP (BY SIMILARITY).
SQ SEQUENCE 602 AA; 67435 MW; 98F67C990196EEC4 CRC64;
Query Match 61.0%; Score 36; DB 1; Length 602;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 YGSFDY 10
DB 472 YGSFDY 477
RESULT 15
FAND_ECOLI STANDARD; PRT; 783 AA.
AC P12050;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE OUTER MEMBRANE USHER PROTEIN FAND PRECURSOR.
GN FAND.
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OS Escherichia coli.
OG Plasmid pFK99.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B41;
RX MEDLINE; 89160266.
RA Roosendaal B., Bakker D., de Graaf F.K.;
RT "The nucleotide sequence of the fanD gene encoding the large outer
RT membrane protein involved in the biosynthesis of K99 fimbriae.";
RL Nucleic Acids Res. 17:1263-1263(1989).
RN [2]
RP SEQUENCE OF 1-20 FROM N.A.
RC Roosendaal B., Gaastra W., de Graaf F.K.;
RT "The nucleotide sequence of the gene encoding the K99 subunit of
RT enterotoxigenic Escherichia coli.";
RL FEMS Microbiol. Lett. 22:253-258(1984).
RN [3]
RP SEQUENCE OF 770-783 FROM N.A.
RC STRAIN-B41;
RX MEDLINE; 91312125.
RA Bakker D., Vader C.E.M., Roosendaal B., Mool F.R., Oudega B.,
RA de Graaf F.K.;
RT "Structure and function of periplasmic chaperone-like proteins
RT involved in the biosynthesis of K88 and K99 fimbriae in
RT enterotoxigenic Escherichia coli.";
RL Mol. Microbiol. 5:875-886(1991).
CC -1- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF K99 FIMBRIAL
CC SUBUNITS ACROSS THE OUTER MEMBRANE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. OUTER MEMBRANE
CC (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FIMBRIAL EXPORT USHER FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X13560; CAA31911.1; -.
DR EMBL; M35282; -: NOT_ANNOTATED_CDS.
DR EMBL; X56001; CAA39473.1; -.
DR PIR; S02755; S02755.
DR PROSITE; PS01151; FIMBRIAL_USHER; 1.
DR PFAM; PF00577; Usher; 1.
KW Outer membrane; Transmembrane; Fimbria; Transport; Signal; Plasmid.
FT SIGNAL 1 ? POTENTIAL.
FT CHAIN ? 783 OUTER MEMBRANE USHER PROTEIN FAND.
FT DISULFID 763 782 POTENTIAL.
SQ SEQUENCE 783 AA; 87156 MW; 23BDE3923A9B7069 CRC64;

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Query Match          61.0%; Score 36; DB 1; Length 783;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YGSEFDY 10
Db 354 YGSEFDY 359

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Search completed: May 27, 2000, 20:07:15
Job time: 987 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:38:40 ; Search time 199.56 Seconds
(without alignments)
3.474 Million cell updates/sec

Title: US-09-016-061-64
Perfect score: 59
Sequence: 1 ARHNGSFDY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SPTREMBL_12.*
1: sp-archaea.*
2: sp-bacteria.*
3: sp-fungi.*
4: sp-human.*
5: sp-invertebrate.*
6: sp-mammal.*
7: sp-mhc.*
8: sp-organelle.*
9: sp-phage.*
10: sp-plant.*
11: sp-rodent.*
12: sp-virus.*
13: sp-vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	42	71.2	79	7 019191	019191 prionailuru
2	42	71.2	79	7 019192	019192 prionailuru
3	42	71.2	79	7 019380	019380 felis silve
4	42	71.2	79	7 019381	019381 felis silve
5	42	71.2	79	7 019382	019382 felis silve
6	42	71.2	79	7 019396	019396 felis silve
7	42	71.2	79	7 019397	019397 felis silve
8	42	71.2	79	7 019405	019405 felis silve
9	42	71.2	79	7 019406	019406 felis silve
10	42	71.2	79	7 019407	019407 felis silve
11	42	71.2	79	7 019408	019408 felis silve
12	42	71.2	79	7 019435	019435 felis silve
13	42	71.2	83	7 02XS06	02XS06 odocolleus
14	42	71.2	83	7 02XS25	02XS25 odocolleus
15	42	71.2	83	7 02XS24	02XS24 odocolleus
16	40	67.8	89	7 019495	019495 gallus gall
17	39	66.1	544	1 P95960	P95960 sulfolobus
18	38	64.4	39	7 P79474	P79474 cervus elap
19	38	64.4	39	7 P79477	P79477 cervus elap
20	38	64.4	39	7 P79478	P79478 cervus elap

21	38	64.4	39	7	P79479	P79479 cervus elap
22	38	64.4	81	7	Q30568	Q30568 macaca fasc
23	38	64.4	81	7	Q30571	Q30571 macaca fasc
24	38	64.4	81	7	Q30737	Q30737 macaca neme
25	38	64.4	81	7	Q30739	Q30739 macaca neme
26	38	64.4	81	7	Q30563	Q30563 macaca fasc
27	38	64.4	81	7	Q30740	Q30740 macaca neme
28	38	64.4	82	7	Q95598	Q95598 phasianus c
29	38	64.4	82	7	Q30606	Q30606 macaca mula
30	38	64.4	82	7	Q30608	Q30608 macaca mula
31	38	64.4	82	7	Q30637	Q30637 macaca mula
32	38	64.4	82	7	Q30638	Q30638 macaca mula
33	38	64.4	82	7	Q30658	Q30658 macaca mula
34	38	64.4	82	7	Q30659	Q30659 macaca mula
35	38	64.4	82	7	Q30666	Q30666 macaca mula
36	38	64.4	82	7	Q30667	Q30667 macaca mula
37	38	64.4	82	7	Q30668	Q30668 macaca mula
38	38	64.4	82	7	Q19287	Q19287 macaca mula
39	38	64.4	82	7	Q19288	Q19288 macaca mula
40	38	64.4	83	7	O98002	O98002 ovis aries
41	38	64.4	85	7	Q30796	Q30796 ovis aries
42	38	64.4	85	7	Q30800	Q30800 ovis aries
43	38	64.4	85	7	Q30803	Q30803 ovis aries
44	38	64.4	85	7	Q30812	Q30812 ovis aries
45	38	64.4	85	7	P79966	P79966 capra aegag

ALIGNMENTS

RESULT 1
ID 019191 PRELIMINARY; PRT; 79 AA.
AC 019191;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
GN MHCMAIR-DRB.

OS Prionailurus bengalensis iriomotensis (Iriomote cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Prionailurus.

RL J. Immunol. 158:2822-2833(1997).

DR EMBL; U51546; AAB65582.1; -.

DR PFAM; PF00969; MHC_II_beta; 1.

RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB genes".

RL J. Immunol. 158:2822-2833(1997).

DR EMBL; U51546; AAB65582.1; -.

DR PFAM; PF00969; MHC_II_beta; 1.

KW MHC.

FT NON_TER 1 1

FT NON_TER 79 79

SQ SEQUENCE 79 AA; 9582 MW; 8EEF2C7D CRC32;

Query Match 71.2%; Score 42; DB 7; Length 79;

Best Local Similarity 87.5%; Pred. No. 0.79;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNGSFD 9

Db 72 RHNGVGF 79

RESULT 2

ID 019192 PRELIMINARY; PRT; 79 AA.

AC 019192;

DT 01-JAN-1998 (TREMBLrel. 05, Created)

DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)

DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)

DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
GN MHCMAIR-DRB.
OS Prionailurus bengalensis iriomotensis (Iriomote cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Prionailurus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97211851.
RA YUHKI N., O'BRIEN S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
genes.";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51498; AAB65533.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 9582 MW; ED9F80F0 CRC32;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 0.79;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
|||||
Db 72 RHNYGVFD 79

RESULT 3
O19380 PRELIMINARY; PRT; 79 AA.
ID O19380
AC O19380
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
GN MHCFECA-DRB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97211851.
RA YUHKI N., O'BRIEN S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
genes.";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51498; AAB65533.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 9659 MW; F352AD23 CRC32;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 0.79;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
|||||
Db 72 RHNYGVFD 79

RESULT 4
O19381 PRELIMINARY; PRT; 79 AA.
ID O19381
AC O19381
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).

GN MHCFECA-DRB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97211851.
RA YUHKI N., O'BRIEN S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
genes.";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51499; AAB65534.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 9610 MW; 1F7FB873 CRC32;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 0.79;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
|||||
Db 72 RHNYGVFD 79

RESULT 5
O19382 PRELIMINARY; PRT; 79 AA.
ID O19382
AC O19382
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
GN MHCFECA-DRB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97211851.
RA YUHKI N., O'BRIEN S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
genes.";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51500; AAB65535.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 9421 MW; CB203F17 CRC32;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 0.79;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
|||||
Db 72 RHNYGVFD 79

RESULT 6
O19396 PRELIMINARY; PRT; 79 AA.
ID O19396
AC O19396
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
GN MHCFECA-DRB.

OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97211851.
 RA YUHKI N., O'BRIEN S.J.;
 RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
 RT genes.";
 RL J. Immunol. 158:2822-2833(1997).
 DR EMBL; U51514; AAB65549.1; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 9625 MW; 5AC8163D CRC32;

Query Match 71.2%; Score 42; DB 7; Length 79;
 Best Local Similarity 87.5%; Pred. No. 0.79;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
 | | | | |
 Db 72 RHNYGVFD 79

RESULT 7
 O19397
 ID O19397 PRELIMINARY; PRT; 79 AA.
 AC O19397;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
 GN MHCFECA-DRB.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97211851.
 RA YUHKI N., O'BRIEN S.J.;
 RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
 RT genes.";
 RL J. Immunol. 158:2822-2833(1997).
 DR EMBL; U51515; AAB65550.1; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 9641 MW; D50F56AA CRC32;

Query Match 71.2%; Score 42; DB 7; Length 79;
 Best Local Similarity 87.5%; Pred. No. 0.79;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
 | | | | |
 Db 72 RHNYGVFD 79

RESULT 8
 O19405
 ID O19405 PRELIMINARY; PRT; 79 AA.
 AC O19405;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
 GN MHCFECA-DRB.
 OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97211851.
 RA YUHKI N., O'BRIEN S.J.;
 RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
 RT genes.";
 RL J. Immunol. 158:2822-2833(1997).
 DR EMBL; U51523; AAB65558.1; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 9590 MW; E9169F1F CRC32;

Query Match 71.2%; Score 42; DB 7; Length 79;
 Best Local Similarity 87.5%; Pred. No. 0.79;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
 | | | | |
 Db 72 RHNYGVFD 79

RESULT 9
 O19406
 ID O19406 PRELIMINARY; PRT; 79 AA.
 AC O19406;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
 GN MHCFECA-DRB.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97211851.
 RA YUHKI N., O'BRIEN S.J.;
 RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
 RT genes.";
 RL J. Immunol. 158:2822-2833(1997).
 DR EMBL; U51524; AAB65559.1; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 9466 MW; 89AFA39A CRC32;

Query Match 71.2%; Score 42; DB 7; Length 79;
 Best Local Similarity 87.5%; Pred. No. 0.79;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
 | | | | |
 Db 72 RHNYGVFD 79

RESULT 10
 O19407
 ID O19407 PRELIMINARY; PRT; 79 AA.
 AC O19407;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
 GN MHCFECA-DRB.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97211851.
RA YUHKI N., O'BRIEN S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
genes.";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51525; AAB65560.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 9485 MW; 9EDE935A CRC32;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 0.79;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
| | | | |
Db 72 RHNYGVFD 79

RESULT 11
O19408 PRELIMINARY; PRT; 79 AA.
ID O19408;
AC O19408;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
GN MHCFCGA-DRB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97211851.
RA YUHKI N., O'BRIEN S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
genes.";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51526; AAB65561.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 9496 MW; FE4A825E CRC32;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 0.79;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
| | | | |
Db 72 RHNYGVFD 79

RESULT 12
O19435 PRELIMINARY; PRT; 79 AA.
ID O19435;
AC O19435;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
GN MHCFCGA-DRB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97211851.
RA YUHKI N., O'BRIEN S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
genes.";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51983; AAB65590.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 9407 MW; 1CC2BF4F CRC32;

Query Match 71.2%; Score 42; DB 7; Length 79;
Best Local Similarity 87.5%; Pred. No. 0.79;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
| | | | |
Db 72 RHNYGVFD 79

RESULT 13
O9XS06 PRELIMINARY; PRT; 83 AA.
ID O9XS06;
AC O9XS06;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE MHC CLASS II ANTIGEN (FRAGMENT).
GN ODVI-DRB.
OS Odocolleus virginianus (white-tailed deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Odocolleinae; Odocolleus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 99216441.
RA VAN DEN BUSSCHE R.A., HOOFFER S.R., LOCHMILLER R.L.;
RT "Characterization of Mhc-DRB allelic diversity in white-tailed deer
RT (Odocolleus virginianus) provides insight into Mhc-DRB allelic
evolution within Cervidae.";
RL Immunogenetics 49:429-437(1999).
DR EMBL; AF082163; AAD37819.1; -.
FT NON_TER 1 1
FT NON_TER 83 83
SQ SEQUENCE 83 AA; 9932 MW; 079E010E CRC32;

Query Match 71.2%; Score 42; DB 7; Length 83;
Best Local Similarity 87.5%; Pred. No. 0.83;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
| | | | |
Db 72 RHNYGVFD 79

RESULT 14
O9XR25 PRELIMINARY; PRT; 83 AA.
ID O9XR25;
AC O9XR25;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE MHC CLASS II ANTIGEN (FRAGMENT).
GN ODVI-DRB.
OS Odocolleus virginianus (white-tailed deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Odocolleinae; Odocolleus.

```
RN SEQUENCE FROM N.A.
RX MEDLINE; 99216441.
RA VAN DEN BUSSCHE R.A., HOOPER S.R., LOCHMILLER R.L.;
RT "Characterization of Mhc-DRB allelic diversity in white-tailed deer
RT (Odocoileus virginianus) provides insight into Mhc-DRB allelic
RL evolution within Cervidae.";
RL Immunogenetics 49:429-437(1999).
DR EMBL; AF082174; AAD37830.1; -.
FT NON_TER 1
FT NON_TER 83
SQ SEQUENCE 83 AA; 9842 MW; 4E3B8130 CRC32;

Query Match      71.2%; Score 42; DB 7; Length 83;
Best Local Similarity 87.5%; Pred. No. 0.83;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
Db 72 RHNYGVFD 79

RESULT 15
Q9XRZ4
ID Q9XRZ4 PRELIMINARY; PRT; 83 AA.
AC Q9XRZ4;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE MHC CLASS II ANTIGEN (FRAGMENT).
GN ODVI-DRB.
OS Odocoileus virginianus (white-tailed deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
OC Odocoileinae; Odocoileus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 99216441.
RA VAN DEN BUSSCHE R.A., HOOPER S.R., LOCHMILLER R.L.;
RT "Characterization of Mhc-DRB allelic diversity in white-tailed deer
RT (Odocoileus virginianus) provides insight into Mhc-DRB allelic
RL evolution within Cervidae.";
RL Immunogenetics 49:429-437(1999).
DR EMBL; AF082175; AAD37831.1; -.
FT NON_TER 1
FT NON_TER 83
SQ SEQUENCE 83 AA; 9923 MW; 848647C3 CRC32;

Query Match      71.2%; Score 42; DB 7; Length 83;
Best Local Similarity 87.5%; Pred. No. 0.83;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFD 9
Db 72 RHNYGVFD 79
```

Search completed: May 27, 2000, 19:38:40
Job time: 2373 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:21:35 ; Search time 148.45 Seconds
(without alignments)
1.596 Million cell updates/sec

Title: US-09-016-061-64
Perfect score: 59
Sequence: 1 ARHNYGSFDY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	10	1 W76022	LM609 grafted anti
2	51	86.4	10	1 W76010	LM609 grafted anti
3	51	86.4	117	1 W76001	Vitaxin antibody h
4	51	86.4	117	1 W76003	LM609 antibody hea
5	50	84.7	10	1 W76023	LM609 grafted anti
6	49	83.1	117	1 R79157	Human IgE receptor
7	49	83.1	117	1 R79155	Human IgE receptor
8	49	83.1	117	1 W27357	Heavy chain variab
9	49	83.1	117	1 W27526	Heavy chain variab
10	49	83.1	117	1 W27354	Heavy chain variab
11	49	83.1	239	1 W73874	Human antiFc epsil
12	49	83.1	242	1 W73876	Human antiFc epsil
13	48	81.4	10	1 W76021	LM609 grafted anti
14	46	78.0	10	1 W76039	LM609 grafted anti
15	46	78.0	10	1 W76040	LM609 grafted anti
16	46	78.0	10	1 W76024	LM609 grafted anti
17	46	78.0	10	1 W76020	LM609 grafted anti
18	46	78.0	10	1 W76025	LM609 grafted anti
19	46	78.0	10	1 W76026	LM609 grafted anti
20	46	78.0	10	1 W76027	LM609 grafted anti
21	46	78.0	10	1 W76028	LM609 grafted anti
22	46	78.0	10	1 W76029	LM609 grafted anti
23	46	78.0	10	1 W76030	LM609 grafted anti
24	43	72.9	110	1 W84099	Murine vitronectin
25	43	72.9	117	1 W84093	Vitronectin alpha-
26	43	72.9	117	1 W84097	Humanised anti-alp
27	41	69.5	10	1 W76037	LM609 grafted anti
28	41	69.5	10	1 W76038	LM609 grafted anti
29	40	67.8	8	1 W27343	CDR3 from murine a
30	37	62.7	36	1 W03964	VDJ joint protein,
31	37	62.7	36	1 W41127	VH251 DXp'1 J6 mu
32	37	62.7	111	1 R40173	Humanised IL-5 ant
33	37	62.7	111	1 R87039	MAB 39D10 heavy ch
34	37	62.7	135	1 R40175	Humanised antibody

35	37	62.7	135	1	R40177	Humanised antibody
36	37	62.7	135	1	R40179	Humanised antibody
37	37	62.7	135	1	R40183	Humanised antibody
38	37	62.7	136	1	R40181	Humanised antibody
39	37	62.7	140	1	R87058	CDR grafted anti-I
40	36.5	61.9	256	1	R22568	SCFVB18 construct.
41	36.5	61.9	256	1	R22583	SCFVB18 construct
42	36.5	61.9	256	1	R22584	SCFVB18 construct
43	36.5	61.9	256	1	R22585	SCFVB18 construct
44	36.5	61.9	256	1	R22586	SCFVB18 construct
45	36.5	61.9	256	1	R22587	SCFVB18 construct

ALIGNMENTS

RESULT 1
W76022
ID W76022 standard; Protein; 10 AA.
AC W76022;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #4.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis; primer; V-H region; CDR;
complementarity determining region.
Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSY INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49859.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
integrin - and related grafted antibodies based on murine monoclonal
LM609, also related nucleic acid, used to treat, prevent or diagnose
angiogenesis or restenosis
Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
LM609 heavy and light chain variable region. LM609 and the antibody
vitaxin bind selectively to integrin alphaVbeta3 and can be used to
inhibit binding of alphaVbeta3 to a ligand and thus block
integrin-mediated signal transduction. This is useful in the treatment,
prevention and diagnosis of alphaVbeta3-mediated disease, specifically
angiogenesis and restenosis of blood vessels (but also e.g. (non-)immune inflammation,
diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
arthritis, macular degeneration, osteoporosis etc.). The antibodies
contain non-murine framework regions so are suitable for use in humans.
Enhanced types of LM609 have affinity more than 90 times greater than
that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 100.0%; Score 59; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00028;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARHNYGSFDY 10
| | | | | | | | | |
Db 1 ARHNYGSFDY 10

RESULT 2
W76010
ID W76010 standard; Protein; 10 AA.
AC W76010;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #1.
KW Vitaxin; antibody; variable region; heavy chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49847.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Disclosure; Page 40; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 86.4%; Score 51; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0059;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
 |||||
 Db 1 ARHNYGSFAY 10

RESULT 3
 W76001 ID W76001 standard; Protein; 117 AA.
 AC W76001;
 DT 02-NOV-1998 (first entry)
 DE Vitaxin antibody heavy chain variable region protein fragment.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49820.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 1; Fig 1a; 129pp; English.
 CC This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated

CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 SQ Sequence 117 AA;

Query Match 86.4%; Score 51; DB 1; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.074;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
 |||||
 Db 97 ARHNYGSFAY 106

RESULT 4
 W76003 ID W76003 standard; Protein; 117 AA.
 AC W76003;
 DT 02-NOV-1998 (first entry)
 DE LM609 antibody heavy chain variable region protein fragment.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49822.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 43; Fig 2a; 129pp; English.
 CC This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 SQ Sequence 117 AA;

Query Match 86.4%; Score 51; DB 1; Length 117;
 Best Local Similarity 90.0%; Pred. No. 0.074;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
 |||||
 Db 97 ARHNYGSFAY 106

RESULT 5
 W76023 ID W76023 standard; Protein; 10 AA.
 AC W76023;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #5.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angioestasis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49860.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 84.7%; Score 50; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0087;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ARHNYGSFDY 10
 |||||
 DB 1 ARHNYGSFY 10

RESULT 6
 R79157
 ID R79157 standard; peptide; 117 AA.
 AC R79157;
 DT 04-MAR-1996 (first entry)
 DE Human IgE receptor-binding antibody-related peptide heavy chain.
 KW Immunoglobulin E; antibody; receptor; monoclonal; detection;
 KW complementarity determining region.
 OS Mus sp.
 FH Key Location/Qualifiers
 FT region 31..35
 FT /label= CDR1H
 FT /note= "all CDR regions are claimed"
 FT region 50..66
 FT /label= CDR2H
 FT /note= "all CDR regions are claimed"
 FT region 99..106
 FT /label= CDR3H
 FT /note= "all CDR regions are claimed"

PN J07165799-A.
 PD 27-JUN-1995.
 PF 22-OCT-1993; 264792.
 PR 22-OCT-1993; JP-264792.
 PA (ASAK) ASahi BREWERIES LTD.
 PA (NIKK-) NIKKA WHISKEY KK.
 PA (TORI) TORII YAHUKIN KK.
 PA (TSUR/) TSURA T.
 DR WPI: 95-261292/34.
 DR N-PSDB; Q96284.
 PT Novel monoclonal antibody against human high-affinity IgE receptor -

PT and DNA fragment encoding the MAb, for the specific identification
 PS of human Fc-epsilon RI
 PS Claim 5; Page 14; 20pp; Japanese.
 CC Polypeptides which specifically recognise human IgE receptor (Fc-
 CC epsilon-RI) have been isolated and sequenced. The new peptides are
 CC related to a monoclonal antibody against Fc-epsilon-RI and are
 CC either heavy or light chain molecules. The heavy chain molecules
 CC have the general formula FRI-CDR1H-FR2-CDR2H-FR3-CDR3H-FR4 (corresp.
 CC to R79153, R79155, R79157, R79159 and R79161) and are encoded by
 CC Q96280, Q96282, Q96284, Q96286 and Q96288. FRI is a polypeptide
 CC having 29-36 amino acids (aa), FR2 is a 10-16 aa polypeptide, FR3 is
 CC a 33-35 aa polypeptide and FR4 is a 12-14 aa polypeptide. Similarly
 CC the light chains have the general formula FR5-CDR1L-FR6-CDR2L-FR7-
 CC CDR3L-FR8, (corresp. to R79154, R79156, R79158, R79160 and R79162)
 CC and are encoded by Q96281, Q96283, Q96285, Q96287 and Q96289. FR5
 CC is a 23-28 aa polypeptide, FR6 is a 14-16 aa polypeptide, FR7 is a
 CC 30-34 aa polypeptide and FR8 is a 9-11 aa polypeptide. All the
 CC peptides are derived from mouse hybridoma cells and are useful in
 CC the detection of the human Fc-epsilon-RI or for the elucidation of
 CC an antigen recognising region of a monoclonal antibody against
 CC human Fc-epsilon-RI.
 SQ Sequence 117 AA;

Query Match 83.1%; Score 49; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 0.16;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ARHNYGSFDY 10
 |||||
 DB 97 ARHNYGMDY 106

RESULT 7
 R79155
 ID R79155 standard; peptide; 117 AA.
 AC R79155;
 DT 04-MAR-1996 (first entry)
 DE Human IgE receptor-binding antibody-related peptide heavy chain.
 KW Immunoglobulin E; antibody; receptor; monoclonal; detection;
 KW complementarity determining region.
 OS Mus sp.
 FH Key Location/Qualifiers
 FT region 31..35
 FT /label= CDR1H
 FT /note= "all CDR regions are claimed"
 FT region 50..66
 FT /label= CDR2H
 FT /note= "all CDR regions are claimed"
 FT region 99..106
 FT /label= CDR3H
 FT /note= "all CDR regions are claimed"

PN J07165799-A.
 PD 27-JUN-1995.
 PF 22-OCT-1993; 264792.
 PR 22-OCT-1993; JP-264792.
 PA (ASAK) ASahi BREWERIES LTD.
 PA (NIKK-) NIKKA WHISKEY KK.
 PA (TORI) TORII YAHUKIN KK.
 PA (TSUR/) TSURA T.
 DR WPI: 95-261292/34.
 DR N-PSDB; Q96282.
 PT Novel monoclonal antibody against human high-affinity IgE receptor -
 PT and DNA fragment encoding the MAb, for the specific identification
 PS of human Fc-epsilon RI
 PS Claim 3; Page 13; 20pp; Japanese.
 CC Polypeptides which specifically recognise human IgE receptor (Fc-
 CC epsilon-RI) have been isolated and sequenced. The new peptides are
 CC related to a monoclonal antibody against Fc-epsilon-RI and are
 CC either heavy or light chain molecules. The heavy chain molecules
 CC have the general formula FRI-CDR1H-FR2-CDR2H-FR3-CDR3H-FR4 (corresp.
 CC to R79153, R79155, R79157, R79159 and R79161) and are encoded by
 CC Q96280, Q96282, Q96284, Q96286 and Q96288. FRI is a polypeptide


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CC having 29-36 amino acids (aa), FR2 is a 10-16 aa polypeptide, FR3 is
CC a 33-35 aa polypeptide and FR4 is a 12-14 aa polypeptide. Similarly
CC the light chains have the general formula FR5-CDRL1-FR6-CDRL2-FR7-
CC CDR31-FR8, (corresp. to R79154, R79156, R79158, R79160 and R79162)
CC and are encoded by Q96281, Q96283, Q96285, Q96287 and Q96289. FR5
CC is a 23-28 aa polypeptide, FR6 is a 14-16 aa polypeptide, FR7 is a
CC 30-34 aa polypeptide and FR8 is a 9-11 aa polypeptide. All the
CC peptides are derived from mouse hybridoma cells and are useful in
CC the detection of the human Fc-epsilon-RI or for the elucidation of
CC an antigen recognising region of a monoclonal antibody against
CC human Fc-epsilon-RI.
CC Sequence 117 AA;

Query Match      83.1%; Score 49; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
Db      ||||| ||
       97 ARHNYGMDY 106

RESULT 8
W27357
ID W27357 standard; Protein; 117 AA.
AC W27357;
DT 16-DEC-1997 (first entry)
DE Heavy chain variable region of chimeric human CRA2 antibody.
KW Complementarity determining region; CDR; murine; mouse; human;
KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
KW IgE; MAb; heavy chain; variable region; humanised; semi-chimeric;
KW chimeric; treatment; prevention; disease; allergy; CRA2.
OS Chimeric - Homo sapiens.
OS Chimeric - Mus spp.
OS Synthetic.
PN J09191886-A.
PD 29-JUL-1997.
PF 19-JAN-1996; 024816.
PR 19-JAN-1996; JP-024816.
PA (ASAK ) ASahi BREWERIES LTD.
PA (NIKK-) NIKKA WHISKEY KK.
PA (TORI ) TORII YAKUHIIN KK.
PA (TSUR/) TSURA T.
DR WPI; 97-429186/40.
PT Humanised, semi-chimeric and chimeric antibodies against human
PT high-affinity IgE receptor - useful medicinally and have low
PS Claim 8; Page 15; 26pp; Japanese.
CC The present sequence, the heavy chain variable region of a
CC chimeric human CRA2 antibody (Ab), comprises complementarity
CC determining regions (CDR) from a murine, anti-human high affinity
CC immunoglobulin E (IgE) receptor, monoclonal Ab (MAb). The
CC humanised chimeric MAb can be used to treat or prevent diseases,
CC specifically allergies, associated with the receptor, and has very
CC low antigenicity in humans.
CC Sequence 117 AA;

Query Match      83.1%; Score 49; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
Db      ||||| ||
       97 ARHNYGMDY 106

RESULT 9
W27526
ID W27526 standard; Protein; 117 AA.
AC W27526;
DT 16-DEC-1997 (first entry)
DE Heavy chain variable region of human CRA2 antibody.
KW Complementarity determining region; CDR; murine; mouse; human;
KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
KW IgE; MAb; heavy chain; variable region; humanised; semi-chimeric;
KW chimeric; treatment; prevention; disease; allergy; CRA2.
OS Homo sapiens.
PN J09191886-A.
PD 29-JUL-1997.
PF 19-JAN-1996; 024816.
PR 19-JAN-1996; JP-024816.
PA (ASAK ) ASahi BREWERIES LTD.
PA (NIKK-) NIKKA WHISKEY KK.
PA (TORI ) TORII YAKUHIIN KK.
PA (TSUR/) TSURA T.
DR WPI; 97-429186/40.
PT Humanised, semi-chimeric and chimeric antibodies against human
PT high-affinity IgE receptor - useful medicinally and have low
PS Claim 2; Page 13; 26pp; Japanese.
CC The present sequence, the heavy chain variable region of a
CC antibody (Ab) CRA2, was used in the preparation of a humanised or
CC semi-chimeric monoclonal Ab (MAb), comprising complementarity
CC determining regions (CDR) from a murine, anti-human high affinity
CC immunoglobulin E (IgE) receptor, MAB. The humanised, semi-chimeric
CC or chimeric MAB can be used to treat or prevent diseases,
CC specifically allergies, associated with the receptor, and has very
CC low antigenicity in humans.
CC Sequence 117 AA;

Query Match      83.1%; Score 49; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
Db      ||||| ||
       97 ARHNYGMDY 106

RESULT 10
W27354
ID W27354 standard; Protein; 117 AA.
AC W27354;
DT 16-DEC-1997 (first entry)
DE Heavy chain variable region of human CRA2 antibody.
KW Complementarity determining region; CDR; murine; mouse; human;
KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
KW IgE; MAb; heavy chain; variable region; humanised; semi-chimeric;
KW chimeric; treatment; prevention; disease; allergy; CRA2.
OS Homo sapiens.
PN J09191886-A.
PD 29-JUL-1997.
PF 19-JAN-1996; 024816.
PR 19-JAN-1996; JP-024816.
PA (ASAK ) ASahi BREWERIES LTD.
PA (NIKK-) NIKKA WHISKEY KK.
PA (TORI ) TORII YAKUHIIN KK.
PA (TSUR/) TSURA T.
DR WPI; 97-429186/40.
DR N-PSDB; T90025.
PT Humanised, semi-chimeric and chimeric antibodies against human
PT high-affinity IgE receptor - useful medicinally and have low
PS antigenicity in humans
PS Disclosure; Fig 1; 26pp; Japanese.
CC The cDNA encoding the present antibody (Ab) CRA2, was used in the preparation
CC of a humanised or semi-chimeric monoclonal Ab (MAb), comprising
CC complementarity determining regions (CDR) from a murine, anti-human
CC high affinity immunoglobulin E (IgE) receptor, MAB. The humanised,
CC semi-chimeric or chimeric MAB can be used to treat or prevent
CC diseases, specifically allergies, associated with the receptor, and
CC has very low antigenicity in humans.
CC Sequence 117 AA;

```

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DE Heavy chain variable region of human CRA2 antibody.
KW Complementarity determining region; CDR; murine; mouse; human;
KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
KW IgE; MAb; heavy chain; variable region; humanised; semi-chimeric;
KW chimeric; treatment; prevention; disease; allergy; CRA2.
OS Homo sapiens.
PN J09191886-A.
PD 29-JUL-1997.
PF 19-JAN-1996; 024816.
PR 19-JAN-1996; JP-024816.
PA (ASAK ) ASahi BREWERIES LTD.
PA (NIKK-) NIKKA WHISKEY KK.
PA (TORI ) TORII YAKUHIIN KK.
PA (TSUR/) TSURA T.
DR WPI; 97-429186/40.
PT Humanised, semi-chimeric and chimeric antibodies against human
PT high-affinity IgE receptor - useful medicinally and have low
PS antigenicity in humans
PS Claim 2; Page 13; 26pp; Japanese.
CC The present sequence, the heavy chain variable region of the human
CC antibody (Ab) CRA2, was used in the preparation of a humanised or
CC semi-chimeric monoclonal Ab (MAb), comprising complementarity
CC determining regions (CDR) from a murine, anti-human high affinity
CC immunoglobulin E (IgE) receptor, MAB. The humanised, semi-chimeric
CC or chimeric MAB can be used to treat or prevent diseases,
CC specifically allergies, associated with the receptor, and has very
CC low antigenicity in humans.
CC Sequence 117 AA;

Query Match      83.1%; Score 49; DB 1; Length 117;
Best Local Similarity 80.0%; Pred. No. 0.16;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFDY 10
Db      ||||| ||
       97 ARHNYGMDY 106

RESULT 10
W27354
ID W27354 standard; Protein; 117 AA.
AC W27354;
DT 16-DEC-1997 (first entry)
DE Heavy chain variable region of human CRA2 antibody.
KW Complementarity determining region; CDR; murine; mouse; human;
KW high affinity; immunoglobulin E; receptor; monoclonal antibody;
KW IgE; MAb; heavy chain; variable region; humanised; semi-chimeric;
KW chimeric; treatment; prevention; disease; allergy; CRA2.
OS Homo sapiens.
PN J09191886-A.
PD 29-JUL-1997.
PF 19-JAN-1996; 024816.
PR 19-JAN-1996; JP-024816.
PA (ASAK ) ASahi BREWERIES LTD.
PA (NIKK-) NIKKA WHISKEY KK.
PA (TORI ) TORII YAKUHIIN KK.
PA (TSUR/) TSURA T.
DR WPI; 97-429186/40.
DR N-PSDB; T90025.
PT Humanised, semi-chimeric and chimeric antibodies against human
PT high-affinity IgE receptor - useful medicinally and have low
PS antigenicity in humans
PS Disclosure; Fig 1; 26pp; Japanese.
CC The cDNA encoding the present antibody (Ab) CRA2, was used in the preparation
CC of a humanised or semi-chimeric monoclonal Ab (MAb), comprising
CC complementarity determining regions (CDR) from a murine, anti-human
CC high affinity immunoglobulin E (IgE) receptor, MAB. The humanised,
CC semi-chimeric or chimeric MAB can be used to treat or prevent
CC diseases, specifically allergies, associated with the receptor, and
CC has very low antigenicity in humans.
CC Sequence 117 AA;

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Query Match 83.1%; Score 49; DB 1; Length 117;
 Best Local Similarity 80.0%; Pred. No. 0.16;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ARHNYGSFDY 10
 DB 97 ARHNYGMDY 106
 ||||| ||
 FT Key Location/Qualifiers
 FT Peptide 1..19 /note= "signal peptide"
 FT Protein 20..239 /note= "mature protein"
 FT J11000174-A.
 PN 06-JAN-1999.
 PD 06-JAN-1999.
 PF 13-JUN-1997; 171232.
 PR 13-JUN-1997; JP-171232.
 PA (ASAK) ASAHI BREWERIES LTD.
 PA (NIKK-) NIKKA WHISKEY KK.
 PA (TORI) TORII YAKUHIN KK.
 PA (TSUR/) TSURA T.
 DR WPI: 99-124394/11.
 DR N-PSDB: X01214.
 PT Preparing an antibody Fab fragment using yeast - in high yield
 PS Claim 6; Page 7; 13pp; Japanese.
 CC This sequence represents a human antiFc epsilon RI alpha chain antibody.
 CC produced using the method of the invention. The method is for preparing
 CC an antibody Fab fragment using the yeast Pichia pastoris as the host
 CC cell. The method can prepare an antibody Fab fragment cost efficiently
 CC and in high yield.
 SQ Sequence 239 AA;

Query Match 83.1%; Score 49; DB 1; Length 239;
 Best Local Similarity 80.0%; Pred. No. 0.33;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ARHNYGSFDY 10
 DB 116 ARHNYGMDY 125
 ||||| ||
 FT Key Location/Qualifiers
 FT Peptide 1..22 /note= "signal peptide"
 FT Protein 23..242 /note= "mature protein"
 FT J11000174-A.
 PN 06-JAN-1999.
 PD 06-JAN-1999.
 PF 13-JUN-1997; 171232.
 PR 13-JUN-1997; JP-171232.
 PA (ASAK) ASAHI BREWERIES LTD.
 PA (NIKK-) NIKKA WHISKEY KK.
 PA (TORI) TORII YAKUHIN KK.

PA (TSUR/) TSURA T.
 DR WPI: 99-124394/11.
 DR N-PSDB: X01216.
 PT Preparing an antibody Fab fragment using yeast - in high yield
 PS Claim 6; Page 9-10; 13pp; Japanese.
 CC This sequence represents a human antiFc epsilon RI alpha chain antibody.
 CC produced using the method of the invention. The method is for preparing
 CC an antibody Fab fragment using the yeast Pichia pastoris as the host
 CC cell. The method can prepare an antibody Fab fragment cost efficiently
 CC and in high yield.
 SQ Sequence 242 AA;

Query Match 83.1%; Score 49; DB 1; Length 242;
 Best Local Similarity 80.0%; Pred. No. 0.33;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 ARHNYGSFDY 10
 DB 119 ARHNYGMDY 128
 ||||| ||
 FT Key Location/Qualifiers
 FT Peptide 1..19 /note= "signal peptide"
 FT Protein 20..239 /note= "mature protein"
 FT J11000174-A.
 PN 06-JAN-1999.
 PD 06-JAN-1999.
 PF 13-JUN-1997; 171232.
 PR 13-JUN-1997; JP-171232.
 PA (ASAK) ASAHI BREWERIES LTD.
 PA (NIKK-) NIKKA WHISKEY KK.
 PA (TORI) TORII YAKUHIN KK.
 PA (TSUR/) TSURA T.
 DR WPI: 99-124394/11.
 DR N-PSDB: X01214.
 PT Preparing an antibody Fab fragment using yeast - in high yield
 PS Claim 6; Page 7; 13pp; Japanese.
 CC This sequence represents a human antiFc epsilon RI alpha chain antibody.
 CC produced using the method of the invention. The method is for preparing
 CC an antibody Fab fragment using the yeast Pichia pastoris as the host
 CC cell. The method can prepare an antibody Fab fragment cost efficiently
 CC and in high yield.
 SQ Sequence 239 AA;

Query Match 81.4%; Score 48; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.019;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ARHNYGSFDY 10
 DB 1 ARHNYGSYAY 10
 ||||| |
 FT Key Location/Qualifiers
 FT Peptide 1..22 /note= "signal peptide"
 FT Protein 23..242 /note= "mature protein"
 FT J11000174-A.
 PN 06-JAN-1999.
 PD 06-JAN-1999.
 PF 13-JUN-1997; 171232.
 PR 13-JUN-1997; JP-171232.
 PA (ASAK) ASAHI BREWERIES LTD.
 PA (NIKK-) NIKKA WHISKEY KK.
 PA (TORI) TORII YAKUHIN KK.

Query Match 81.4%; Score 48; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.019;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ARHNYGSFDY 10
 DB 1 ARHNYGSYAY 10
 ||||| |
 FT Key Location/Qualifiers
 FT Peptide 1..22 /note= "signal peptide"
 FT Protein 23..242 /note= "mature protein"
 FT J11000174-A.
 PN 06-JAN-1999.
 PD 06-JAN-1999.
 PF 13-JUN-1997; 171232.
 PR 13-JUN-1997; JP-171232.
 PA (ASAK) ASAHI BREWERIES LTD.
 PA (NIKK-) NIKKA WHISKEY KK.
 PA (TORI) TORII YAKUHIN KK.

RESULT 14

W76039
ID W76039 standard; Protein; 10 AA.
AC W76039;
DE LM609 grafted antibody V-H region CDR3 protein fragment #15.
DT 02-NOV-1998 (first entry)
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW Vitaxin; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49876.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 43; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 78.0%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
| | | | | | | |
Db 1 ARHNYGSF 8

Search completed: May 27, 2000, 19:21:35
Job time: 1589 sec

PT angiogenesis or restenosis
PS Claim 62; Page 43; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 78.0%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.04;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
| | | | | | | |
Db 1 ARHNYGSF 8

RESULT 15
W76040
ID W76040 standard; Protein; 10 AA.
AC W76040;
DE LM609 grafted antibody V-H region CDR3 protein fragment #16.
DT 02-NOV-1998 (first entry)
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW Vitaxin; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49877.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose

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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:26:42 ; Search time 163.56 Seconds
(without alignments)
3.585 Million cell updates/sec

Title: US-09-016-061-66
Perfect score: 60
Sequence: 1 ARHNYGSPYY 10
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues
Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_63:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	39	65.0	113	2 S26468	Ig heavy chain V r
2	39	65.0	2288	2 T29999	hypothetical prote
3	38	63.3	25	2 PH1886	Ig heavy chain V r
4	38	63.3	25	2 PH1700	Ig heavy chain V r
5	38	63.3	56	2 E49038	Ig lambda chain V
6	38	63.3	130	2 S06817	Ig heavy chain V r
7	38	63.3	144	2 T38634	40s ribosomal prot
8	38	63.3	233	2 S76857	hypothetical prote
9	38	63.3	377	2 I50147	3beta-hydroxy-belt
10	38	63.3	1144	2 A36968	PI-like adhesin pr
11	37	61.7	102	2 S14581	Ig heavy chain V r
12	37	61.7	192	2 T38535	probable transloca
13	37	61.7	386	2 S51436	probable membrane
14	37	61.7	641	2 JC6017	zinc-finger transc
15	36	60.0	82	2 I51106	Major Histocompati
16	36	60.0	89	2 S38688	MHC class II histo
17	36	60.0	89	2 S38683	MHC class II histo
18	36	60.0	89	2 S38684	MHC class II histo
19	36	60.0	225	2 I47095	MHC class II OVAR-
20	36	60.0	306	2 B28170	reaction center pr
21	36	60.0	446	2 T19625	hypothetical prote
22	36	60.0	470	2 H71667	glutamate--tRNA li
23	36	60.0	786	2 S37031	probable succinogl
24	36	60.0	2161	1 A45389	genome polyprotein
25	35.5	59.2	45	2 PL0094	Ig heavy chain V r
26	35	58.3	3	2 S36850	Ig heavy chain V r
27	35	58.3	27	2 PH1719	Ig heavy chain V r
28	35	58.3	98	2 B24754	Ig heavy chain V r
29	35	58.3	108	2 S26316	Ig heavy chain V r
30	35	58.3	110	2 S26317	Ig heavy chain V r

RESULT 1

S26468
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26468
R:Kavaler, J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S26468
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <KAV>
A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 65.0%; Score 39; DB 2; Length 113;
Best Local Similarity 66.7%; Pred. No. 4.4;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSPY 9
Db 93 ARHPYGNYY 101

RESULT 2

T29999
hypothetical protein zc8.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T29999
R:Latrelle, P.; Bradshaw, H.
submitted to the EMBL Data Library, July 1996
A:Description: The sequence of C. elegans cosmid zc8.
A:Reference number: Z20719
A:Accession: T29999
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-2288 <LAT>
A:Cross-references: EMBL:U64862; PIDN:AAB52624.1; GSPDB:GN00028; CESP:zc8.4
A:Experimental source: strain Bristol N2; clone zc8
C:Genetics:
A:Gene: CESP:zc8.4
A:Map position: 10
A:Introns: 43/2; 80/3; 110/3; 153/2; 274/3; 738/2; 1249/1; 1392/3; 1454/1; 1602/1; 16

Query Match 65.0%; Score 39; DB 2; Length 2288;
Best Local Similarity 60.0%; Pred. No. 86;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
: | | | | |
Db 34 SRSNYGEFY 43

RESULT 3

PH1686
Ig heavy chain V region (clone NP-6-17) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1686
R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607
A:Accession: PH1686
A:Molecule type: mRNA
A:Residues: 1-25 <MCH>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 63.3%; Score 38; DB 2; Length 25;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
: | | | | |
Db 13 ARYYGSTY 22

RESULT 4

PH1700
Ig heavy chain V region (clone NP-7-13) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 17-Mar-1999
C:Accession: PH1700
R:McHeyzer-Williams, M.G.; McLean, M.J.; Lalor, P.A.; Nossal, G.J.V.
J. Exp. Med. 178, 295-307, 1993
A:Title: Antigen-driven B cell differentiation in vivo.
A:Reference number: PH1675; MUID:93301607
A:Accession: PH1700
A:Molecule type: mRNA
A:Residues: 1-25 <MCH>
A:Experimental source: B cell
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 63.3%; Score 38; DB 2; Length 25;
Best Local Similarity 70.0%; Pred. No. 1.5;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
: | | | | |
Db 13 ARYYGSSYY 22

RESULT 5

E49038
Ig lambda chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
C:Accession: E49038
R:Weiss, U.; Zobebelein, R.; Rajewsky, K.
Eur. J. Immunol. 22, 511-517, 1992
A:Title: Accumulation of somatic mutants in the B cell compartment after primary immunization.
A:Reference number: A49038; MUID:92164733
A:Accession: E49038
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-56 <WEI>
A:Cross-references: GB:S85736; NID:g246322; PIDN:AAB21563.1; PID:g246323
A:Experimental source: spleen
A:Note: sequence extracted from NCBI backbone (NCBIN:85736, NCBIP:85804)
C:Keywords: heterotetramer; immunoglobulin

Query Match 63.3%; Score 38; DB 2; Length 56;
Best Local Similarity 70.0%; Pred. No. 3.3;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
: | | | | |
Db 42 ARYYGSSYY 51

RESULT 6

S06817
Ig heavy chain V region (clone 11c7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1991 #sequence_revision 11-Nov-1994 #text_change 23-Jul-1999
C:Accession: S06817
R:Miller III, A.; Glasel, J.A.
J. Mol. Biol. 209, 763-778, 1989
A:Title: Comparative sequence and immunochemical analyses of murine monoclonal anti-m
A:Reference number: S06815; MUID:90064531
A:Accession: S06817
A:Molecule type: mRNA
A:Residues: 1-130 <MIL>
A:Cross-references: EMBL:X17165; NID:g51917; PIDN:CAA35043.1; PID:g930155
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>
F:22-96/Disulfide bonds: #status predicted

Query Match 63.3%; Score 38; DB 2; Length 130;
Best Local Similarity 75.0%; Pred. No. 7.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFY 10
: | | | | |
Db 103 YNYGSHY 110

RESULT 7

T38634
40S ribosomal protein S10 - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T38634
R:McLean, J.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z21722
A:Accession: T38634
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-144 <MCL>
A:Cross-references: EMBL:Z98979; PIDN:CAB11701.1; GSPDB:GN00066; SPDB:SPAC31G5.17c
A:Experimental source: strain 972h-; cosmid c31G5
C:Genetics:
A:Gene: SPDB:SPAC31G5.17c
A:Map position: 1
A:Introns: 26/1

Query Match 63.3%; Score 38; DB 2; Length 144;
Best Local Similarity 66.7%; Pred. No. 8.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFY 10
: | | | | |
Db 58 RYNGWFY 66

```
RESULT 8
S76857
hypothetical protein - Synecocystis sp. (strain PCC 6803)
C:Species: Synecocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S76857
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
s.
A:Reference number: S74322; MUID:97061201
A:Accession: S76857
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-233 <KAN>
A:Cross-references: EMBL:D90917; GB:AB001339; NID:g1653836; PIDN:BAA18769.1; PID:d101950
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 63.3%; Score 38; DB 2; Length 233;
Best Local Similarity 55.6%; Pred. No. 14;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFY 10
||:::|
Db 98 RHYSGTLY 106

RESULT 9
I50147
3beta-hydroxy-Delta5-steroid dehydrogenase multifunctional protein - chicken
N:Contains: 3beta-hydroxy-Delta5-steroid dehydrogenase (BC 1.1.1.145); steroid Delta-5
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 11-Jun-1999
C:Accession: I50147; I50220
R:Nakabayashi, O.; Nomura, O.; Nishimori, K.; Mizuno, S.
Gene 162, 261-265, 1995
A:Title: The cDNA cloning and transient expression of a chicken gene encoding a 3 beta-h
A:Reference number: I50147; MUID:96032354
A:Accession: I50147
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-377 <NAK>
A:Cross-references: GB:D43762; NID:g1019355; PIDN:BAA07819.1; PID:g1019356
A:Accession: I50220
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-377 <NA2>
A:Cross-references: GB:D43763; NID:g1019357; PIDN:BAA07820.1; PID:g1019358
C:Superfamily: 3beta-hydroxy-Delta5-steroid dehydrogenase
C:Keywords: intramolecular oxidoreductase; isomerase; NAD; oxidoreductase; steroid biosy

Query Match 63.3%; Score 38; DB 2; Length 377;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
||| |
Db 250 ARHNGQFY 259

RESULT 10
A36968
PI-like adhesin precursor - Mycoplasma pirum
C:Species: Mycoplasma pirum
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 07-Dec-1999
C:Accession: A36968
R:Tham, T.N.; Ferris, S.; Bahraoui, E.; Canarelli, S.; Montagnier, L.; Blanchard, A.
```

```
J. Bacteriol. 176, 781-788, 1994
A:Title: Molecular characterization of the PI-like adhesin gene from Mycoplasma pirum
A:Reference number: A36968; MUID:94131957
A:Accession: A36968
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1144 <THA>
A:Cross-references: GB:L19685; NID:g404770; PIDN:AAC36866.1; PID:g404771
C:Genetics:
A:Genetic code: SGC3
```

```
Query Match 63.3%; Score 38; DB 2; Length 1144;
Best Local Similarity 55.6%; Pred. No. 65;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 2 RHNYGSFY 10
: |||::|
Db 885 KQNYGSFY 893
```

```
RESULT 11
SI4581
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999
C:Accession: SI4581
R:Chen, Q.; Stenzel-Poore, M.; Rittenberg, M.B.
submitted to the EMBL Data Library, March 1991
A:Description: Natural polyclonal antibodies differ from Ag-induced antibodies in V
A:Reference number: SI4484
A:Accession: SI4581
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-102 <CHE>
A:Cross-references: EMBL:X58653; NID:g51295; PIDN:CAA41510.1; PID:g51296
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>
```

```
Query Match 61.7%; Score 37; DB 2; Length 102;
Best Local Similarity 70.0%; Pred. No. 9;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 1 ARHNYGSFY 10
||:::|
Db 89 ARWHYGSFY 98
```

```
RESULT 12
T38535
probable translocation protein - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C:Accession: T38535
R:Oliver, K.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Wood, V.
submitted to the EMBL Data Library, September 1997
A:Reference number: Z21748
A:Accession: T38535
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-192 <OLI>
A:Cross-references: EMBL:Z99165; PIDN:CAB16260.1; GSPDB:GN00066; SPDB:SPAC2F3.02
A:Experimental source: strain 972h-; cosmid c2F3
C:Genetics:
A:Gene: SPDB:SPAC2F3.02
A:Map position: 1
```

```
Query Match 61.7%; Score 37; DB 2; Length 192;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

QY 2 RHNYGSFY 10
I:||||
Db 139 RNYGKCY 147

RESULT 13

S51436
probable membrane protein YLR191w - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein L9470.1

C:Species: Saccharomyces cerevisiae

C:Date: 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 06-Feb-1998

C:Accession: S51436

R:Wohldmann, P.

submitted to the EMBL Data Library, November 1994

A:Description: The sequence of S. cerevisiae cosmid 9470.

A:Reference number: S51414

A:Accession: S51436

A:Molecule type: DNA

A:Residues: 1-386 <WOH>

A:Cross-references: EMBL:U17246; NID:g577192; PID:g577193; MIPS:YLR191w

C:Genetics:

A:Gene: SGD:PEX13

A:Cross-references: SGD:S0004181; MIPS:YLR191w

A:Map position: 12R

C:Superfamily: SH3 homology

C:Keywords: transmembrane protein

F:264-280/Domain: transmembrane #status predicted <TMM>

F:313-367/Domain: SH3 homology <SH3>

Query Match

61.7%; Score 37; DB 2; Length 386;

Best Local Similarity 85.7%; Pred. No. 34;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSFY 9

I:|||||

Db 117 NNYGSFY 123

RESULT 14

JC6017

zinc-finger transcription factor pacc - Penicillium chrysogenum

N:Alternate names: Pacc protein

C:Species: Penicillium chrysogenum

C:Date: 15-Aug-1996 #sequence_revision 18-Oct-1996 #text_change 09-Sep-1997

C:Accession: JC6017

R:Suarez, T.; Penalba, M.A.

Mol. Microbiol. 20, 529-540, 1996

A:Title: Characterization of a Penicillium chrysogenum gene encoding a Pacc transcription factor

A:Reference number: JC6017; MUID:96347125

A:Accession: JC6017

A:Molecule type: mRNA

A:Residues: 1-641 <SUA>

A:Cross-references: GB:U44726; NID:g1403693; PID:g1403694

A:Experimental source: NRRL1951

C:Genetics:

A:Gene: pacc

A:Introns: 74/3

C:Function:

A:Description: an activator of transcription of the isopenicillin N synthase, and it med

C:Keywords: transcription factor; zinc finger

F:1-52/Region: alanine/threonine-rich

F:30-50/Region: conserved

F:58-144/Region: zinc fingers

F:290-299/Region: glycine-rich

Query Match

61.7%; Score 37; DB 2; Length 641;

Best Local Similarity 62.5%; Pred. No. 55;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFY 10

I:||||
Db 210 HSYGNLY 217

RESULT 15

I51106

Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)

C:Species: Phasianus colchicus (ring-necked pheasant)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999

C:Accession: I51106

R:Witzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.

Immunogenetics 39, 395-403, 1994

A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-ne

A:Reference number: I51103; MUID:94245280

A:Accession: I51106

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-82 <WIT>

A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927

C:Superfamily: class II histocompatibility antigen; Immunoglobulin homology

Query Match

60.0%; Score 36; DB 2; Length 82;

Best Local Similarity 85.7%; Pred. No. 11;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

I:|||||

Db 75 RHNYGVF 81

Search completed: May 27, 2000, 19:26:43

Job time: 1766 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 20:07:15 ; Search time 69.28 Seconds
(without alignments)
4.396 Million cell updates/sec

Title: US-09-016-061-66
Perfect score: 60
Sequence: 1 ARHNYGSFYY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	38	63.3	144	1 RS10_SCHPO	O14112 schizosacch
2	37	61.7	386	1 PEXD_YEAST	P80667 saccharomyc
3	36	60.0	305	1 RCYM_RHORI	P10718 rhodospiril
4	36	60.0	470	1 SYE2_RICPR	P92ct8 rickettsia
5	36	60.0	786	1 EXOP_RHIME	P33698 rhizobium m
6	35	58.3	316	1 YX12_CAEEL	Q11123 caenorhabdi
7	35	58.3	583	1 INV3_DAUCA	Q39693 daucus caro
8	35	58.3	592	1 INV1_DAUCA	P26792 daucus caro
9	35	58.3	592	1 INV2_DAUCA	Q39692 daucus caro
10	34	56.7	275	1 IF2A_PVRHO	O38655 pyrococcus
11	34	56.7	284	1 IPYR_PICPA	O13505 pichia past
12	34	56.7	286	1 IPYR_KLULA	P13998 kluyveromyc
13	34	56.7	286	1 IPYR_YEAST	P00817 saccharomyc
14	34	56.7	306	1 RCYM_CHLAU	P09438 chloroflexu
15	34	56.7	323	1 RCYM_RHOVI	P06010 rhodopseu
16	34	56.7	361	1 LIMA_MOUSE	P53776 mus musculu
17	34	56.7	1135	1 NINS_DROME	P10677 drosophila
18	34	56.7	1501	1 NINL_DROME	P10676 drosophila
19	33	55.0	347	1 UL33_HSV6U	P52380 herpes simp
20	33	55.0	349	1 PHOE_KLEOX	Q01606 klebsiella
21	33	55.0	349	1 XYJ9_YEAST	P41903 saccharomyc
22	33	55.0	351	1 PHOE_KLEPN	P30704 klebsiella
23	33	55.0	359	1 OM21_HAEIN	P43839 haemophilus
24	33	55.0	360	1 OM26_HAEIN	Q48216 haemophilus
25	33	55.0	361	1 OM22_HAEIN	P20149 haemophilus
26	33	55.0	361	1 OM29_HAEIN	Q48217 haemophilus
27	33	55.0	363	1 OM2B_HAEIN	Q48220 haemophilus
28	33	55.0	367	1 OM2A_HAEIN	Q48219 haemophilus
29	33	55.0	369	1 OM27_HAEIN	Q48218 haemophilus
30	33	55.0	371	1 OM25_HAEIN	P46027 haemophilus
31	33	55.0	385	1 OM23_HAEIN	P46025 haemophilus
32	33	55.0	386	1 OM24_HAEIN	P46026 haemophilus
33	33	55.0	423	1 VI07_VACCC	P20501 vaccinia vi
34	33	55.0	423	1 VI07_VACCV	P12926 vaccinia vi

35	33	55.0	423	1	VI07_VARV	P33003 variola vir
36	33	55.0	448	1	NCAP_CVHOC	P33469 human coron
37	33	55.0	473	1	SYE_AQUAE	O6771 aquifex aeo
38	33	55.0	494	1	RNHL_CRIFA	Q07762 crithidia f
39	33	55.0	512	1	PNTA_HAEIN	P43842 haemophilus
40	33	55.0	514	1	LIM_HALRO	Q25132 halocynthia
41	33	55.0	527	1	NU2M_ACACA	Q37376 acanthamoeb
42	33	55.0	550	1	MPT1_XENLA	P30309 xenopus lae
43	33	55.0	650	1	CG45_YEAST	Q08032 saccharomyc
44	33	55.0	715	1	ADSV_BOVIN	Q28046 bos taurus
45	33	55.0	1323	1	RRPO_SMYEA	P28897 strawberry

ALIGNMENTS

RESULT 1
RS10_SCHPO
ID RS10_SCHPO STANDARD; PRT; 144 AA.
AC O14112;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 40S RIBOSOMAL PROTEIN S10.
GN RPS10 OR SPAC31G5.17C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
OC Schizosaccharomycetaceae; Schizosaccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-972;
RA McLean J., Harris D., Barrell B.G., Rajandream M.A., Wood V.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE S10E FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; 298979; CAB11701.1; -.
KW Ribosomal protein.
SQ SEQUENCE 144 AA; 16275 MW; C0F58FEBEDB8905 CRC64;

Query Match 63.3%; Score 38; DB 1; Length 144;
Best Local Similarity 66.7%; Pred. No. 4;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Oy 2 RHNYGSFYY 10
Db 58 RYNGWFYY 66
1:1:1111

RESULT 2
PEXD_YEAST
ID PEXD_YEAST STANDARD; PRT; 386 AA.
AC P80667;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PEROXISOMAL MEMBRANE PROTEIN PAS20 (PEROXIN-13).
GN PEX13 OR PAS20 OR YER191W OR L9470.1.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97011156.
RA Elgersma Y., Kwast L., Klein A., Voorn-Brouwer T., van den Berg M.,

RA Tabak H.F., Distel B.;
RT "The SH3 domain of the Saccharomyces cerevisiae peroxisomal membrane
RT protein Pex13p functions as a docking site for Pex5p, a mobile
RT receptor for the import pTsl-containing proteins.";
RL J. Cell Biol. 135:97-109(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favetto A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
RA Hallsworth K., Hawkins J., Hillier L., Jler M., Johnson D.,
RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
RA Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
RA Taich A., Trevasakis E., Vignati D., Wilcox L., Wohlman P., Vaudin M.,
RA Wilson R., Waterston R.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
RC STRAIN-S288C;
RX MEDLINE; 97011157.
RA Erdmann R., Blobel G.;
RT Identification of Pex13p a peroxisomal membrane receptor for the
RT Pts1 recognition factor.;
RL J. Cell Biol. 135:111-121(1996).
CC -!- FUNCTION: COMPONENT OF THE PEROXISOMAL TRANSLLOCATION MACHINERY
CC WITH PEX14 AND PEX17. INTERACTS WITH THE Pts1 RECEPTOR
(PAS10/PEX5).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PEROXISOMAL.
CC -!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -----
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CC -----
DR EMBL; S82971; AAB46885.1; -;
DR EMBL; U37420; AAA79308.1; -;
DR EMBL; U17246; AAB67453.1; -;
DR EMBL; U14913; AAB67448.1; -;
DR HSP; Q06187; 1AWW.
DR SGD; L003024; PAS20.
DR PRINTS; PR00452; SH3DOMAIN.
DR PROSITE; PS50002; SH3; 1.
DR PFAM; PF00018; SH3; 1.
KW Peroxisome; Transport; Protein transport; Transmembrane; SH3 domain.
FT DOMAIN 1 263 LUMENAL (POTENTIAL).
FT TRANSMEM 264 280 POTENTIAL.
FT DOMAIN 281 386 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 306 372 SH3.
SQ SEQUENCE 386 AA; 42706 MW; DBEA9A2372185860 CRC64;

Query Match 61.7%; Score 37; DB 1; Length 386;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSFY 9
Db 117 HNYGSFY 123

RESULT 3
RCM_RHURU STANDARD; PRT; 305 AA.
AC P10718;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE REACTION CENTER PROTEIN M CHAIN (PHOTOSYNTHETIC REACTION CENTER M
DE SUBUNIT).

GN PUFM.
OS Rhodospirillum rubrum.
OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
OC Rhodospirillum.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88227960.
RA Belanger G., Berard J., Corriveau P., Gingras G.;
RT "The structural genes coding for the L and M subunits of
RT Rhodospirillum rubrum photoreaction center.";
RL J. Biol. Chem. 263:7632-7638(1988).
RN [2]
RP SEQUENCE OF 1-50.
RX MEDLINE; 84133817.
RA Theiller R., Suter F., Zuber H.;
RT N-terminal sequences of subunits L and M of the photosynthetic
RT reaction centre from Rhodospirillum rubrum G-9+. Separation of the
RT subunits by gel filtration on hydroxypropylated Sephadex G 100 in
RT organic solvents.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:1765-1776(1983).
CC -!- FUNCTION: THE REACTION CENTER IS A MEMBRANE-BOUND COMPLEX THAT
CC MEDIATES THE INITIAL PHOTOCHEMICAL EVENT IN THE ELECTRON TRANSFER
CC PROCESS OF PHOTOSYNTHESIS.
CC -!- SUBUNIT: REACTION CENTER IS COMPOSED OF FOUR BACTERIOCHLOROPHYLLS,
CC TWO BACTERIOPEOPHYTINS, TWO UBIQUINONES, ONE IRON, AND THREE
CC HIGHLY HYDROPHOBIC POLYPEPTIDE CHAINS (DESIGNATED L, M, AND H).
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC -!- SIMILARITY: BELONGS TO THE REACTION CENTER L/M CHAINS / PSBA /
CC PSBD FAMILY.
CC -----
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CC -----
DR EMBL; J03731; AAA26465.1; -;
DR PIR; B28170; B28170.
DR HSP; P02953; 2RCR.
DR PRINTS; PR00256; REACTNCENTRE.
DR PROSITE; PS00244; REACTION_CENTER; 1.
DR PFAM; PF00124; photoRC; 1.
KW Transmembrane; Electron transport; Photosynthesis; Reaction center;
KW INIT_MET 0 0
FT TRANSMEM 52 78
FT TRANSMEM 110 139
FT TRANSMEM 142 167
FT TRANSMEM 197 225
FT TRANSMEM 259 285
FT METAL 200 200
FT METAL 217 217
FT METAL 232 232
FT METAL 264 264
FT BINDING 250 250
SQ SEQUENCE 305 AA; 34017 MW; 75B2A5236F0EDB79 CRC64;

Query Match 60.0%; Score 36; DB 1; Length 305;
Best Local Similarity 71.4%; Pred. No. 20;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFY 10
Db 190 NYGNFFY 196

RESULT 4
SYE2_RICPR STANDARD; PRT; 470 AA.
ID SYE2_RICPR
AC Q9ZCT8;

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DR EMBL; U39744; AA80440.1; -
 DR WORMPEP; C03F11.2; C803914.
 KW Hypothetical protein.
 SQ SEQUENCE 316 AA; 35107 MW; 6A725FCAC21CF676 CRC64;

Query Match 58.3%; Score 35; DB 1; Length 316;
 Best Local Similarity 60.0%; Pred. No. 31;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNGSFYY 10
 Db 69 ARHFGSYEY 78

RESULT 7
 INV3_DAUCA STANDARD; PRT; 583 AA.
 ID INV3_DAUCA
 AC Q39693;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 3 PRECURSOR (EC 3.2.1.26)
 DE (SUCROSE-6-PHOSPHATE HYDROLASE 3) (INVERTASE 3) (CELL WALL BETA-
 DE FRUCTOSIDASE 3).
 GN INV3.

OS Daucus carota (Carrot).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. QUEEN ANNE'S LACE;
 RX MEDLINE; 93306787.

RA Lorenz K., Lienhard S., Sturm A.;
 RT "Structural organization and differential expression of carrot beta-
 RT fructofuranosidase genes: identification of a gene coding for a
 RT flower bud-specific isozyme."
 RL Plant Mol. Biol. 28:189-194(1995).

CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN PHLOEM UNLOADING AND IN
 CC STRESS RESPONSE.

CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING BETA-D-
 CC FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES.

CC -1- SUBCELLULAR LOCATION: IONICALLY BOUND TO THE CELL WALL.

CC -1- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.

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DR EMBL; X78423; CAA55188.1; -
 DR PROSITE; P500609; GLYCOSYL_HYDROL_F32; 1.
 DR PFAM; PF00251; Glyco_hydro_32; 1.
 KW Hydrolase; Glycosidase; Glycoprotein; Cell wall; Zymogen; Signal.
 FT SIGNAL 1 ?
 FT PROPEP ? ?
 FT CHAIN ? 583
 FT BETA-FRUCTOFURANOSIDASE, INSOLUBLE
 FT ISOENZYME 3.
 FT CARBOHYD 164 164
 FT CARBOHYD 280 280
 FT CARBOHYD 303 303
 FT CARBOHYD 340 340

FT CARBOHYD 561 561 POTENTIAL.
 SQ SEQUENCE 583 AA; 66381 MW; 1DBF591CD94749AF CRC64;

Query Match 58.3%; Score 35; DB 1; Length 583;
 Best Local Similarity 62.5%; Pred. No. 58;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYSGFY 9
 Db 313 RYDYGNEY 320

RESULT 8
 INV1_DAUCA STANDARD; PRT; 592 AA.
 ID INV1_DAUCA
 AC P26792;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 1 PRECURSOR (EC 3.2.1.26)
 DE (SUCROSE-6-PHOSPHATE HYDROLASE 1) (INVERTASE 1) (CELL WALL BETA-
 DE FRUCTOSIDASE 1).
 GN INV1.

OS Daucus carota (Carrot).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.

RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC STRAIN=CV. QUEEN ANNE'S LACE;
 RX MEDLINE; 93005650.

RA Sturm A., Chrispeels M.J.;

RT "cDNA cloning of carrot extracellular beta-fructosidase and its
 RT expression in response to wounding and bacterial infection."
 RL Plant Cell 2:1107-1119(1990).
 RN [2]
 RP SEQUENCE FROM N.A.

RX MEDLINE; 94035200.

RA Ramloch-Lorenz K., Knudsen S., Sturm A.;

RT "Molecular characterization of the gene for carrot cell wall beta-
 RT fructosidase."
 RL Plant J. 4:545-554(1993).

CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN PHLOEM UNLOADING AND IN
 CC STRESS RESPONSE.

CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING BETA-D-
 CC FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES.

CC -1- SUBCELLULAR LOCATION: IONICALLY BOUND TO THE CELL WALL.

CC -1- TISSUE SPECIFICITY: IN LEAVES AND ROOTS OF YOUNG PLANTS.

CC -1- INDUCTION: IN RESPONSE TO WOUNDING AND BACTERIAL INFECTION.

CC -1- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.

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DR EMBL; M58362; AAA03516.1; -
 DR EMBL; X69321; CAA49162.1; -
 DR PIR; JQ0991; JQ0991.
 DR PROSITE; P500609; GLYCOSYL_HYDROL_F32; 1.
 DR PFAM; PF00251; Glyco_hydro_32; 1.
 KW Hydrolase; Glycosidase; Glycoprotein; Cell wall; Zymogen; Signal.
 FT SIGNAL 1 31
 FT PROPEP 32 48
 FT CHAIN 49 592
 FT BETA-FRUCTOFURANOSIDASE, INSOLUBLE
 FT ISOENZYME 1.
 FT ACT_SITE 74 74
 FT CARBOHYD 170 170
 FT CARBOHYD 195 195
 FT N-LINKED (GLCNAC. . .) (COMPLEX).
 FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 311 311 N-LINKED (GLCNAC...) (COMPLEX).
FT CARBOHYD 348 348 N-LINKED (GLCNAC...) (HIGH MANNOS).
FT CARBOHYD 570 570 N-LINKED (GLCNAC...) (POTENTIAL).
FT CONFLICT 133 133 R -> W (IN REF. 2).
FT CONFLICT 487 487 A -> V (IN REF. 2).
SQ SEQUENCE 592 AA; 66813 MW; E3DF85355D277D0C CRC64;

Query Match 58.3%; Score 35; DB 1; Length 592;
Best Local Similarity 62.5%; Pred. No. 58;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9
DB 321 RYDYGNYF 328
I::|::|

RESULT 9
INV2_DAUCA
ID INV2_DAUCA STANDARD; PRT; 592 AA.
AC Q39692;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 2 PRECURSOR (EC 3.2.1.26)
DE (SUCROSE-6-PHOSPHATE HYDROLASE 2) (INVERTASE 2) (CELL WALL BETA-FRUCTOSIDASE 2).
GN INV2.
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. QUEEN ANNE'S LACE;
RX MEDLINE; 95306787.
RA Lorenz K., Lienhard S., Sturm A.;
RT "Structural organization and differential expression of carrot beta-fructofuranosidase genes: identification of a gene coding for a flower bud-specific isozyme.";
RT Plant Mol. Biol. 28:189-194(1995).
RL
CC -!- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN PHLOEM UNLOADING AND IN STRESS RESPONSE.
CC
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING BETA-D-FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES.
CC -!- SUBCELLULAR LOCATION: IONICALLY BOUND TO THE CELL WALL.
CC -!- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
CC
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CC
CC EMBL; X78424; CAA55189.1; -.
CC PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.
DR PFAM; PF00251; Glyco_hydro_32; 1.
DR Hydrolase; Glycosidase; Glycoprotein; Cell wall; Zymogen; Signal.
KW SIGNAL
FT PROPEP 1 ? POTENTIAL.
FT CHAIN 7 ? POTENTIAL.
FT ACT_SITE 75 75 BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 2.
FT CARBOHYD 171 171 BY SIMILARITY.
FT CARBOHYD 195 195 POTENTIAL.
FT CARBOHYD 310 310 POTENTIAL.
FT CARBOHYD 347 347 POTENTIAL.
FT CARBOHYD 568 568 POTENTIAL.
SQ SEQUENCE 592 AA; 67397 MW; 2734603836709133 CRC64;

Query Match 58.3%; Score 35; DB 1; Length 592;
Best Local Similarity 62.5%; Pred. No. 58;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9
DB 320 RYDYGNYF 327
I::|::|

RESULT 10
IF2A_PYRHO
ID IF2A_PYRHO STANDARD; PRT; 275 AA.
AC O58655;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
GN PH0961.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE; 98344137.
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
CC
CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA (BY SIMILARITY).
CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA CHAIN (BY SIMILARITY).
CC
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CC
CC EMBL; AP000004; BAA30058.1; -.
DR PFAM; PF00575; Sl; 1.
KW Initiation factor; Protein biosynthesis.
SQ SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;

Query Match 56.7%; Score 34; DB 1; Length 275;
Best Local Similarity 83.3%; Pred. No. 40;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
DB 23 HNYGAF 28
I::|::|

RESULT 11
IPYR_PICPA
ID IPYR_PICPA STANDARD; PRT; 284 AA.
AC O13505;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-HYDROLASE) (PPASE).
GN IPPI.
OS Pichia pastoris (Yeast).

CC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 RN Saccharomycetaceae; Pichia.
 [1]
 RC SEQUENCE FROM N.A.
 RC STRAIN=NREL Y-11430;
 RX MEDLINE; 99034033.
 RA Cosano I.C., Alvarez P., Molina M., Nombela C.;
 RT "Cloning and sequence analysis of the Pichia pastoris TRP1 and
 RT HIS3 genes.";
 CC Yeast 14:861-867(1998).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; AJ001000; CAA04453.1; -.
 DR HSSP; P00817; IWGI.
 DR PROSITE; PS00387; PPASE; 1.
 DR PFAM; PF00719; Pyrophosphatase; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 284 AA; 31937 MW; 3DAD2790D7775D6 CRC64;

 Query Match 56.7%; Score 34; DB 1; Length 284;
 Best Local Similarity 83.3%; Pred. No. 41;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HNYGSF 8
 DB 91 HNYGAF 96
 ||||:|
 RESULT 12
 IPYR_KLULA STANDARD; PRT; 286 AA.
 AC P13998;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI OR IPP.
 OS Kluyveromyces lactis (Yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 CC Saccharomycetaceae; Kluyveromyces.
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 89189093.
 RA Stark M.J.R., Milner J.S.;
 RT "Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a
 RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
 RT and histone H3.";
 RL Yeast 5:35-50(1989).
 RN [2]
 RN SIMILARITY TO E. COLI AND YEAST PPASES.
 RX MEDLINE; 90254161.
 RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RT "Conservation of functional residues between yeast and E. coli
 RT inorganic pyrophosphatases.";

RL Biochim. Biophys. Acta 1038:338-345(1990).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; X14230; CAA32446.1; -.
 DR PIR; S07894; PWVKL.
 DR HSSP; P00817; IWGI.
 DR PROSITE; PS00387; PPASE; 1.
 DR PFAM; PF00719; Pyrophosphatase; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 286 AA; 32034 MW; 11647F4ABD916A2F CRC64;

 Query Match 56.7%; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 42;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HNYGSF 8
 DB 91 HNYGAF 96
 ||||:|
 RESULT 13
 IPYR_YEAST STANDARD; PRT; 286 AA.
 ID AC P00817;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI OR PPAL OR PPA OR YBR011C OR YBR0202.
 OS Saccharomyces cerevisiae (Baker's yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 CC Saccharomycetaceae; Saccharomyces.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=X2180;
 RX MEDLINE; 89083474.
 RA Kolakowski L.F. Jr., Schloesser M., Cooperman B.S.;
 RT "Cloning, molecular characterization and chromosome localization of
 RT the inorganic pyrophosphatase (PPA) gene from S. cerevisiae.";
 RL Nucleic Acids Res. 16:10441-10452(1988).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=S288C;
 RA Entian K.-D., Koetter P., Rose M., Li Z., Thermann R., Brendel M.,
 RA Baur A., Boles E., Miosga T., Schaaff-Gerstenschlaeger I.,
 RA Zimmermann F.K.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE.. 78087552.
 RX Cohen S.A., Steiner R., Keim P.S., Heinrichson R.L.;
 RT "Covalent structural analysis of yeast inorganic pyrophosphatase.";
 RL J. Biol. Chem. 253:889-897(1978).
 RN [4]
 RN SEQUENCE OF 25-35 AND 239-251.

ID RCEN_CHLAW STANDARD; PRT; 306 AA.
 AC P09438;
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE REACTION CENTER PROTEIN M CHAIN (PHOTOSYNTHETIC REACTION CENTER M
 DE SUBUNIT).
 GN PUFM.
 OS Chloroflexus aurantiacus.
 OC Bacteria; Green non-sulfur bacteria; Chloroflexaceae group;
 OC Chloroflexaceae; Chloroflexus.
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE; 88242827.
 RA Ochinnikov Y.A., Abdulaev N.G., Shmuckler B.E., Zargarov A.A.,
 RA Kutuzov M.A., Telezhinskaya I.N., Levina N.B., Zolotarev A.S.;
 RT "Photosynthetic reaction centre of Chloroflexus aurantiacus. Primary
 RT structure of M-subunit.";
 RL FEBS Lett. 232:364-368(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-J10-FL;
 RX MEDLINE; 89210866.
 RA Shiozawa J.A., Lottspeich F., Oesterheld D., Feick R.;
 RT "The primary structure of the Chloroflexus aurantiacus
 RT reaction-center polypeptides.";
 RL Eur. J. Biochem. 180:75-84(1989).
 CC -|- FUNCTION: THE REACTION CENTER IS A MEMBRANE-BOUND COMPLEX THAT
 CC MEDIATES THE INITIAL PHOTOCHEMICAL EVENT IN THE ELECTRON TRANSFER
 CC PROCESS OF PHOTOSYNTHESIS.
 CC -|- SUBUNIT: REACTION CENTER IS COMPOSED OF FOUR BACTERIOCHLOROPHYLLS,
 CC TWO BACTERIOPEOPHYTINS, TWO UBIQUINONES, ONE IRON, AND TWO
 CC HIGHLY HYDROPHOBIC POLYPEPTIDE CHAINS (DESIGNATED L AND M).
 CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -|- SIMILARITY: BELONGS TO THE REACTION CENTER L/M CHAINS / PSBA /
 CC PSBD FAMILY.
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 CC -----
 DR EMBL; X07847; CAA30694.1; -.
 DR EMBL; X14979; CAA33103.1; -.
 DR PIR; S03567; WNJXM.
 DR HSP; P02953; 2RCR.
 DR PROSITE; PS00244; REACTION_CENTER; 1.
 DR PFAM; PF00124; photoRC; 1.
 KW Transmembrane; Electron transport; Photosynthesis; Reaction center;
 KW Iron; Magnesium.
 FT INIT MET 0 0
 FT MOD_RES 1 1 BLOCKED.
 FT TRANSMEM 44 68 POTENTIAL.
 FT TRANSMEM 102 122 POTENTIAL.
 FT TRANSMEM 132 152 POTENTIAL.
 FT TRANSMEM 195 215 POTENTIAL.
 FT TRANSMEM 256 276 POTENTIAL.
 FT METAL 191 191 MAGNESIUM (BACTERIOCHLOROPHYLL B).
 FT METAL 208 208 IRON (NON HAEM).
 FT METAL 235 235 IRON (NON HAEM).
 FT METAL 255 255 IRON (NON HAEM).
 SQ SEQUENCE 306 AA; 34835 MW; D8A938C32A5B86B1 CRC64;

Query Match 56.7%; Score 34; DB 1; Length 306;
 Best Local Similarity 83.3%; Pred. No. 44;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 5 YGSEFY 10
 ||:|

Db 182 YGNFY 187
 RESULT 15
 RCEN_RHOVI STANDARD; PRT; 323 AA.
 AC P06010;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE REACTION CENTER PROTEIN M CHAIN (PHOTOSYNTHETIC REACTION CENTER M
 DE SUBUNIT).
 GN PUFM.
 OS Rhodospseudomonas viridis.
 OC Bacteria; Proteobacteria; alpha subdivision; Ancylobacter group;
 OC Blastochloris.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DSM 133;
 RA Michel H., Weyer K.A., Gruenberg H., Dunger I., Oesterheld D.,
 RA Lottspeich F.;
 RT "The 'light' and 'medium' subunits of the photosynthetic reaction
 RT centre from Rhodospseudomonas viridis: isolation of the genes,
 RT nucleotide and amino acid sequence.";
 RL EMBO J. 5:1149-1158(1986).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
 RA Deisenhofer J., Epp O., Miki K., Huber R., Michel H.;
 RT "Structure of the protein subunits in the photosynthetic reaction
 RT centre of Rhodospseudomonas viridis at 3-A resolution.";
 RL Nature 318:618-624(1985).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).
 RX MEDLINE; 85083091.
 RA Deisenhofer J., Epp O., Miki K., Huber R., Michel H.;
 RT "X-ray structure analysis of a membrane protein complex. Electron
 RT density map at 3-A resolution and a model of the chromophores of the
 RT photosynthetic reaction center from Rhodospseudomonas viridis.";
 RL J. Mol. Biol. 180:385-398(1984).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.45 ANGSTROMS).
 RC STRAIN-DSM 133;
 RX MEDLINE; 98035456.
 RA Lancaster C.R.D., Michel H.;
 RT "The coupling of light-induced electron transfer and proton uptake as
 RT derived from crystal structures of reaction centres from
 RT Rhodospseudomonas viridis modified at the binding site of the
 RT secondary quinone, QB.";
 RL Structure 5:1339-1359(1997).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS).
 RC STRAIN-DSM 133;
 RX MEDLINE; 99150431.
 RA Lancaster C.R.D., Michel H.;
 RT "Refined crystal structures of reaction centres from Rhodospseudomonas
 RT viridis in complexes with the herbicide atrazine and two chiral
 RT atrazine derivatives also lead to a new model of the bound
 RT carotenoid.";
 RL J. Mol. Biol. 286:883-898(1999).
 CC -|- FUNCTION: THE REACTION CENTER IS A MEMBRANE-BOUND COMPLEX THAT
 CC MEDIATES THE INITIAL PHOTOCHEMICAL EVENT IN THE ELECTRON TRANSFER
 CC PROCESS OF PHOTOSYNTHESIS.
 CC -|- SUBUNIT: REACTION CENTER IS COMPOSED OF FOUR BACTERIOCHLOROPHYLLS,
 CC TWO BACTERIOPEOPHYTINS, TWO UBIQUINONES, ONE IRON, AND THREE
 CC HIGHLY HYDROPHOBIC POLYPEPTIDE CHAINS (DESIGNATED L, M, AND H).
 CC -|- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -|- SIMILARITY: BELONGS TO THE REACTION CENTER L/M CHAINS / PSBA /
 CC PSBD FAMILY.
 CC -----
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DR EMBL: X03915; CAA27551.1; -.
DR PIR; B25102; B25102.
DR PDB; 1PRC; 15-OCT-94.
DR PDB; 2PRC; 01-APR-99.
DR PDB; 3PRC; 01-APR-99.
DR PDB; 4PRC; 01-APR-99.
DR PDB; 5PRC; 01-APR-99.
DR PDB; 6PRC; 06-APR-99.
DR PDB; 7PRC; 06-APR-99.
DR PDB; 8PRC; 06-APR-99.
DR PRINTS; PR00256; REACTNCENTRE.
DR PROSITE; PS00244; REACTION_CENTER; 1.
DR PFAM; PF00124; Photoc; 1.
KW Transmembrane; Electron transport; Photosynthesis; Reaction center;
KW Iron; Magnesium; 3D-structure.
FT INIT_MET 0 0
FT TRANSMEM 52 78
FT TRANSMEM 110 139
FT TRANSMEM 142 167
FT TRANSMEM 197 225
FT TRANSMEM 259 285
FT METAL 200 200
FT METAL 217 217
FT METAL 232 232
FT METAL 264 264
FT BINDING 250 250
FT HELIX 3 5
FT TURN 6 6
FT STRAND 12 13
FT HELIX 25 27
FT STRAND 28 29
FT STRAND 33 34
FT TURN 36 37
FT HELIX 38 40
FT TURN 41 41
FT STRAND 45 46
FT STRAND 49 50
FT HELIX 52 76
FT TURN 77 79
FT HELIX 81 90
FT STRAND 93 93
FT TURN 101 102
FT TURN 107 110
FT HELIX 111 137
FT TURN 138 139
FT HELIX 143 159
FT TURN 160 160
FT HELIX 161 166
FT TURN 167 167
FT HELIX 169 171
FT STRAND 175 175
FT TURN 177 178
FT HELIX 179 190
FT TURN 191 192
FT HELIX 194 196
FT TURN 198 223
FT TURN 224 224
FT HELIX 225 227
FT TURN 228 230
FT HELIX 232 237
FT HELIX 241 254
FT HELIX 260 284
FT STRAND 285 285
FT TURN 286 288
FT STRAND 289 289
FT HELIX 292 298
FT TURN 299 300
FT STRAND 312 312
FT HELIX 315 317
FT TURN 319 320

SQ SEQUENCE 323 AA; 35904 MW; F1E62D99418D8125 CRC64;

Query Match 56.7%; Score 34; DB 1; Length 323;
Best Local Similarity 83.3%; Pred. No. 47;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 YGSFYY 10
Db 191 YGNFYY 196
||:||||

Search completed: May 27, 2000, 20:07:16
Job time: 988 sec

Result No.	Score	Query		Length	DB	ID	Description
		Match					
1	39	65.0	2288	5	Q23081		Q23081 caenorhabdi
2	38	63.3	89	7	O19495		O19495 gallus gall
3	38	63.3	147	3	O13614		O13614 schizosacc
4	38	63.3	233	2	P74653		P74653 synechocyst
5	38	63.3	377	13	Q911997		Q911997 gallus gall
6	38	63.3	502	10	O9XG35		O9XG35 guillardia
7	38	63.3	1144	2	Q50371		Q50371 mycoplasma
8	37	61.7	192	3	O14085		O14085 schizosacc
9	37	61.7	333	2	Q47734		Q47734 enterococc
10	37	61.7	410	11	Q922E9		Q922e9 mus musculu
11	37	61.7	643	3	Q01864		Q01864 penicillium
12	37	61.7	806	5	O97288		O97288 plasmodium
13	37	61.7	897	2	O85661		O85661 proteus mir
14	37	61.7	1289	5	O01495		O01495 caenorhabdi
15	36	60.0	39	7	P79474		P79474 cervus elap
16	36	60.0	39	7	P79477		P79477 cervus elap
17	36	60.0	39	7	P79478		P79478 cervus elap
18	36	60.0	39	7	P79479		P79479 cervus elap
19	36	60.0	78	6	O97835		O97835 ovis aries
20	36	60.0	78	6	O97839		O97839 ovis aries

RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U64862; AAB52624.1; -.
 SQ SEQUENCE 2288 AA; 262172 MW; 6AD20DAC CRC32;

Query Match 65.0%; Score 39; DB 5; Length 2288;
 Best Local Similarity 60.0%; Pred. No. 1.4e+02;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNGSFY 10
 Db 34 SRSNYGEFYW 43

RESULT 2
 ID 019495 PRELIMINARY; PRT; 89 AA.

DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE MHC CLASS II BETA 1 DOMAIN (FRAGMENT).
 GN B-LBI.

OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
 OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=15.151-5; TISSUE=BURSA;
 RA PHARR G.T., DODGSON J.B., HUNT H.D., BACON L.D.;

RL Immunogenetics 47:350-354(1998).

DR EMBL; U91532; AAC15813.1; -.
 DR PFAM; PF00969; MHC_II_beta; 1.

KW MHC.

FT NON_TER 1 1
 FT NON_TER 89 89

SQ SEQUENCE 89 AA; 10724 MW; FDAC6024 CRC32;

Query Match 63.3%; Score 38; DB 7; Length 89;
 Best Local Similarity 85.7%; Pred. No. 6.5;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYSGF 8
 Db 75 RHNYSGF 81

RESULT 3

ID 013614 PRELIMINARY; PRT; 147 AA.

AC 013614;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)

DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)

DT 01-AUG-1998 (TrEMBLrel. 07, Last annotation update)

DE P1023 PROTEIN.

GN P1023.

OS Schizosaccharomyces pombe (Fission yeast).

OC Eukaryota; Fungi; Ascomycota; Archiascomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=972 H-;

RA KUSHIDA N., YAMAZAKI S., TANAKA T., JINNO K., HAIKAWA Y., YAMAZAKI J.,

RA YAMAMOTO S., SEKINE M., OGUCHI A., NAGAI Y., SAKAI K.,

RA OGURA K., OTSUKA R., KUDOH Y., YANAGIDA M., MACHIDA M., ZHANG M.Q.;

RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB004535; BAA21402.1; -.
 SQ SEQUENCE 147 AA; 16443 MW; EFEDC779 CRC32;

Query Match 63.3%; Score 38; DB 3; Length 147;

Best Local Similarity 66.7%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYSGFY 10
 Db 58 RYNGWFY 66

RESULT 4

ID P74653 PRELIMINARY; PRT; 233 AA.

AC P74653;

DT 01-FEB-1997 (TrEMBLrel. 02, Created)

DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)

DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)

DE HYPOTHETICAL 24.7 KD PROTEIN.

OS Synechocystis sp. (strain PCC 6803).

OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=PCC6803;

RA TABATA S.;

RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=PCC6803;

RX MEDLINE; 97061201.

RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,

RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,

RA HOSOUCHI T., MATSUNO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,

RA SHIMPO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,

RA TABATA S.;

RT "Sequence analysis of the genome of the unicellular cyanobacterium

RT Synechocystis sp. strain PCC6803. II. Sequence determination of the

RT entire genome and assignment of potential protein-coding regions.";

RL DNA Res. 3:109-136(1996).

DR EMBL; D90917; BAA18769.1; -.
 KW Hypothetical protein.

SQ SEQUENCE 233 AA; 24737 MW; 287B8255 CRC32;

Query Match 63.3%; Score 38; DB 2; Length 233;
 Best Local Similarity 55.6%; Pred. No. 18;
 Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYSGFY 10
 Db 98 RHYGTLY 106

RESULT 5

ID Q91997 PRELIMINARY; PRT; 377 AA.

AC Q91997;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)

DE 3BETA-HYDROXYSTEROID DEHYDROGENASE/DELTA5-DELTA4 ISOMERASE.

OS Gallus gallus (Chicken).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;

OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE-ADRENAL GLAND;

RX MEDLINE; 96032354.

RA NAKABAYASHI O., NOMURA O., NISHIMORI K., MIZUNO S.;

RT "The cDNA cloning and transient expression of a chicken gene encoding

RT a 3 beta-hydroxysteroid dehydrogenase/delta 5-->4 isomerase unique to

RL major steroidogenic tissues.";

RL Gene 162:261-265(1995).

DR EMBL; D43763; BAA07820.1; -.
 DR EMBL; D43762; BAA07819.1; -.
 DR PFAM; PF01073; 3beta_HSD; 1.

KW Isomerase.
SQ SEQUENCE 377 AA; 42881 MW; 9C38B8E9 CRC32;

Query Match 63.3%; Score 38; DB 13; Length 377;
Best Local Similarity 70.0%; Pred. No. 30;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNGSFYY 10
| | | | |
Db 250 ARHTRGQFYY 259

RESULT 6

Q9XG35 PRELIMINARY; PRT; 502 AA.
AC Q9XG35;
DT 01-NOV-1999 (TRENBLrel. 12, Created)
DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
DE T-COMPLEX PROTEIN 1 GAMMA SUBUNIT.
GN TCP3.
OS Guillardia theta (Cryptomonas phi).
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
RN [1]
RP SEQUENCE FROM N.A.
RA ZAUNER S., FRAUNHOLZ M., WASTL J., PENNY S.L., CAVALIER-SMITH T.,
RA MAIER U., DOUGLAS S.;
RT "Aberrant telomeres, overlapping genes and chloroplast protein-
RT encoding functions in an unusually compact eukaryotic genome -the
RT cryptomonad nucleomorph.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ010592; CAB40401.1; -;
SQ SEQUENCE 502 AA; 57514 MW; F60B836D CRC32;

Query Match 63.3%; Score 38; DB 10; Length 502;
Best Local Similarity 62.5%; Pred. No. 41;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFY 10
| | | | |
Db 444 HKYKYY 451

RESULT 7

Q50371 PRELIMINARY; PRT; 1144 AA.
AC Q50371;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DE P1-LIKE ADHESIN.
OS Mycoplasma pirum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Mycoplasmataceae; Mycoplasma.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BER;
RX MEDLINE: 94131957.
RA THAM T.N., FERRIS S., BAHAOU E., CANARELLI S., MONTAGNIER L.,
RA BLANCHARD A.;
RT "Molecular characterization of the P1-like adhesin gene from
RT Mycoplasma pirum.";
RL J. Bacteriol. 176:781-788(1994).
DR EMBL: L15685; AAC36866.1; -;
SQ SEQUENCE 1144 AA; 126732 MW; 081F55F1 CRC32;

Query Match 63.3%; Score 38; DB 2; Length 1144;
Best Local Similarity 55.6%; Pred. No. 98;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFY 10
: | | | | : |
Db 885 KQNYGSFY 893

RESULT 8

O14085 PRELIMINARY; PRT; 192 AA.
AC O14085;
DT 01-NOV-1998 (TRENBLrel. 08, Created)
DT 01-NOV-1998 (TRENBLrel. 08, Last sequence update)
DE PUTATIVE TRANSLLOCATION PROTEIN C2F3.02.
GN SPAC2F3.02.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Archiascomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA OLIVER K., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WOOD V.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -!- SIMILARITY: TO YAST SEC72.
DR EMBL: Z99165; CAB16260.1; -;
KW Hypothetical protein; Transport; Protein transport.
SQ SEQUENCE 192 AA; 21657 MW; F2E478E CRC32;

Query Match 61.7%; Score 37; DB 3; Length 192;
Best Local Similarity 66.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFY 10
: | | | | : |
Db 139 RNYGKCY 147

RESULT 9

Q47734 PRELIMINARY; PRT; 333 AA.
AC Q47734;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DE ORF14.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Enterococcaceae;
OC Enterococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DS16; TRANSPOSON=TN916;
RX MEDLINE: 95207419.
RA FLANNAGAN S.E., ZITZOW L.A., SU Y.A., CLEWELL D.B.;
RT "Nucleotide sequence of the 18-kb conjugative transposon Tn916 from
RT Enterococcus faecalis.";
RL Plasmid 32:350-354(1994).
DR EMBL: U09422; AAB60019.1; -;
DR PFAM: PF00877; NLP_C_P60.1.
SQ SEQUENCE 333 AA; 36781 MW; 9216B415 CRC32;

Query Match 61.7%; Score 37; DB 2; Length 333;
Best Local Similarity 55.6%; Pred. No. 40;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFY 10
: | | | | : |
Db 186 RNYGNMFY 194

RESULT 10

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Q922E9          PRELIMINARY;          PRT;      410 AA.
AC Q922E9;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE HYPOTHETICAL 46.2 KD PROTEIN.
GN GNG3LG.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C; TISSUE=BRAIN;
RX MEDLINE; 99009337.
RA DOWNES G.B., COPELAND N.G., JENKINS N.A., GAUTAM N.;
RT "Structure and mapping of the G protein gamma3 subunit gene and a
RT divergently transcribed novel gene, gng3lg."
RL Genomics 53:220-230(1998).
DR EMBL; AF069954; AAC77923.1; -.
KW Hypothetical protein.
SQ SEQUENCE 410 AA; 46169 MW; 0021E5CC CRC32;

Query Match          61.7%; Score 37; DB 11; Length 410;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YGSFY 10
Db 76 YGSFY 81

RESULT 11
Q01864          PRELIMINARY;          PRT;      643 AA.
AC Q01864;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE TRANSCRIPTION FACTOR PACC.
GN PACC.
OS Penicillium chrysogenum.
OC Eukaryota; Fungi; Ascomycota; Euascomycetes; Plectomycetes;
OC Eurotiales; Trichocomaceae; anamorphic Trichocomaceae; Penicillium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL1951;
RX MEDLINE; 96347125.
RA SUAREZ T., PENALVA M.A.;
RT "Characterization of a Penicillium chrysogenum gene encoding a PACC
RT transcription factor and its binding sites in the divergent pcbAB-pcbC
RT promoter of the penicillin biosynthetic cluster."
RL Mol. Microbiol. 20:529-540(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL1951;
RA SUAREZ T., PENALVA M.A.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL1951;
RA SUAREZ T.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MEDIATES REGULATION OF BOTH ACID- AND ALKALINE-EXPRESSED
CC GENES BY AMBIENT PH. AT ALKALINE AMBIENT PH, IT ACTIVATES
CC TRANSCRIPTION OF ALKALINE-EXPRESSED GENES (INCLUDING PACC ITSELF)
CC AND REPRESSES TRANSCRIPTION OF ACID- EXPRESSED GENES (BY
CC SIMILARITY). SPECIFICALLY RECOGNIZES THE CONSENSUS SEQUENCE 5'-
CC GCCARG-3'.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- DEVELOPMENTAL STAGE: HIGHER EXPRESSION IN OLDER MYCELIA.
CC -1- INDUCTION: BY ALKALINE CONDITIONS.

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CC -1- PTM: ACTIVATED BY C-TERMINAL PROTEOLYTIC CLEAVAGE WHICH IS
CC STIMULATED UNDER ALKALINE GROWTH CONDITIONS (BY SIMILARITY).
CC -1- SIMILARITY: TO FUNGAL TRANSCRIPTION FACTORS PACC, AND TO YEAST
CC PROTEIN RIM1.
DR EMBL; U44726; AAC36492.1; -.
DR PROSITE; PS00028; ZINC_FINGER_C2H2; 1.
DR PRINTS; PR00048; ZINC_FINGER.
KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
KW Nuclear protein; Repressor; Activator.
FT DOMAIN 36 44 POLY-ALA.
FT ZN_FING 60 83 C2H2-TYPE.
FT ZN_FING 96 118 C2H2-TYPE.
FT ZN_FING 126 146 C2H2-TYPE.
FT DOMAIN 233 251 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 292 301 POLY-GLY.
SQ SEQUENCE 643 AA; 68823 MW; 0AA070E0 CRC32;

Query Match          61.7%; Score 37; DB 3; Length 643;
Best Local Similarity 62.5%; Pred. No. 80;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFY 10
Db 212 HSYGNLYY 219

RESULT 12
O97288          PRELIMINARY;          PRT;      806 AA.
AC O97288;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE PFC0940C PROTEIN.
GN PFC0940C.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RA OLIVER K., BOWMAN S., HARRIS D., LAWSON D., QUAIL M., BARRELL B.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL034559; CAB39034.1; -.
SQ SEQUENCE 806 AA; 98328 MW; 7EFB873F CRC32;

Query Match          61.7%; Score 37; DB 5; Length 806;
Best Local Similarity 71.4%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSFY 10
Db 319 NYGTY 325

RESULT 13
O85661          PRELIMINARY;          PRT;      897 AA.
AC O85661;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE REGULATOR OF SWARMING BEHAVIOR PRECURSOR.
GN RSBA.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BB2000;
RA MELCH M., SCHNEIDER R., WALKER K., BELAS R.;
RT "RSBA: A regulator of Proteus mirabilis swarming behavior."

```

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF071215; AAC82660.1; -
 DR PFAM; PF00512; signal; 1.
 KW SIGNAL.
 FT CHAIN 32 897 REGULATOR OF SWARMING BEHAVIOR.
 FT CHAIN 32 897
 SQ SEQUENCE 897 AA; 103862 MW; D21F2D31 CRC32;

Query Match 61.7%; Score 37; DB 2; Length 897;
 Best Local Similarity 66.7%; Pred. No. 1.1e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFY 10
 I:| | | |
 Db 134 RNNYSLLY 142

RESULT 14
 O01495 PRELIMINARY; PRT; 1289 AA.
 AC O01495;
 DT 01-JUL-1997 (TReMBLrel. 04, Created)
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
 DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
 DE SIMILARITY TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY.
 GN C34G6.4.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditida; Rhabditidae;
 OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE; 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SHALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA LANGSTON Z., ROHLFING T.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA WATERSTON R.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U97407; AAB52482.1; -
 DR HSSP; P13569; 1NBD.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 2.
 DR PFAM; PF00664; ABC_membrane; 2.
 DR PFAM; PF00005; ABC_tran; 2.
 KW ATP-binding; Transport.
 SQ SEQUENCE 1289 AA; 143065 MW; 35FC8DC3 CRC32;

Query Match 61.7%; Score 37; DB 5; Length 1289;
 Best Local Similarity 85.7%; Pred. No. 1.7e+02;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NYGSFY 10
 | | | | |
 Db 35 NYGIFY 41

RESULT 15

P79474 PRELIMINARY; PRT; 39 AA.
 ID P79474;
 AC P79474;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
 DE MHC CLASS II DBB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
 OC Cervinae; Cervus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SWARBRICK P.A., CRAWFORD A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63077; AAB37777.1; -
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4767 MW; E01AA287 CRC32;

Query Match 60.0%; Score 36; DB 7; Length 39;
 Best Local Similarity 85.7%; Pred. No. 6.1;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 | | | | |
 Db 25 RHNYGVF 31

Search completed: May 27, 2000, 19:38:41
 Job time: 2374 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:21:35 ; Search time 148.45 Seconds
(without alignments)
1.596 Million cell updates/sec

Title: US-09-016-061-66
Perfect score: 60
Sequence: 1 ARHNYGSFYY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	10	1 W76023	LM609 grafted anti
2	53	88.3	10	1 W76039	LM609 grafted anti
3	53	88.3	10	1 W76040	LM609 grafted anti
4	51	85.0	10	1 W76010	LM609 grafted anti
5	51	85.0	117	1 W76001	Vitaxin antibody h
6	51	85.0	117	1 W76003	LM609 antibody hea
7	50	83.3	10	1 W76022	LM609 grafted anti
8	48	80.0	10	1 W76038	LM609 grafted anti
9	48	80.0	10	1 W76021	LM609 grafted anti
10	46	76.7	10	1 W76020	LM609 grafted anti
11	46	76.7	10	1 W76024	LM609 grafted anti
12	46	76.7	10	1 W76025	LM609 grafted anti
13	46	76.7	10	1 W76026	LM609 grafted anti
14	46	76.7	10	1 W76027	LM609 grafted anti
15	46	76.7	10	1 W76028	LM609 grafted anti
16	46	76.7	10	1 W76029	LM609 grafted anti
17	46	76.7	10	1 W76030	LM609 grafted anti
18	43	71.7	110	1 W84099	Vitronectin alpha-
19	43	71.7	117	1 W84093	Murine vitronectin
20	43	71.7	117	1 W84097	Humanised anti-alp
21	41	68.3	10	1 W76037	LM609 grafted anti
22	41	68.3	256	1 R22568	ScFvB18 construct.
23	41	68.3	256	1 R22583	ScFvB18 construct
24	41	68.3	256	1 R22584	ScFvB18 construct
25	41	68.3	256	1 R22585	ScFvB18 construct
26	41	68.3	256	1 R22586	ScFvB18 construct
27	41	68.3	256	1 R22587	ScFvB18 construct
28	40	66.7	117	1 R79157	Human IGE receptor
29	40	66.7	117	1 R79155	Human IGE receptor
30	40	66.7	117	1 W27357	Heavy chain variab
31	40	66.7	117	1 W27526	Heavy chain variab
32	40	66.7	117	1 W27354	Heavy chain variab
33	40	66.7	239	1 W73874	Human antiFc epsil
34	40	66.7	242	1 W73876	Human antiFc epsil

35 38 63.3 122 1 R30145 MAb 1-3-1 variable
36 38 63.3 1144 1 R76059 Mycoplasma pirum a
37 37 61.7 36 1 W03964 VDJ joint protein,
38 37 61.7 36 1 W41127 VH251 DXP/1 J6 mu
39 37 61.7 256 1 R22582 ScFvB18 construct
40 37 61.7 334 1 W63695 Human secreted pro
41 37 61.7 462 1 W73623 Human secreted pro
42 35 58.3 33 1 W03958 VDJ joint protein,
43 35 58.3 33 1 W41121 VH251 DHQ52 J6 mu
44 34 56.7 119 1 W01578 Lead binding MAb 8
45 34 56.7 123 1 W19881 CEA-specific antib

ALIGNMENTS

RESULT 1

W76023
ID W76023 standard; Protein; 10 AA.
AC W76023;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #5.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49860.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PS Claim 62: Page 41: 129pp: English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 100.0%; Score 60; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00029;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFYY 10
| | | | | | | | | |
Db 1 ARHNYGSFYY 10

RESULT 2

W76039
ID W76039 standard; Protein; 10 AA.
AC W76039;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #15.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49876.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 43; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region, LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 88.3%; Score 53; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.004;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
 | | | | | | | |
 DB 1 ARHNYGSFY 9

RESULT 3
 W76040
 ID W76040 standard; Protein; 10 AA.
 AC W76040;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #16.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49877.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 43; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region, LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 88.3%; Score 53; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.004;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
 | | | | | | | |
 DB 1 ARHNYGSFY 9

RESULT 4
 W76010
 ID W76010 standard; Protein; 10 AA.
 AC W76010;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #1.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49847.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Disclosure; Page 40; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region, LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 85.0%; Score 51; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0085;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
 | | | | | | | |
 DB 1 ARHNYGSFY 10

RESULT 5
 W76001
 ID W76001 standard; Protein; 117 AA.

AC W76001;
 DT 02-NOV-1998 (first entry)
 DE Vitaxin antibody heavy chain variable region protein fragment.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB: V49820.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 1; Fig 1a; 129pp; English.
 CC This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 CC Sequence 117 AA;

Query Match 85.0%; Score 51; DB 1; Length 117;
 Best Local Similarity 90.0%; Pred. NO. 0.11;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
 | | | | | | | |
 Db 97 ARHNYGSFAY 106

RESULT 6
 W76003
 ID W76003 standard; Protein; 117 AA.
 AC W76003;
 DT 02-NOV-1998 (first entry)
 DE LM609 antibody heavy chain variable region protein fragment.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB: V49822.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 43; Fig 2a; 129pp; English.
 CC This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus

CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 CC Sequence 117 AA;

Query Match 85.0%; Score 51; DB 1; Length 117;
 Best Local Similarity 90.0%; Pred. NO. 0.11;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
 | | | | | | | |
 Db 97 ARHNYGSFAY 106

RESULT 7
 W76022
 ID W76022 standard; Protein; 10 AA.
 AC W76022;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #4.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB: V49859.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 CC Sequence 10 AA;

Query Match 83.3%; Score 50; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. NO. 0.012;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
 | | | | | | | |
 Db 1 ARHNYGSFDY 10

RESULT 8
 W76038
 ID W76038 standard; Protein; 10 AA.

```

AC W76038;
DE 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #14.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49875.
DR Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PT Claim 62; Page 43; 129pp; English.
PS
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 80.0%; Score 48; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.026;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
   |||||:|
DB 1 ARHNYGSYAY 10

RESULT 10
ID W76020 standard; Protein; 10 AA.
AC W76020;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #2.
DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49857.
DR Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PT Claim 62; Page 41; 129pp; English.
PS
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 76.7%; Score 46; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.055;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
   |||||:|
DB 1 ARHNGSFAY 10

```

PT	Integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose
PS	angiogenesis or restenosis
PS	Claim 62; Page 41; 129pp; English.
CC	W76007-W76040 are protein fragments of the grafted monoclonal antibody LM609 heavy and light chain variable region. LM609 and the antibody
CC	vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC	inhibit binding of alphavbeta3 to a ligand and thus block
CC	integrin-mediated signal transduction. This is useful in the treatment,
CC	prevention and diagnosis of alphavbeta3-mediated disease, specifically,
CC	angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC	diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC	arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC	contain non-murine framework regions so are suitable for use in humans.
CC	Enhanced types of LM609 have affinity more than 90 times greater than
CC	that of parent the parent antibody.
SQ	Sequence 10 AA;
Query Match 76.7%; Score 46; DB 1; Length 10;	
Best Local Similarity 100.0%; Pred. No. 0.055;	
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
QY	1 ARHNYGSF 8
Db	1 ARHNYGSF 8
RESULT	13
W76026	ID W76026 standard; Protein; 10 AA.
AC	W76026;
DT	02-NOV-1998 (first entry)
DE	LM609 grafted antibody V-H region CDR3 protein fragment #8.
KW	Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW	LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW	diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW	neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW	macular degeneration; osteoporosis; primer; V-H region; CDR;
KW	complementarity determining region.
OS	Mus sp.
PN	WO9833919-A2.
PD	06-AUG-1998.
PF	30-JAN-1998; U01826.
PR	30-JAN-1997; US-791391.
PA	(IXSY-) IXSYS INC.
PI	Glaser SM, Huse WD;
DR	WFI; 98-437472/37.
DR	N-PSDB; V49863.
PT	Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT	Integrin - and related grafted antibodies based on murine monoclonal
PT	LM609, also related nucleic acid, used to treat, prevent or diagnose
PT	angiogenesis or restenosis
PS	Claim 62; Page 41; 129pp; English.
CC	W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC	LM609 heavy and light chain variable region. LM609 and the antibody
CC	vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC	inhibit binding of alphavbeta3 to a ligand and thus block
CC	integrin-mediated signal transduction. This is useful in the treatment,
CC	prevention and diagnosis of alphavbeta3-mediated disease, specifically,
CC	angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC	diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC	arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC	contain non-murine framework regions so are suitable for use in humans.
CC	Enhanced types of LM609 have affinity more than 90 times greater than
CC	that of parent the parent antibody.
SQ	Sequence 10 AA;
Query Match 76.7%; Score 46; DB 1; Length 10;	
Best Local Similarity 100.0%; Pred. No. 0.055;	
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0	

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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:26:43 ; Search time 163.56 seconds
(without alignments)
3.585 Million cell updates/sec

Title: US-09-016-061-68
Perfect score: 54
Sequence: 1 ARHNYGSPAS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_63: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	40	74.1	446	2 T19625	hypothetical prote
2	39	72.2	89	2 S38688	MHC class II histo
3	39	72.2	89	2 S38683	MHC class II histo
4	39	72.2	89	2 S38684	MHC class II histo
5	39	72.2	225	2 I47095	MHC class II OVAR-
6	36	66.7	65	2 S17441	hypothetical prote
7	36	66.7	82	2 I51106	Major Histocompat
8	36	66.7	360	2 S48566	hypothetical prote
9	35	64.8	85	2 I59634	MHC class II DR-be
10	35	64.8	89	2 S38676	MHC class II histo
11	35	64.8	89	2 S38680	MHC class II histo
12	35	64.8	89	2 S57512	MHC class II histo
13	35	64.8	98	1 WMBF72	gene 7 protein - p
14	35	64.8	98	1 WMBF79	gene 7 protein - p
15	35	64.8	123	2 D32339	MHC class II histo
16	35	64.8	200	2 D32526	MHC class II histo
17	35	64.8	221	2 I45939	MHC cell surface g
18	35	64.8	227	2 C27060	class II histocomp
19	35	64.8	286	2 I54287	gene HLA-DRB1 prot
20	35	64.8	266	2 A27618	class II histocomp
21	35	64.8	266	2 I54295	lymphocyte antigen
22	35	64.8	313	1 A05213	cytochrome c-type
23	35	64.8	347	2 S43771	phosphatidylcholin
24	34	63.0	108	2 S26316	Ig heavy chain v r
25	34	63.0	110	2 S26317	Ig heavy chain v r
26	34	63.0	115	2 S37265	MHC class II histo
27	34	63.0	210	1 B69265	conserved hypothet
28	34	63.0	263	2 A45838	MHC class II histo
29	34	63.0	265	2 B39797	MHC class II histo
30	34	63.0	275	2 D71087	probable translati

31 34 63.0 275 2 G75130 translation initia
32 34 63.0 279 2 T05421 hypothetical prote
33 34 63.0 287 1 PWBV inorganic pyrophos
34 34 63.0 287 1 PWBV inorganic pyrophos
35 33 61.1 80 2 I54469 MHC HLA-DR-beta-1
36 33 61.1 80 2 I68777 MHC HLA-DR-beta-1
37 33 61.1 81 2 I54550 HLA DRB1*1202 - hu
38 33 61.1 87 2 S38681 major histocompati
39 33 61.1 87 2 S38682 major histocompati
40 33 61.1 87 2 S38685 major histocompati
41 33 61.1 167 2 T16454 hypothetical prote
42 33 61.1 232 2 I51220 major histocompati
43 33 61.1 232 2 B48381 MHC class II histo
44 33 61.1 258 2 T36268 probable DNA-bindi
45 33 61.1 258 2 F72616 hypothetical prote

ALIGNMENTS

RESULT 1

T19625

hypothetical protein C31H5.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T19625

R:Kershaw, J. submitted to the EMBL Data Library, April 1997

A:Reference number: Z19153

A:Accession: T19625

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-446 <WIL>

A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6

A:Experimental source: clone C31H5

C:Genetics:

A:Gene: CESP:C31H5.6

A:Map position: 1

A:Introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3

Query Match 74.1%; Score 40; DB 2; Length 446;
Best Local Similarity 77.8%; Pred. No. 3.7;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10

Db 51 RHNYGSHAA 59

RESULT 2

S38688

MHC class II histocompatibility antigen HLA-DR-08 beta chain - Galago senegalensis (f

C:Species: Galago senegalensis

C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997

C:Accession: S38688

R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.

submitted to the EMBL Data Library, November 1993

A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduce

A:Reference number: S38676

A:Accession: S38688

A:Molecule type: DNA

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:Z27158

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 72.2%; Score 39; DB 2; Length 89;
Best Local Similarity 77.8%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAS 10

Db 1111111111

```
Db 75 RHNYGVFES 83

RESULT 3
MHC class II histocompatibility antigen HLA-DR-03 beta chain - Galago senegalensis (frag
C:Species: Galago senegalensis
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997
C:Accession: S38683
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced f
A:Reference number: S38676
A:Accession: S38683
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:227153
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 72.2%; Score 39; DB 2; Length 89;
Best Local Similarity 77.8%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
Db 75 RHNYGVFES 83

RESULT 4
MHC class II histocompatibility antigen HLA-DR-04 beta chain - Galago senegalensis (frag
C:Species: Galago senegalensis
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997
C:Accession: S38684
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced f
A:Reference number: S38676
A:Accession: S38684
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:227154
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 72.2%; Score 39; DB 2; Length 89;
Best Local Similarity 77.8%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
Db 75 RHNYGVFES 83

RESULT 5
MHC class II OVAR-DR-beta-3 - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 23-Jul-1999
C:Accession: I47095
R:Fabb, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.
Anim. Genet. 24, 249-255, 1993
A:Title: Isolation, characterization and evolution of ovine major histocompatibility com
A:Reference number: I47095; MUID:94057592
A:Accession: I47095
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-225 <FAB>
A:Cross-references: GB:L04790; NID:g458880; PIDN:AAA16562.1; PID:g458881
C:Genetics:
A:Gene: OVAR-DRB3
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 72.2%; Score 39; DB 2; Length 225;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
Db 68 RHNYGVFES 76

RESULT 6
hypothetical protein (rpl2 5' region) - garden pea chloroplast (fragment)
C:Species: chloroplast Pisum sativum (garden pea)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 11-Jun-1999
C:Accession: S17441
R:Nagano, Y.; Ishikawa, H.; Matsuno, R.; Sasaki, Y.
Plant Mol. Biol. 17, 541-545, 1991
A:Title: Nucleotide sequence and expression of the ribosomal protein L2 gene in pea c
A:Reference number: S17441; MUID:91355950
A:Accession: S17441
A:Molecule type: DNA
A:Residues: 1-65 <NAG>
A:Cross-references: EMBL:X59015; NID:g12175; PIDN:CAA41754.1; PID:g388252
C:Genetics:
A:Genome: chloroplast
C:Superfamily: cytochrome c-type synthesis protein
C:Keywords: chloroplast

Query Match 66.7%; Score 36; DB 2; Length 65;
Best Local Similarity 75.0%; Pred. No. 3.2;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAS 10
Db 57 HSYGSFTS 64

RESULT 7
Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)
C:Species: Phasianus colchicus (ring-necked pheasant)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
C:Accession: I51106
R:Witzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.
Immunogenetics 39, 395-403, 1994
A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-ne
A:Reference number: I51103; MUID:94245280
A:Accession: I51106
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-82 <WIT>
A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 66.7%; Score 36; DB 2; Length 82;
Best Local Similarity 85.7%; Pred. No. 4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 75 RHNYGVF 81

RESULT 8
hypothetical protein YLR215c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein L8167.23
C:Species: Saccharomyces cerevisiae
C:Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 24-Nov-1999
```

C;Accession: S48566
R;Pauley, A.
submitted to the EMBL Data Library, September 1994
A;Description: The sequence of S. cerevisiae cosmid 8167.
A;Reference number: S48545
A;Accession: S48566
A;Molecule type: DNA
A;Residues: 1-360 <PAU>
A;Cross-references: EMBL:U14913; NID:g544497; PIDN:AA67444.1; PID:g544519; GSPDB:GN0001
C;Genetics:
A;Gene: MIPS:YLR215C
A;Map position: 12R
C;Superfamily: Saccharomyces cerevisiae hypothetical protein YLR215c

Query Match 66.7%; Score 36; DB 2; Length 360;
Best Local Similarity 77.8%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSPAS 10
|||||: |
Db 304 RHNTGRFAS 312

RESULT 9
I59634
MHC class II DR-beta-1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
C;Accession: I59634
R;Lin, Y.N.; Ren, E.C.; Chan, S.H.
Tissue Antigens 41, 204-205, 1993
A;Title: A new DR11 allele in Singaporean Chinese.
A;Reference number: I59634; MUID:93369836
A;Accession: I59634
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-85 <RES>
A;Cross-references: GB:M98436; NID:gl87890; PIDN:AAA59693.1; PID:gl87891
C;Genetics:
A;Gene: HLA-DRB1-11
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.8%; Score 35; DB 2; Length 85;
Best Local Similarity 66.7%; Pred. No. 6.4;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSPAS 10
|||||: |
Db 75 RHNYGAVES 83

RESULT 10
S38676
MHC class II histocompatibility antigen HLA-DR-01 beta chain - Galago moholi (fragment)
C;Species: Galago moholi
C;Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999
C;Accession: S38676
R;Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A;Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced f
A;Reference number: S38676
A;Accession: S38676
A;Molecule type: DNA
A;Residues: 1-89 <FIG>
A;Cross-references: EMBL:227130; NID:g415801; PIDN:CAA81657.1; PID:e214692; PID:gl132545
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.8%; Score 35; DB 2; Length 89;
Best Local Similarity 66.7%; Pred. No. 6.7;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSPAS 10
|||||: |
Db 75 RHNYGAVES 83

RESULT 11
S38680
MHC class II histocompatibility antigen HLA-DR-05 beta chain - Galago moholi (fragmen
C;Species: Galago moholi
C;Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 23-Jul-1999
C;Accession: S38680
R;Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A;Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduce
A;Reference number: S38676
A;Accession: S38680
A;Molecule type: DNA
A;Residues: 1-89 <FIG>
A;Cross-references: EMBL:227134; NID:g415805; PIDN:CAA81661.1; PID:e214696; PID:gl1332
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.8%; Score 35; DB 2; Length 89;
Best Local Similarity 66.7%; Pred. No. 6.7;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSPAS 10
|||||: |
Db 75 RHNYGAVES 83

RESULT 12
S57512
MHC class II histocompatibility antigen HLA-DR beta 1 chain DRB1*08 precursor - human
C;Species: Homo sapiens (man)
C;Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 23-Jul-1999
C;Accession: S57512; I79647
R;Versluis, L.F.; Savelkoul, P.; van der Zwan, A.W.; van den Berg-Loonen, E.; Tilianus
submitted to the EMBL Data Library, June 1995
A;Reference number: S57512
A;Accession: S57512
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-89 <VER>
A;Cross-references: EMBL:X88854; NID:g887451; PIDN:CAA61324.1; PID:g887452
R;Gyllenstein, U.B.; Sundvall, M.; Erlich, H.A.
Proc. Natl. Acad. Sci. U.S.A. 88, 3686-3690, 1991
A;Title: Allelic diversity is generated by intraexon sequence exchange at the DRB1 lo
A;Reference number: I59196; MUID:91219437
A;Accession: I79647
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-73 <RES>
A;Cross-references: GB:M63196; NID:gl81762; PIDN:AAA52321.1; PID:gl81763
C;Genetics:
A;Gene: GDB:HLA-DRB1
A;Cross-references: GDB:120642
A;Map position: 6p21.3-6p21.3
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.8%; Score 35; DB 2; Length 89;
Best Local Similarity 66.7%; Pred. No. 6.7;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSPAS 10
|||||: |
Db 75 RHNYGAVES 83

RESULT 13
WMBP72

gene 7 protein - phage PZA

C:Species: phage PZA
A:Note: host Bacillus subtilis
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 23-Jul-1999
C:Accession: A24831
R:Paces, V.; Vicek, C.; Urbaneck, P.
Gene 44, 107-114, 1986
A:Title: Nucleotide sequence of the late region of Bacillus subtilis phage PZA, a close
A:Reference number: A91550; MUID:87031573
A:Accession: A24831
A:Molecule type: DNA
A:Residues: 1-98 <PAC>
A:Cross-references: GB:M1813; GB:M13904; GB:M13905; NID:g216046; PIDN:AAA8483.1; PID:g
C:Genetics:
A:Gene: 7
C:Superfamily: phage PZA gene 7 protein
C:Keywords: late protein

Query Match 64.8%; Score 35; DB 1; Length 98;

Best Local Similarity 77.8%; Pred. No. 7.4;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10

| | | | |

Db 33 RVNYGSFVS 41

RESULT 14

WMBPF9

gene 7 protein - phage phi-29
N:Alternate names: head morphogenesis protein
C:Species: phage phi-29
A:Note: host Bacillus subtilis
C:Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 23-Jul-1999
C:Accession: A28923; A25816
R:Innis, C.A.; Garvey, K.J.; Ito, J.
Nucleic Acids Res. 14, 7129, 1986
A:Title: Nucleotide sequence of phage phi-29 gene 7: structure of intergenic spacer betw
A:Reference number: A28923; MUID:87016351
A:Accession: A28923
A:Molecule type: DNA
A:Residues: 1-98 <INN>
A:Cross-references: GB:X04386; NID:g15522; PIDN:CAA27974.1; PID:g15524
R:Vlcek, C.; Paces, V.
Gene 46, 215-225, 1986
A:Title: Nucleotide sequence of the late region of Bacillus phage phi-29 completes the
A:Reference number: A25816; MUID:87106857
A:Accession: A25816
A:Molecule type: DNA
A:Residues: 1-98 <VLC>
A:Cross-references: GB:M14782; NID:g215323; PIDN:AAA32279.1; PID:g215324
C:Genetics:
A:Gene: 7
C:Superfamily: phage PZA gene 7 protein
C:Keywords: head protein; late protein

Query Match

64.8%; Score 35; DB 1; Length 98;

Best Local Similarity 77.8%; Pred. No. 7.4;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10

| | | | |

Db 33 RVNYGSFVS 41

RESULT 15

C25239

MHC class II histocompatibility antigen HLA-DR-2-MN2-2 beta chain precursor - human (fra
C:Species: Homo sapiens (man)
C:Date: 28-Sep-1987 #sequence_revision 28-Sep-1987 #text_change 03-May-1996
C:Accession: C25239

R;Wu, S.; Saunders, T.L.; Bach, F.H.

Nature 324, 676-679, 1986

A:Title: Polymorphism of human Ia antigens generated by reciprocal intergenic exchange

A:Reference number: A25239; MUID:87090380

A:Accession: C25239

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-123 <WUS>

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match

64.8%; Score 35; DB 2; Length 123;

Best Local Similarity 66.7%; Pred. No. 9.3;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10

| | | | |

Db 109 RHNYGAVES 117

Search completed: May 27, 2000, 19:26:43

Job time: 1766 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 20:07:16 ; Search time 69.28 Seconds
(without alignments)
4.396 Million cell updates/sec

Title: US-09-016-061-68
Perfect score: 54
Sequence: 1 ARHNYGSFAS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	66.7	65	1 CCSA_PEA	P31172 pisum sativ
2	36	66.7	328	1 CCSA_ARATH	P56770 arabidopsis
3	35	64.8	98	1 VG7_BPPH2	P13848 bacterioph
4	35	64.8	98	1 VG7_BPP2A	P07533 bacterioph
5	35	64.8	313	1 CCSA_TOBAC	P12216 nicotiana t
6	34	63.0	275	1 IF2A_PYRHO	O58655 pyrococcus
7	34	63.0	284	1 IPYR_PICPA	O13505 pichia past
8	34	63.0	286	1 IPYR_KUOLA	P13998 kluyveromyc
9	34	63.0	286	1 IPYR_YEAST	P00817 saccharomyc
10	33	61.1	266	1 HB2D_CANFA	P18470 canis fami
11	33	61.1	322	1 FATB_VIBAN	P11460 vibrio angu
12	33	61.1	398	1 PF21_ARATH	Q04088 arabidopsis
13	33	61.1	448	1 NCAP_CVHOC	P33469 human coron
14	33	61.1	470	1 SYE2_RICPR	Q92ct8 rickettsia
15	33	61.1	473	1 SYE_AQUAE	O67271 aquifex aeo
16	33	61.1	639	1 Y119_MYCTU	Q50614 mycobacteri
17	33	61.1	682	1 VG50_BPML5	Q05262 mycobacteri
18	33	61.1	1254	1 MDR3_CAEEL	P34713 caenorhabdi
19	32	59.3	65	1 CCSA_OENBE	P31565 oenothera b
20	32	59.3	196	1 WBBJ_ECOLI	P37750 escherichia
21	32	59.3	198	1 HB2G_HUMAN	P01911 homo sapien
22	32	59.3	213	1 PNCA_ECOLI	P21369 escherichia
23	32	59.3	251	1 SAST_ANAPL	P00633 anas platyr
24	32	59.3	266	1 HB2A_HUMAN	P01913 homo sapien
25	32	59.3	266	1 HB2B_HUMAN	P01912 homo sapien
26	32	59.3	266	1 HB2C_HUMAN	P01914 homo sapien
27	32	59.3	266	1 HB2D_HUMAN	P13759 homo sapien
28	32	59.3	266	1 HB2E_HUMAN	P04229 homo sapien
29	32	59.3	266	1 HB2F_HUMAN	P13758 homo sapien
30	32	59.3	266	1 HB2H_HUMAN	P13760 homo sapien
31	32	59.3	266	1 HB2I_HUMAN	P20039 homo sapien
32	32	59.3	266	1 HB2J_HUMAN	P13761 homo sapien
33	32	59.3	321	1 CCSA_MAIZE	P46659 zea mays (m
34	32	59.3	321	1 CCSA_ORYZA	P12215 oryza sativ

RESULT 1

CCSA_PEA	ID	CCSA_PEA	STANDARD;	PRT;	65 AA.
AC	P31172;				
DT	01-JUL-1993	(Rel. 26, Created)			
DT	01-JUL-1993	(Rel. 26, Last sequence update)			
DT	01-NOV-1997	(Rel. 35, Last annotation update)			
DE	CYTOCHROME C BIOGENESIS PROTEIN CCSA (FRAGMENT).				
GN	CCSA.				
OS	Pisum sativum (Garden pea).				
OG	Chloroplast.				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;				
OC	core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;				
OC	Pisum.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CV. ALASKA;				
RX	MEDLINE; 91355950.				
RA	Nagano Y., Ishikawa H., Matsuno R., Sasaki Y.;				
RT	"Nucleotide sequence and expression of the ribosomal protein L2 gene				
RT	in pea chloroplasts.";				
RL	Plant Mol. Biol. 17:541-545(1991).				
CC	-!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF				
CC	HEME ATTACHMENT (BY SIMILARITY).				
CC	-!- SIMILARITY: BELONGS TO THE CCNF/CYCK/CCL1/NRFE/CCSA FAMILY.				
CC	-----				
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CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; X59015; CAA41754.1; -.				
DR	PIR; S17441; S17441.				
KW	Cytochrome c-type biogenesis; Chloroplast.				
FT	NON_TER				
SQ	SEQUENCE 65 AA; 7396 MW; 9E523E0C70B102AA CRC64;				

Query Match 66.7%; Score 36; DB 1; Length 65;
Best Local Similarity 75.0%; Pred. No. 0.94;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNYGSFAS 10
Db 57 HSYGSFAS 64

RESULT 2

CCSA_ARATH	ID	CCSA_ARATH	STANDARD;	PRT;	328 AA.
AC	P56770;				
DT	15-FEB-2000 (Rel. 39, Created)				
DT	15-FEB-2000 (Rel. 39, Last sequence update)				

DT 15-FEB-2000 (Rel. 39, Last annotation update)
GN CYTOCHROME C BIOGENESIS PROTEIN CCSA.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euryliophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;
RT "Complete structure of the chloroplast genome of Arabidopsis
thaliana";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCLI/NRFE/CCSA FAMILY.
CC -----
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CC -----
DR EMBL; AF000423; BAA84436.1; -;
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 328 AA; 37732 MW; C88D1508B2924D6F CRC64;

Query Match 66.7%; Score 36; DB 1; Length 328;
Best Local Similarity 75.0%; Pred. No. 5.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNVGSPAS 10
Db |.....|
320 HSYGSFTS 327

RESULT 3
VG7_BPPH2 STANDARD; PRT; 98 AA.
AC P13848;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE HEAD MORPHOGENESIS PROTEIN (LATE PROTEIN GP7).
GN 7.
OS Bacteriophage phi-29.
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Podoviridae.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87106857.
RA Vicek C., Paces V.;
RT "Nucleotide sequence of the late region of Bacillus phage phi 29
completes the 19,285-bp sequence of phi 29 genome. Comparison with
the homologous sequence of phage pZA.";
RL Gene 46:215-225(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87016351.
RA Innis C.A., Garvey K.J., Ito J.;
RT "Nucleotide sequence of phage phi 29 gene 7: structure of intergenic
spacer between the major early and late genes.";
RL Nucleic Acids Res. 14:7129-7129(1986).
CC -----
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CC -----
DR EMBL; M14782; AAA32279.1; -;
DR EMBL; X04386; CAA27974.1; -;
DR PIR; A28923; WMBPF9.
KW Late protein.
SQ SEQUENCE 98 AA; 11266 MW; FF2E7985D2266E14 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 98;
Best Local Similarity 77.8%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSPAS 10
Db |.....|
33 RVNYGSPVS 41

RESULT 4
VG7_BPPZA STANDARD; PRT; 98 AA.
ID VG7_BPPZA
AC P07533;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE HEAD MORPHOGENESIS PROTEIN (LATE PROTEIN GP7).
GN 7.
OS Bacteriophage pZA.
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Podoviridae.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87031573.
RA Paces V., Vicek C., Urbanek P.;
RT "Nucleotide sequence of the late region of Bacillus subtilis phage
pZA, a close relative of phi 29.";
RL Gene 44:107-114(1986).
CC -----
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CC -----
DR EMBL; M11813; AAA88483.1; -;
DR PIR; A24831; WMBP72.
KW Late protein.
SQ SEQUENCE 98 AA; 11281 MW; 444408C39B606A25 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 98;
Best Local Similarity 77.8%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSPAS 10
Db |.....|
33 RVNYGSPVS 41

RESULT 5
CCSA_TOBAC STANDARD; PRT; 313 AA.
ID CCSA_TOBAC
AC P12216;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA.
GN CCSA.
OS Nicotiana tabacum (Common tobacco).
OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Asteridae; euasterids I; Solanales; Solanaceae;
 OC Nicotiana.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, BRIGHT YELLOW 4;
 RA Sugliura M.;
 RL Submitted (AUG-1986) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP COMPLETE GENOME.
 RA Shinzaki K., Ohme M., Tanaka M., Wakasugi T., Hayashida N.,
 RA Matsubayashi T., Zaita N., Chunwongse J., Obokata J.,
 RA Yamaguchi-Shinozaki K., Ohto C., Torazawa K., Meng B.Y., Sugita M.,
 RA Deno H., Kamogashira T., Yamada K., Kusuda J., Takaiwa F., Kato A.,
 RA Tohdoh N., Shimada H., Sugliura M.;
 RT "The complete nucleotide sequence of the tobacco chloroplast genome:
 RT its gene organization and expression.";
 RL EMBO J. 5:2043-2049(1986).
 CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
 CC HEME ATTACHMENT (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.
 CC -----
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 CC -----
 DR EMBL; Z00044; CAA77395.1; -.
 DR PIR; A05213; A05213.
 DR PFAM; PF01578; Cytc_asm; 1.
 KW Cytochrome c-type biogenesis; Chloroplast.
 SQ SEQUENCE 313 AA; 35558 MW; 0C9341F79C47A96 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 313;
 Best Local Similarity 75.0%; Pred. No. 8.1;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAS 10
 Db 303 HSYGSFSPS 310
 I:|||||I

RESULT 6
 ID IF2A_PYRHO STANDARD; PRT; 275 AA.
 AC O58655;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
 GN PH0961.
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-OT3;
 RX MEDLINE; 98344137.
 RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudo H. Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RL DNA Res. 5:55-76(1998).
 CC -1- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
 CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA

CC (BY SIMILARITY).
 CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
 CC CHAIN (BY SIMILARITY).
 CC -----
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 CC -----
 DR EMBL; AP000004; BAA30058.1; -.
 DR PFAM; PF00575; S1; 1.
 KW Initiation factor; Protein biosynthesis.
 SQ SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 275;
 Best Local Similarity 83.3%; Pred. No. 11;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
 Db 23 HNYGAF 28
 I:||||I

RESULT 7
 ID IPYR_PICPA STANDARD; PRT; 284 AA.
 AC O13505;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPP1.
 OS Pichia pastoris (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Pichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NRRL Y-11430;
 RX MEDLINE; 99034033.
 RA Cosano I.C., Alvarez P., Molina M., Nombela C.;
 RT "Cloning and sequence analysis of the Pichia pastoris TRP1, IPP1 and
 RT HIS3 genes.";
 RL Yeast 14:861-867(1998).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- COPACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; AJ001000; CAA04453.1; -.
 DR HSP; P00817; 1WG1.
 DR PROSITE; PS00387; PPASE; 1.
 DR PFAM; PF00719; Pyrophosphatase; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0
 FT ACT_SITE 56 56 BY SIMILARITY.
 FT BINDING 78 78 PROBABLE.
 FT SEQUENCE 284 AA; 31937 MW; 30AD27970D775D6 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 284;

Best Local Similarity 83.3%; Pred. No. 12;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8

|||||

Db 91 HNYGAF 96

RESULT 8

ID IPYR_KLUJA STANDARD; PRT; 286 AA.
AC P13998;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
DE HYDROLASE) (PPASE).
GN IPPI OR IPP.
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Kluyveromyces.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89189093.
RA Stark M.J.R., Milner J.S.;
RT "Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a
RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
RT and histone H3";
RL Yeast 5:35-50(1989).
RN [2]
RP SIMILARITY TO E.COLI AND YEAST PPASES.

RX MEDLINE; 90254161.
RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
RA Cooperman B.S.;
RT "Conservation of functional residues between yeast and E. coli
RT inorganic pyrophosphatases";
RL Biochim. Biophys. Acta 1038:338-345(1990).
CC -|- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
CC -|- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
CC -|- SUBUNIT: HOMODIMER.
CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -|- SIMILARITY: BELONGS TO THE PPASE FAMILY.

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DR EMBL; X14230; CAA32446.1; -
DR PIR; S07894; PWVL.
DR HSP; P00817; IWGL.
DR PROSITE; PS00387; PPASE; 1.
DR PFAM; PF00719; Pyrophosphatase; 1.
KW Hydrolase; Magnesium.
FT INIT MET 0 BY SIMILARITY.
FT ACT_SITE 56 56 PROBABLE.
FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 286 AA; 32034 MW; 11647F4BD916A2F CRC64;

Query Match 63.0%; Score 34; DB 1; Length 286;

Best Local Similarity 83.3%; Pred. No. 12;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8

|||||

Db 91 HNYGAF 96

RESULT 9

ID IPYR_YEAST STANDARD; PRT; 286 AA.
AC P00817;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
DE HYDROLASE) (PPASE).
GN IPPI OR PPAL OR PPA OR YBR011C OR YBR0202.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=X2180;
RX MEDLINE; 89083474.
RA Kolakowski L.F. Jr., Schloesser M., Cooperman B.S.;
RT "Cloning, molecular characterization and chromosome localization of
RT the inorganic pyrophosphatase (PPA) gene from S. cerevisiae";
RL Nucleic Acids Res. 16:10441-10452(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=S288C;
RX Entian K.-D., Koetter P., Rose M., Li Z., Thermann R., Brendel M.,
RA Baur A., Boles E., Miosga T., Schaaff-Gerstenschlaeger I.,
RA Zimmermann F.K.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE.
RX MEDLINE; 78087552.
RA Cohen S.A., Sterner R., Keim P.S., Heinrikson R.L.;
RT "Covalent structural analysis of yeast inorganic pyrophosphatase";
RL J. Biol. Chem. 253:889-897(1978).
RN [4]
RP SEQUENCE OF 25-35 AND 239-251.
RX STRAIN=S288C;
RX MEDLINE; 95203288.
RA Garrels J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a Saccharomyces cerevisiae protein
RT database";
RL Electrophoresis 15:1466-1486(1994).
RN [5]
RP SEQUENCE OF 239-249.
RX STRAIN=ATCC 38531 / Y41;
RX MEDLINE; 97089742.
RA Norbeck J., Blomberg A.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
RT Saccharomyces cerevisiae";
RL FEMS Microbiol. Lett. 137:1-8(1996).
RN [6]
RP ACTIVE SITE.
RX MEDLINE; 80109718.
RA Bond M.W., Chiu N.Y., Cooperman B.S.;
RT "Identification of an arginine important for enzymatic activity
RT within the covalent structure of yeast inorganic pyrophosphatase";
RL Biochemistry 19:94-102(1980).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RA Arutunian E.G., Terzian S.S., Voronova A.A., Kuranova I.P.,
RA Smirnova E.A., Vainstein B.K., Hohne W.E., Hansen G.;
RT "X-ray diffraction study of inorganic pyrophosphatase from baker's
RT yeast at the 3-A resolution";
RL Dokl. Akad. Nauk SSSR 258:1481-1492(1981).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE; 97148342.
RA Heikinheimo P., Lehtonen J., Baykov A., Lahti R., Cooperman B.S.,
RA Goldman A.;
RT "The structural basis for pyrophosphatase catalysis";

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RL Structure 4:1491-1508(1996).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RA Swaminathan K., Cooperman B.S., Lahti R., Voet D.;
RL Submitted (DEC-1997) to the PDB data bank.
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF MUTANTS LYS-78 AND LYS-117.
RX MEDLINE; 99096888.
RA Tuominen V., Heikinheimo P., Kajander T., Torkkel T., Hyytiä T.,
RA Kapyla J., Lahti R., Cooperman B.S., Goldman A.;
RT "The R78K and D117E active-site variants of Saccharomyces cerevisiae
RT soluble inorganic pyrophosphatase: structural studies and mechanistic
RT implications.";
RL J. Mol. Biol. 284:1565-1580(1998).
RN [11]
RP SIMILARITY TO E.COLI AND K.LACTIS PPASES.
RX MEDLINE; 90254161.
RA Lahti R., Kolakowski L.F. Jr., Helonen J., Vihinen M., Pohjanoksa K.,
RA Cooperman B.S.;
RT "Conservation of functional residues between yeast and E. coli
RT inorganic pyrophosphatases.";
RL Biochim. Biophys. Acta 1038:338-345(1990).
CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O -> 2 ORTHOPHOSPHATE.
CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY. IT BINDS UP TO 4 DIVALENT
CC CATIONS PER SUBUNIT, WITH THREE REQUIRED FOR ACTIVITY.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X13253; CAA31629.1; -.
DR EMBL; Z35880; CAA84949.1; -.
DR PIR; S45864; PWBY.
DR PDB; 1YPX; 15-OCT-91.
DR PDB; 1YPP; 07-DEC-96.
DR PDB; 1WGI; 19-NOV-97.
DR PDB; 1WGI; 19-NOV-97.
DR PDB; 1WGI; 19-NOV-97.
DR PDB; 1HUJ; 08-APR-98.
DR PDB; 1HUK; 08-APR-98.
DR PDB; 117E; 23-DEC-98.
DR PDB; 8PRK; 23-DEC-98.
DR SWISS-2DPAGE; P00817; YEAST.
DR YEPD; 7305; -.
DR SGD; L0000872; IPP1.
DR PROSITE; PS00387; PPASE; 1.
DR PFAM; PF00719; Pyrophosphatase; 1.
KW Hydrolase; Magnesium; 3D-structure.
FT INIT_MSET 0
FT ACT_SITE 56 56 PROBABLE.
FT BINDING 78 78 INORGANIC PYROPHOSPHATE.
FT CONFLICT 40 40 N -> D (IN REF. 3).
FT CONFLICT 71 71 D -> N (IN REF. 3).
FT CONFLICT 74 74 MISSING (IN REF. 3).
FT CONFLICT 123 123 E -> Q (IN REF. 3).
FT CONFLICT 136 136 Q -> E (IN REF. 3).
FT CONFLICT 186 186 N -> D (IN REF. 3).
FT CONFLICT 224 224 D -> N (IN REF. 3).
FT CONFLICT 266 266 L -> P (IN REF. 2).
FT STRAND 4 7
FT STRAND 16 20
FT STRAND 25 25
FT TURN 28 30
FT TURN 38 41
FT STRAND 45 55
FT STRAND 55 55

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FT STRAND 79 79
FT TURN 97 98
FT TURN 111 112
FT STRAND 121 123
FT TURN 131 132
FT STRAND 135 135
FT STRAND 138 146
FT STRAND 151 158
FT TURN 160 161
FT TURN 165 167
FT HELIX 172 175
FT TURN 176 177
FT TURN 179 180
FT HELIX 182 197
FT STRAND 203 203
FT HELIX 205 207
FT STRAND 210 210
FT HELIX 212 230
FT TURN 231 231
FT TURN 245 246
FT TURN 248 249
FT TURN 251 252
FT TURN 255 260
FT TURN 274 275
SQ SEQUENCE 286 AA; 32184 MW; F29390260B60C8B2 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 286;
Best Local Similarity 83.3%; Pred. NO. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 91 HNYGAF 96
||||:|

RESULT 10
HB2D_CANFA STANDARD; PRT; 266 AA.
AC P18470;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE DLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 BETA CHAIN PRECURSOR.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Canidae; Canis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90316610.
RA Sarmiento U.M., Storb R.;
RT "Nucleotide sequence of a dog DRB cDNA clone.";
RL Immunogenetics 31:396-399(1990).
CC -----
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CC -----
DR EMBL; M29511; AAA30874.1; -.
DR PIR; A45844; A45844.
DR HSSP; P13760; 2SEB.
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC II; Transmembrane; Glycoprotein; Signal.
FT SIGNAL 1 29
FT CHAIN 30 266
FT DOMAIN 30 124
FT DR-1 BETA CHAIN.
FT DLA CLASS II HISTOCOMPATIBILITY ANTIGEN,
FT EXTRACELLULAR BETA-1.

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FT DOMAIN 125 227 EXTRACELLULAR BETA-2.
 FT TRANSMEM 228 250
 FT DOMAIN 251 266 CYTOPLASMIC TAIL.
 FT DISULFID 44 108 BY SIMILARITY.
 FT DISULFID 146 202 BY SIMILARITY.
 FT CARBOHYD 48 POTENTIAL.
 SQ SEQUENCE 266 AA; 30151 MW; 4E8297BBF1ACDD67 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 266;
 Best Local Similarity 66.7%; Pred. No. 17;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHYNGSFAS 10
 ||||| I
 DB 109 RHYNGVIES 117

RESULT 11
 FATB_VIBAN
 ID FATB_VIBAN STANDARD; PRT; 322 AA.
 AC P11460;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE FERRIC ANGUIBACTIN-BINDING PROTEIN PRECURSOR.
 GN FATB.
 OS Vibrio anguillarum.
 OG Plasmid pJMI.
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-775;
 RX MEDLINE; 88139336.
 RA Actis L.A., Tolmasky M.E., Farrell D.H., Crosa J.H.;
 RT "Genetic and molecular characterization of essential components of
 the vibrio anguillarum plasmid-mediated iron-transport system.";
 RL J. Biol. Chem. 263:2853-2860(1988).
 RN [2]
 RP SEQUENCE OF 1-154 FROM N.A.
 RC STRAIN-775;
 RX MEDLINE; 92084677.
 RA Koester W.L., Actis L.A., Waldbeser L.S., Tolmasky M.E., Crosa J.H.;
 RT "Molecular characterization of the iron transport system mediated by
 the pJM1 plasmid in Vibrio anguillarum 775.";
 RL J. Biol. Chem. 266:23829-23833(1991).
 CC -!- FUNCTION: BINDS FERRIC ANGUIBACTIN; PART OF THE BINDING-PROTEIN-
 DEPENDENT TRANSPORT SYSTEM FOR UPTAKE OF FERRIC ANGUIBACTIN.
 CC -!- SUBCELLULAR LOCATION: ATTACHED TO THE INNER MEMBRANE BY A LIPID
 ANCHOR (POTENTIAL).
 CC -!- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
 PROTEIN FAMILY 8.
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EMBL; J03529; AAA91580.1; -.
 DR EMBL; M74068; AAA25643.1; ALT_INIT.
 DR PIR; A29928; A29928.
 DR PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
 DR PFAM; PF01497; Peripla_BP_2; 1.
 KW Transport; Iron transport; Signal; Inner membrane; Lipoprotein;
 KW Plasmid.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 322 FERRIC ANGUIBACTIN-BINDING PROTEIN.
 FT LIPID 23 23 N-ACYL DIGLYCERIDE (POTENTIAL).
 SQ SEQUENCE 322 AA; 35635 MW; FB8674EED5CF73F7 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 322;
 Best Local Similarity 75.0%; Pred. No. 21;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 3 HNYGSFAS 10
 ||||| I
 DB 203 HNYGSFSS 210

RESULT 12
 PF21_ARATH
 ID PF21_ARATH STANDARD; PRT; 398 AA.
 AC Q04088;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE POSSIBLE TRANSCRIPTION FACTOR POSF21.
 GN POSF21.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 OC Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV_ZURICH; TISSUE-LEAF;
 RX MEDLINE; 93251100.

RA Aeschbacher R.A., Schrott M., Potrykus I., Saul M.W.;
 RT "Isolation and molecular characterization of Posf21, an Arabidopsis
 thaliana gene which shows characteristics of a b-Zip class
 transcription factor";
 RL Plant J. 1:303-316(1991).
 CC -!- FUNCTION: PUTATIVE TRANSCRIPTION FACTOR WITH AN ACTIVATORY
 ROLE.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR.
 CC -!- DEVELOPMENTAL STAGE: EXPRESSED CONSTITUTIVELY AT A LOW LEVEL IN
 YOUNG SEEDLINGS AND IN ROOTS, STEMS AND LEAVES OF MATURE
 ARABIDOPSIS PLANTS.
 CC -!- SIMILARITY: TO OTHER BZIP PROTEINS.
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EMBL; X61031; CAA43366.1; -.
 DR PROSITE; PS00036; BZIP_BASIC; FALSE_NEG.
 DR PFAM; PF00170; bzip; 1.
 KW Transcription regulation; DNA-binding; Nuclear protein.
 FT DNA_BIND 203 222 BASIC MOTIF.
 FT DOMAIN 229 264 LEUCINE-ZIPPER.
 FT DOMAIN 340 364 POLY-GLN.
 FT DOMAIN 354 372 POLY-GLN.
 SQ SEQUENCE 398 AA; 44689 MW; 2DAA9EC9B9C14D11 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 398;
 Best Local Similarity 85.7%; Pred. No. 26;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NYGSFAS 10
 ||||| I
 DB 305 NYGSFSS 311

RESULT 13
 NCAP_CVHOC
 ID NCAP_CVHOC STANDARD; PRT; 448 AA.
 AC P33469;

```
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE NUCLEOCAPSID PROTEIN.
GN N.
OS Human coronavirus (strain OC43).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
[1]
RN PIR: A60003; A60003.
RX MEDLINE; 89243809.
RA Kamahora T., Soe L.H., Lai M.M.C.;
RT "Sequence analysis of nucleocapsid gene and leader RNA of human
RL coronavirus OC43."
RL Virus Res. 12:1-9(1989).
DR PIR: A60003; A60003.
DR PFAM; PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 448 AA; 49316 MW; 5193ABIAE0D75626 CRC64;

Query Match
Best Local Similarity 61.1%; Score 33; DB 1; Length 448;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
   |||||
DB 103 RHNRGSF 109

RESULT 14
SYE2_RICPR
ID SYE2_RICPR STANDARD; PRT; 470 AA.
AC Q9ZCT8;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE 2 (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE 2)
DE (GLURS 2).
GN GLTX2 OR RP623.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
[1]
RN PIR: A60003; A60003.
RX MEDLINE; 99039499.
RA Andersson S.G.E., Zomrodipour A., Andersson J.O.,
RA Sichertitz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria."
RL Nature 396:133-140(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) -> AMP +
CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
-----
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-----
EMBL; AJ235272; CAA15066.1; -.
DR HSSP; P27000; 1GLN.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE NEG.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
   SIMILAR 239 243 "KMSKS" REGION.
```

```
FT BINDING 242 242 ATP (BY SIMILARITY).
SQ SEQUENCE 470 AA; 53696 MW; DF1CE50A20B8A9FD CRC64;

Query Match
Best Local Similarity 61.1%; Score 33; DB 1; Length 470;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
   |||||
DB 31 ARHNRGKF 38

RESULT 15
SYE_AQUAE
ID SYE_AQUAE STANDARD; PRT; 473 AA.
AC O67271;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE)
DE (GLURS).
GN GLTX OR AQ_1221.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
[1]
RN PIR: A60003; A60003.
RX MEDLINE; 98196666.
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujaay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus."
RL Nature 392:353-358(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) -> AMP +
CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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-----
EMBL; AE000729; AAC07230.1; -.
DR PRINTS; PR00987; TRNASYNTHGLU.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
DR PFAM; PF00749; TRNA-synt_lc; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
   SIMILAR 242 246 "KMSKS" REGION.
FT BINDING 245 245 ATP (BY SIMILARITY).
SQ SEQUENCE 473 AA; 55121 MW; 5CB4D1590973E07A CRC64;
```

```
Query Match
Best Local Similarity 61.1%; Score 33; DB 1; Length 473;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
   |||||
DB 31 ARHNRGKF 38
```

Search completed: May 27, 2000, 20:07:17
Job time: 989 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:38:41 ; Search time 199.56 Seconds
(without alignments)
3.474 Million cell updates/sec

Title: US-09-016-061-68
Perfect score: 54
Sequence: 1 ARHNYGSPAS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL12:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	41	75.9	89	7 O19495	O19495 gallus gall
2	40	74.1	446	5 O62086	O62086 caenorhabdi
3	39	72.2	39	7 P79474	P79474 cervus elap
4	39	72.2	39	7 P79477	P79477 cervus elap
5	39	72.2	39	7 P79478	P79478 cervus elap
6	39	72.2	39	7 P79479	P79479 cervus elap
7	39	72.2	82	7 Q30606	Q30606 macaca mula
8	39	72.2	82	7 Q30608	Q30608 macaca mula
9	39	72.2	82	7 Q30637	Q30637 macaca mula
10	39	72.2	82	7 Q30638	Q30638 macaca mula
11	39	72.2	82	7 Q30658	Q30658 macaca mula
12	39	72.2	82	7 Q30659	Q30659 macaca mula
13	39	72.2	82	7 Q30659	Q30659 macaca mula
14	39	72.2	82	7 Q30667	Q30667 macaca mula
15	39	72.2	82	7 Q30668	Q30668 macaca mula
16	39	72.2	82	7 O19287	O19287 macaca mula
17	39	72.2	82	7 O19288	O19288 macaca mula
18	39	72.2	83	7 O98002	O98002 ovis aries
19	39	72.2	85	7 Q30796	Q30796 ovis aries
20	39	72.2	85	7 Q30800	Q30800 ovis aries

21	39	72.2	85	7 Q30803	Q30803 ovis aries
22	39	72.2	85	7 Q30812	Q30812 ovis aries
23	39	72.2	85	7 P79966	P79966 capra aegag
24	39	72.2	85	7 P79967	P79967 capra aegag
25	39	72.2	85	7 P79968	P79968 capra aegag
26	39	72.2	86	7 Q30326	Q30326 bos taurus
27	39	72.2	89	7 O19210	O19210 capra hircu
28	39	72.2	89	7 O19212	O19212 capra hircu
29	39	72.2	89	7 Q30521	Q30521 galago sene
30	39	72.2	89	7 Q30522	Q30522 galago sene
31	39	72.2	89	7 Q30526	Q30526 galago sene
32	39	72.2	89	7 Q30217	Q30217 homo sapien
33	39	72.2	107	7 Q9XRW7	Q9XRW7 phasianus c
34	39	72.2	225	7 Q30844	Q30844 ovis aries
35	39	72.2	232	7 Q9XRW6	Q9XRW6 phasianus c
36	39	72.2	266	7 Q30632	Q30632 macaca mula
37	39	72.2	611	2 Q9X5S2	Q9X5S2 streptomyce
38	36	66.7	78	6 O97835	O97835 ovis aries
39	36	66.7	78	6 O97839	O97839 ovis aries
40	36	66.7	78	6 O97844	O97844 ovis aries
41	36	66.7	78	6 O97968	O97968 ovis aries
42	36	66.7	79	7 O19191	O19191 prionalluru
43	36	66.7	79	7 O19192	O19192 prionalluru
44	36	66.7	79	7 O19380	O19380 felis silve
45	36	66.7	79	7 O19381	O19381 felis silve

ALIGNMENTS

RESULT 1

O19495
ID O19495 PRELIMINARY; PRT; 89 AA.
AC O19495;
DC 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE MHC CLASS II BETA 1 DOMAIN (FRAGMENT).
GN B-LBI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauaria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=15.151-5; TISSUE=BURSA;
RA PHARR G.T., DODGSON J.B., HUNT H.D., BACON L.D.;
RL Immunogenetics 47:350-354(1998).
DR EMBL; U91532; AAC15813.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.

FT NON_TER 1 1
FT NON_TER 89 89
SQ SEQUENCE 89 AA; 10724 MW; FDAC6024 CRC32;

Query Match 75.9%; Score 41; DB 7; Length 89;
Best Local Similarity 77.8%; Pred. No. 0.58;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSEAS 10
Db 75 RHNYGDFES 83

RESULT 2

O62086
ID O62086 PRELIMINARY; PRT; 446 AA.
AC O62086;
DC 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)
DE C3IH5.6 PROTEIN.
GN C3IH5.6.

OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentes; Rhabditia; Rhabditida;
 OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA KERSHAW J.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KRISTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEN R.,
 RA SMAILDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WAYSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RL Nature 368:32-38(1994).
 DR EMBL; 293778; CAB07846.1; -.
 SQ SEQUENCE 446 AA; 50763 MW; B347C0C8 CRC32;

Query Match 74.1%; Score 40; DB 5; Length 446;
 Best Local Similarity 77.8%; Pred. No. 4.8;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
 Db [111111];
 Db 51 RHNYGSAAA 59

RESULT 3
 P79474
 ID P79474 PRELIMINARY; PRT; 39 AA.
 AC P79474;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea; Cervidae;
 OC Cervinae; Cervus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SWARRICK P.A., CRAWFORD A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63077; AAB37777.1; -.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4767 MW; E01AA287 CRC32;

Query Match 72.2%; Score 39; DB 7; Length 39;
 Best Local Similarity 77.8%; Pred. No. 0.6;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
 Db [111111];
 Db 25 RHNYGVFES 33

RESULT 4
 P79477
 ID P79477 PRELIMINARY; PRT; 39 AA.
 AC P79477;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)

DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea; Cervidae;
 OC Cervinae; Cervus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SWARRICK P.A., CRAWFORD A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63080; AAB37780.1; -.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match 72.2%; Score 39; DB 7; Length 39;
 Best Local Similarity 77.8%; Pred. No. 0.6;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
 Db [111111];
 Db 25 RHNYGVFES 33

RESULT 5
 P79478
 ID P79478 PRELIMINARY; PRT; 39 AA.
 AC P79478;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea; Cervidae;
 OC Cervinae; Cervus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SWARRICK P.A., CRAWFORD A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63081; AAB37781.1; -.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match 72.2%; Score 39; DB 7; Length 39;
 Best Local Similarity 77.8%; Pred. No. 0.6;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
 Db [111111];
 Db 25 RHNYGVFES 33

RESULT 6
 P79479
 ID P79479 PRELIMINARY; PRT; 39 AA.
 AC P79479;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea; Cervidae;
 OC Cervinae; Cervus.
 RN [1]
 RP SEQUENCE FROM N.A.

RA SWARRICK P.A., CRAWFORD A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63082; AAC37782.1; -.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match 72.2%; Score 39; DB 7; Length 39;
 Best Local Similarity 77.8%; Pred. No. 0.6;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
 Db 25 RHNYGVFES 33
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RESULT 7
 Q30606 PRELIMINARY; PRT; 82 AA.
 ID Q30606;
 AC Q30606;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE MAJOR HISTOCOMPATIBILITY COMPLEX CLASS II (FRAGMENT).
 GN MHC-DRB.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Cercopitheidae; Cercopitheinae;
 OC Macaca.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97152405.
 RA KNAPP L.A., CADAVID L.F., EBERLE M.E., KNECHTLE S.J., BONTROP R.E.,
 RT "Identification of new mamu-DRB alleles using DGGE and direct
 sequencing.";
 RL Immunogenetics 45:171-179(1997).
 DR EMBL; U57948; AAC50981.1; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 82 82
 SQ SEQUENCE 82 AA; 9921 MW; A871F869 CRC32;

Query Match 72.2%; Score 39; DB 7; Length 82;
 Best Local Similarity 77.8%; Pred. No. 1.3;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
 Db 73 RHNYGVFES 81
 |||||

RESULT 8
 Q30608 PRELIMINARY; PRT; 82 AA.
 ID Q30608;
 AC Q30608;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE MAJOR HISTOCOMPATIBILITY COMPLEX CLASS II (FRAGMENT).
 GN MHC-DRB.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Cercopitheidae; Cercopitheinae;
 OC Macaca.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97152405.
 RA KNAPP L.A., CADAVID L.F., EBERLE M.E., KNECHTLE S.J., BONTROP R.E.,

RA WATKINS D.I.;
 RT "Identification of new mamu-DRB alleles using DGGE and direct
 sequencing.";
 RL Immunogenetics 45:171-179(1997).
 DR EMBL; U57950; AAC50983.1; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 82 82
 SQ SEQUENCE 82 AA; 9880 MW; 84AB3DAA CRC32;

Query Match 72.2%; Score 39; DB 7; Length 82;
 Best Local Similarity 77.8%; Pred. No. 1.3;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
 Db 73 RHNYGVFES 81
 |||||

RESULT 9
 Q30637 PRELIMINARY; PRT; 82 AA.
 ID Q30637;
 AC Q30637;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).
 GN MHC DR-BETA 1.
 OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Cercopitheidae; Cercopitheinae;
 OC Macaca.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-1KM; TISSUE=BLOOD;
 RX MEDLINE; 93123123.
 RA SLIERENDREGT B.L., VAN NOORT J.T., BAKAS R.M., OTTING N., JONKER M.,
 RA BONTROP R.E.;
 RT "Evolutionary stability of transspecies major histocompatibility
 complex class II DRB lineages in humans and rhesus monkeys.";
 RL Hum. Immunol. 35:29-39(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-1KM; TISSUE=BLOOD;
 RA SLIERENDREGT B.L.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Z26140; CRA81141.1; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 82 82
 SQ SEQUENCE 82 AA; 10024 MW; 9D3AA6A2 CRC32;

Query Match 72.2%; Score 39; DB 7; Length 82;
 Best Local Similarity 77.8%; Pred. No. 1.3;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAS 10
 Db 73 RHNYGVFES 81
 |||||

RESULT 10
 Q30638 PRELIMINARY; PRT; 82 AA.
 ID Q30638;
 AC Q30638;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-NOV-1998 (Tremblrel. 08, Last annotation update)
 DE MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).


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GN MHC DR-BETA 1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae;
OC Macaca.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1KL; TISSUE=BLOOD;
RX MEDLINE; 93123123.
RA SLIERENDREGT B.L.; VAN NOORT J.T., BAKAS R.M., OTTING N., JONKER M.,
RA BONTROP R.E.;
RT "Evolutionary stability of transspecies major histocompatibility
complex class II DRB lineages in humans and rhesus monkeys.";
RL Hum. Immunol. 35:29-39(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1KL; TISSUE=BLOOD;
RA SLIERENDREGT B.L.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z26141; CAA81142.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 9953 MW; CC45E3FD CRC32;

Query Match 72.2%; Score 39; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHYGVSFAS 10
Db 73 RHYGVFES 81

RESULT 11
ID Q30658 PRELIMINARY; PRT; 82 AA.
AC Q30658;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).
GN MHC DR-BETA 5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae;
OC Macaca.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1KL; TISSUE=BLOOD;
RX MEDLINE; 93123123.
RA SLIERENDREGT B.L.; VAN NOORT J.T., BAKAS R.M., OTTING N., JONKER M.,
RA BONTROP R.E.;
RT "Evolutionary stability of transspecies major histocompatibility
complex class II DRB lineages in humans and rhesus monkeys.";
RL Hum. Immunol. 35:29-39(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1KL; TISSUE=BLOOD;
RA SLIERENDREGT B.L.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z26161; CAA81162.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 9964 MW; F161DC3E CRC32;

Query Match 72.2%; Score 39; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHYGVSFAS 10
Db 73 RHYGVFES 81

RESULT 12
ID Q30659 PRELIMINARY; PRT; 82 AA.
AC Q30659;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).
GN MHC DR-BETA 5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae;
OC Macaca.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1KL; TISSUE=BLOOD;
RX MEDLINE; 93123123.
RA SLIERENDREGT B.L.; VAN NOORT J.T., BAKAS R.M., OTTING N., JONKER M.,
RA BONTROP R.E.;
RT "Evolutionary stability of transspecies major histocompatibility
complex class II DRB lineages in humans and rhesus monkeys.";
RL Hum. Immunol. 35:29-39(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1KL; TISSUE=BLOOD;
RA SLIERENDREGT B.L.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z26162; CAA81163.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 9940 MW; 79205B65 CRC32;

Query Match 72.2%; Score 39; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHYGVSFAS 10
Db 73 RHYGVFES 81

RESULT 13
ID Q30666 PRELIMINARY; PRT; 82 AA.
AC Q30666;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).
GN MHC DR-BETA.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae;
OC Macaca.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1KL; TISSUE=BLOOD;
RX MEDLINE; 93123123.
RA SLIERENDREGT B.L.; VAN NOORT J.T., BAKAS R.M., OTTING N., JONKER M.,
RA BONTROP R.E.;
RT "Evolutionary stability of transspecies major histocompatibility
complex class II DRB lineages in humans and rhesus monkeys.";
RL Hum. Immunol. 35:29-39(1992).

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RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=IMP; TISSUE=BLOOD;
RA  SLIERENDREGT B.L.;
RL  Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR  EMBL; Z26170; CAA81171.1; -.
DR  PFAM; PF00969; MHC_II_beta; 1.
KW  MHC.
FT  NON_TER      1
   NON_TER      82
SQ  SEQUENCE      82 AA; 9881 MW; 2B69C7C0 CRC32;

Query Match      72.2%; Score 39; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 RHNYGSFAS 10
Db  73 RHNYGVFES 81

RESULT 14
Q30667
ID  Q30667      PRELIMINARY;      PRT;      82 AA.
AC  Q30667;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE  MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).
GN  MHC DR-BETA.
OS  Macaca mulatta (Rhesus macaque).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC  Eutheria; Primates; Catarrhini; Cercopitheciidae; Cercopitheciinae;
OC  Macaca.
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=IMR; TISSUE=BLOOD;
RX  MEDLINE; 93123123.
RA  SLIERENDREGT B.L.; VAN NOORT J.T., BAKAS R.M., OTTING N., JONKER M.,
   BONTROP R.E.;
RT  "Evolutionary stability of transspecies major histocompatibility
   complex class II DRB lineages in humans and rhesus monkeys.";
RL  Hum. Immunol. 35:29-39(1992).
DR  EMBL; Z26172; CAA81173.1; -.
DR  PFAM; PF00969; MHC_II_beta; 1.
KW  MHC.
FT  NON_TER      1
   NON_TER      82
SQ  SEQUENCE      82 AA; 9894 MW; CC46DD8A CRC32;

Query Match      72.2%; Score 39; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 RHNYGSFAS 10
Db  73 RHNYGVFES 81

Search completed: May 27, 2000, 19:38:41
Job time: 2374 sec

RN  [2]
RP  SEQUENCE FROM N.A.
RC  STRAIN=IMP; TISSUE=BLOOD;
RA  SLIERENDREGT B.L.;
RL  Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR  EMBL; Z26170; CAA81171.1; -.
DR  PFAM; PF00969; MHC_II_beta; 1.
KW  MHC.
FT  NON_TER      1
   NON_TER      82
SQ  SEQUENCE      82 AA; 9881 MW; 2B69C7C0 CRC32;

Query Match      72.2%; Score 39; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 RHNYGSFAS 10
Db  73 RHNYGVFES 81

RESULT 15
Q30668
ID  Q30668      PRELIMINARY;      PRT;      82 AA.
AC  Q30668;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-NOV-1998 (TrEMBLrel. 08, Last annotation update)

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DE  MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).
GN  MHC DR-BETA.
OS  Macaca mulatta (Rhesus macaque).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC  Eutheria; Primates; Catarrhini; Cercopitheciidae; Cercopitheciinae;
OC  Macaca.
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=IKL; TISSUE=BLOOD;
RX  MEDLINE; 93123123.
RA  SLIERENDREGT B.L.; VAN NOORT J.T., BAKAS R.M., OTTING N., JONKER M.,
   BONTROP R.E.;
RT  "Evolutionary stability of transspecies major histocompatibility
   complex class II DRB lineages in humans and rhesus monkeys.";
RL  Hum. Immunol. 35:29-39(1992).
DR  EMBL; Z26172; CAA81173.1; -.
DR  PFAM; PF00969; MHC_II_beta; 1.
KW  MHC.
FT  NON_TER      1
   NON_TER      82
SQ  SEQUENCE      82 AA; 9894 MW; CC46DD8A CRC32;

Query Match      72.2%; Score 39; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 1.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  2 RHNYGSFAS 10
Db  73 RHNYGVFES 81

Search completed: May 27, 2000, 19:38:41
Job time: 2374 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:21:36 ; Search time 148.45 Seconds
(without alignments)
1.596 Million cell updates/sec

Title: US-09-016-061-68
Perfect score: 54
Sequence: 1 ARHNYGSFAS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	54	100.0	10	1 W76024	LM609 grafted anti
2	51	94.4	10	1 W76025	LM609 grafted anti
3	51	94.4	10	1 W76030	LM609 grafted anti
4	50	92.6	10	1 W76026	LM609 grafted anti
5	50	92.6	10	1 W76027	LM609 grafted anti
6	50	92.6	10	1 W76028	LM609 grafted anti
7	50	92.6	10	1 W76029	LM609 grafted anti
8	50	92.6	10	1 W76010	LM609 grafted anti
9	50	92.6	11	1 W76001	Vitaxin antibody h
10	50	92.6	11	1 W76003	LM609 antibody hea
11	49	90.7	10	1 W76037	LM609 grafted anti
12	48	88.9	10	1 W76040	LM609 grafted anti
13	47	87.0	10	1 W76021	LM609 grafted anti
14	46	85.2	10	1 W76039	LM609 grafted anti
15	46	85.2	10	1 W76022	LM609 grafted anti
16	46	85.2	10	1 W76023	LM609 grafted anti
17	45	83.3	10	1 W76020	LM609 grafted anti
18	43	79.6	10	1 W76038	LM609 grafted anti
19	42	77.8	11	1 W84099	Vitronectin alpha-
20	42	77.8	11	1 W84093	Murine vitronectin
21	42	77.8	11	1 W84097	Humanised anti-alp
22	36	66.7	11	1 R79157	Human IGE receptor
23	36	66.7	11	1 R79155	Human IGE receptor
24	36	66.7	11	1 W27357	Heavy chain variab
25	36	66.7	11	1 W27526	Heavy chain variab
26	36	66.7	11	1 W27354	Heavy chain variab
27	36	66.7	11	1 W01578	Lead binding MAB 8
28	36	66.7	239	1 W73874	Human antiFc epsil
29	36	66.7	242	1 W73876	Human antiFc epsil
30	33	61.1	80	1 R13396	HLA-DRw12a antigen
31	33	61.1	80	1 R13397	HLA-DRw12b antigen
32	32	59.3	11	1 W22700	Peptide sequence #
33	32	59.3	15	1 W25799	Synthetic human SI
34	32	59.3	18	1 W27062	Chemically syntheses

ALIGNMENTS

RESULT 1

W76024
ID W76024 standard; Protein; 10 AA.

AC W76024;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #6.

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis; primer; V-H region; CDR;

KW complementarity determining region.

OS Mus sp.

PN WO9833919-A2.

PD 06-AUG-1998.

PF 30-JAN-1998; U01826.

PR 30-JAN-1997; US-791391.

PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

DR WPI; 98-437472/37.

DR N-PSDB: V49861.

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT Integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

PS Claim 62: Page 41: 129pp: English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody

CC vitaxin bind selectively to integrin alphavbeta3 and can be used to

CC inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies

CC contain non-murine framework regions so are suitable for use in humans.

CC Enhanced types of LM609 have affinity more than 90 times greater than

CC that of parent the parent antibody.

SQ Sequence 10 AA;

Query Match 100.0%; Score 54; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00083;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAS 10

Db 1 ARHNYGSFAS 10

RESULT 2

W76025

ID W76025 standard; Protein; 10 AA.

AC W76025;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #7.

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49862.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region; LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 94.4%; Score 51; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0027;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAS 10
 |||||
 DB 1 ARHNYGSFAT 10

RESULT 3
 W76030
 ID W76030 standard; Protein; 10 AA.
 AC W76030;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #12.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49867.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 94.4%; Score 51; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0027;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAS 10
 |||||
 DB 1 ARHNYGSFAA 10

RESULT 4
 W76026
 ID W76026 standard; Protein; 10 AA.
 AC W76026;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #8.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49863.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 92.6%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0041;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 DB 1 ARHNYGSFA 9

RESULT 5
 W76027
 ID W76027 standard; Protein; 10 AA.

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AC W76027;
DE 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #9.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; 001826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB; V49864.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; 001826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB; V49864.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 92.6%; Score 50; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 7
W76029
ID W76029 standard; Protein; 10 AA.
AC W76029;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #11.
DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; 001826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB; V49866.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 92.6%; Score 50; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0041;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9

RESULT 6
W76028
ID W76028 standard; Protein; 10 AA.
AC W76028;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #10.
DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; 001826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB; V49865.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.

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PT	LM609, also related nucleic acid, used to treat, prevent or diagnose	PT	LM609, also related nucleic acid, used to treat, prevent or diagnose
PT	angiogenesis or restenosis	PT	angiogenesis or restenosis
PS	Claim 1; Fig 1a; 129pp; English.	PS	Claim 1; Fig 1a; 129pp; English.
CC	This sequence represents a fragment of the vitaxin antibody variable	CC	This sequence represents a fragment of the vitaxin antibody variable
CC	heavy chain region. Vitaxin and the antibody LM609 bind selectively to	CC	heavy chain region. Vitaxin and the antibody LM609 bind selectively to
CC	integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3	CC	integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
CC	to a ligand and thus block integrin-mediated signal transduction. This is	CC	to a ligand and thus block integrin-mediated signal transduction. This is
CC	useful in the treatment, prevention and diagnosis of alphavbeta3-mediated	CC	useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
CC	disease, specifically angiogenesis and restenosis (but also e.g.	CC	disease, specifically angiogenesis and restenosis (but also e.g.
CC	(non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,	CC	(non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
CC	cancer, psoriasis, rheumatoid arthritis, macular degeneration,	CC	cancer, psoriasis, rheumatoid arthritis, macular degeneration,
CC	osteoporosis etc.). The antibodies contain non-murine framework regions	CC	osteoporosis etc.). The antibodies contain non-murine framework regions
CC	so are suitable for use in humans. Enhanced types of LM609 have affinity	CC	so are suitable for use in humans. Enhanced types of LM609 have affinity
CC	more than 90 times greater than that of parent the parent antibody.	CC	more than 90 times greater than that of parent the parent antibody.
SQ	Sequence 117 AA;	SQ	Sequence 117 AA;
QY	1 ARHNYGSFA 9	QY	1 ARHNYGSFA 9
DB	97 ARHNYGSFA 105	DB	97 ARHNYGSFA 105
RESULT 10		RESULT 10	
ID	W76003 standard; Protein; 117 AA.	ID	W76003 standard; Protein; 117 AA.
AC	W76003;	AC	W76003;
DT	02-NOV-1998 (first entry)	DT	02-NOV-1998 (first entry)
DE	LM609 antibody heavy chain variable region protein fragment.	DE	LM609 antibody heavy chain variable region protein fragment.
KW	Vitaxin; antibody; variable region; heavy chain; light chain; integrin;	KW	Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW	LM609; inhibitor; integrin-mediated signal transduction; treatment;	KW	LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW	diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;	KW	diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW	neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;	KW	neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW	macular degeneration; osteoporosis.	KW	macular degeneration; osteoporosis.
OS	Mus sp.	OS	Mus sp.
PN	WO9833919-A2.	PN	WO9833919-A2.
PD	06-AUG-1998.	PD	06-AUG-1998.
PF	30-JAN-1997; US-791391.	PF	30-JAN-1997; US-791391.
PR	30-JAN-1997; US-791391.	PR	30-JAN-1997; US-791391.
PA	(IXSY-) IXSYS INC.	PA	(IXSY-) IXSYS INC.
PI	Glaser SM, Huse WD;	PI	Glaser SM, Huse WD;
DR	WPI: 98-437472/37.	DR	WPI: 98-437472/37.
DR	N-PSDB; V49822.	DR	N-PSDB; V49822.
PT	Humanised antibody, Vitaxin, that binds selectively to alphavbeta3	PT	Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT	integrin - and related grafted antibodies based on murine monoclonal	PT	integrin - and related grafted antibodies based on murine monoclonal
PT	LM609, also related nucleic acid, used to treat, prevent or diagnose	PT	LM609, also related nucleic acid, used to treat, prevent or diagnose
PT	angiogenesis or restenosis	PT	angiogenesis or restenosis
PS	Claim 43; Fig 2a; 129pp; English.	PS	Claim 43; Fig 2a; 129pp; English.
CC	This sequence represents the LM609 antibody variable heavy chain region.	CC	This sequence represents the LM609 antibody variable heavy chain region.
CC	LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3	CC	LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
CC	and can be used to inhibit binding of alphavbeta3 to a ligand and thus	CC	and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC	block integrin-mediated signal transduction. This is useful in the	CC	block integrin-mediated signal transduction. This is useful in the
CC	treatment, prevention and diagnosis of alphavbeta3-mediated disease,	CC	treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC	specifically angiogenesis and restenosis (but also e.g. (non-)immune	CC	specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC	inflammation, diabetic retinopathy, neovascular glaucoma, cancer,	CC	inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC	psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis	CC	psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC	etc.). The antibodies contain non-murine framework regions so are	CC	etc.). The antibodies contain non-murine framework regions so are
CC	suitable for use in humans. Enhanced types of LM609 have affinity	CC	suitable for use in humans. Enhanced types of LM609 have affinity
CC	more than 90 times greater than that of parent the parent antibody.	CC	more than 90 times greater than that of parent the parent antibody.
SQ	Sequence 117 AA;	SQ	Sequence 117 AA;
QY	1 ARHNYGSFA 9	QY	1 ARHNYGSFA 9
DB	97 ARHNYGSFA 105	DB	97 ARHNYGSFA 105
Query Match	92.6%; Score 50; DB 1; Length 117;	Query Match	92.6%; Score 50; DB 1; Length 117;
Best Local Similarity	100.0%; Pred. No. 0.051;	Best Local Similarity	100.0%; Pred. No. 0.051;
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ARHNYGSFA 9	QY	1 ARHNYGSFA 9
DB	97 ARHNYGSFA 105	DB	97 ARHNYGSFA 105
RESULT 9		RESULT 9	
ID	W76001 standard; Protein; 117 AA.	ID	W76001 standard; Protein; 117 AA.
AC	W76001;	AC	W76001;
DT	02-NOV-1998 (first entry)	DT	02-NOV-1998 (first entry)
DE	Vitaxin antibody heavy chain variable region protein fragment.	DE	Vitaxin antibody heavy chain variable region protein fragment.
KW	Vitaxin; antibody; variable region; heavy chain; light chain; integrin;	KW	Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW	LM609; inhibitor; integrin-mediated signal transduction; treatment;	KW	LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW	diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;	KW	diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW	neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;	KW	neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW	macular degeneration; osteoporosis.	KW	macular degeneration; osteoporosis.
OS	Mus sp.	OS	Mus sp.
PN	WO9833919-A2.	PN	WO9833919-A2.
PD	06-AUG-1998.	PD	06-AUG-1998.
PF	30-JAN-1997; US-791391.	PF	30-JAN-1997; US-791391.
PR	30-JAN-1997; US-791391.	PR	30-JAN-1997; US-791391.
PA	(IXSY-) IXSYS INC.	PA	(IXSY-) IXSYS INC.

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RESULT 11
W76037
ID W76037 standard; Protein; 10 AA.
AC W76037;
DE 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #13.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49874.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62: Page 43: 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 90.7%; Score 49; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0061;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAS 10
   |||||
DB 1 ARHNGSFAS 10

RESULT 12
W76040
ID W76040 standard; Protein; 10 AA.
AC W76040;
DE 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #16.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49877.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

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PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62: Page 43: 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 88.9%; Score 48; DB 1; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.0091;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFAS 10
   |||||
DB 1 ARHNGSFVS 10

RESULT 13
W76021
ID W76021 standard; Protein; 10 AA.
AC W76021;
DE 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #3.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49858.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62: Page 41: 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 87.0%; Score 47; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.014;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```



```

QY 1 ARHNYGSFA 9
   |||||
Db 1 ARHNYGSYA 9

RESULT 14
ID W76039 standard; Protein; 10 AA.
AC W76039;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #15.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR N-PSDB; V49876.
DR WPI; 98-437472/37.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 43; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match      85.2%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
   |||||
Db 1 ARHNYGSF 8

Search completed: May 27, 2000, 19:21:36
Job time: 1590 sec

QY 1 ARHNYGSFA 9
   |||||
Db 1 ARHNYGSYA 9

RESULT 15
ID W76022 standard; Protein; 10 AA.
AC W76022;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #4.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR N-PSDB; V49876.
DR WPI; 98-437472/37.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related nucleic acid, used to treat, prevent or diagnose
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 43; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match      85.2%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
   |||||
Db 1 ARHNYGSF 8

RESULT 15
ID W76022 standard; Protein; 10 AA.
AC W76022;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #4.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.

```


GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:26:43 ; Search time 163.56 Seconds
(without alignments)
3.585 Million cell updates/sec

Title: US-09-016-061-70
Perfect score: 55
Sequence: 1 ARHNYGSFAT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

PIR_63:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	70.9	446	2	T19625
2	37	67.3	448	1	A60003
3	36	65.5	82	2	I51106
4	36	65.5	89	2	S38688
5	36	65.5	89	2	S38683
6	36	65.5	89	2	S38684
7	36	65.5	225	2	I47095
8	35	63.6	31	2	S00685
9	35	63.6	201	2	S38725
10	35	63.6	201	2	S55040
11	35	63.6	262	2	G69040
12	35	63.6	347	2	S43771
13	35	63.6	1101	2	T16840
14	34	61.8	110	2	S26317
15	34	61.8	110	2	S26317
16	34	61.8	210	1	B69265
17	34	61.8	275	2	D71087
18	34	61.8	275	2	G75130
19	34	61.8	287	1	PWBV
20	34	61.8	287	1	PWBV
21	34	61.8	527	2	T39741
22	34	61.8	548	2	T25424
23	33	60.0	65	2	S17441
24	33	60.0	80	2	I34469
25	33	60.0	80	2	I68777
26	33	60.0	81	2	I54550
27	33	60.0	85	2	I59634
28	33	60.0	89	2	S38676
29	33	60.0	89	2	S38680
30	33	60.0	89	2	S57512

31	33	60.0	123	2	C25239
32	33	60.0	167	2	T16454
33	33	60.0	200	2	D32526
34	33	60.0	237	2	C27060
35	33	60.0	266	2	I54287
36	33	60.0	266	2	A27618
37	33	60.0	266	2	I54295
38	33	60.0	279	2	T05421
39	33	60.0	297	2	T32719
40	33	60.0	360	2	S48566
41	33	60.0	383	2	S56179
42	33	60.0	467	1	P2WL33
43	33	60.0	470	2	H71667
44	33	60.0	473	2	D70405
45	33	60.0	512	2	E64119

MHC class II histo
hypotheical prote
class II histocomp
class II histocomp
gene HLA-DRB1 prot
class II histocomp
lymphocyte antigen
hypotheical prote
hypotheical prote
secreted glycoprot
L2 protein - human
glutamate--tRNA 11
glutamate--tRNA 11
NAD(P)+ transhydro

ALIGNMENTS

RESULT 1

T19625

hypotheical protein C31H5.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T19625

R:Kershaw, J. submitted to the EMBL Data Library, April 1997

A:Reference number: Z19153

A:Accession: T19625

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-446 <WIL>

A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6

A:Experimental source: clone C31H5

C:Genetics:

A:Gene: CESP:C31H5.6

A:Map position: 1

A:introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3

Query Match 70.9%; Score 39; DB 2; Length 446;
Best Local Similarity 87.5%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFA 9

Db 51 RHNYGSHA 58

RESULT 2

A60003

nucleocapsid protein - human coronavirus (strain OC43)

C:Species: human coronavirus

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Feb-1999

C:Accession: A60003

R:Kamahora, T.; Soe, L.H.; Lai, M.M.C.

Virus Res. 12, 1-9, 1999

A:Title: Sequence analysis of nucleocapsid gene and leader RNA of human coronavirus O

A:Reference number: A60003; MUID:89243809

A:Accession: A60003

A:Molecule type: genomic RNA

C:Residues: 1-448 <KAM>

A:Gene: N

C:Superfamily: coronavirus nucleocapsid protein

C:Keywords: glycoprotein; nucleocapsid

F:17,221,336,388,408,421/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.3%; Score 37; DB 1; Length 448;
Best Local Similarity 77.8%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY      2 RHNYGSFAT 10
Db      103 RHNRGSFAT 111
||| ||| |
||| ||| |

RESULT  3
I51106
Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)
C:Species: Phasianus colchicus (ring-necked pheasant)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
C:Accession: I51106
R:Wittzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.
Immunogenetics 39, 395-403, 1994
A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-necked pheasant
A:Reference number: I51103; MUID:94245280
A:Accession: I51106
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-82 <WIT>
A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match      65.5%; Score 36; DB 2; Length 82;
Best Local Similarity 85.7%; Pred. No. 4.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 RHNYGSF 8
Db      75 RHNYGVF 81
||| ||| |
||| ||| |

RESULT  4
S38688
MHC class II histocompatibility antigen HLA-DR-08 beta chain - Galago senegalensis (fragment)
C:Species: Galago senegalensis
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997
C:Accession: S38688
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from genomic DNA
A:Reference number: S38688
A:Accession: S38688
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27158
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match      65.5%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 RHNYGSF 8
Db      75 RHNYGVF 81
||| ||| |
||| ||| |

RESULT  5
S38683
MHC class II histocompatibility antigen HLA-DR-03 beta chain - Galago senegalensis (fragment)
C:Species: Galago senegalensis
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997
C:Accession: S38683
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from genomic DNA
A:Reference number: S38676
A:Accession: S38683
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27153
```

```
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match      65.5%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 RHNYGSF 8
Db      75 RHNYGVF 81
||| ||| |
||| ||| |

RESULT  6
S38684
MHC class II histocompatibility antigen HLA-DR-04 beta chain - Galago senegalensis (fragment)
C:Species: Galago senegalensis
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997
C:Accession: S38684
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from genomic DNA
A:Reference number: S38676
A:Accession: S38684
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27154
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match      65.5%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 4.6;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 RHNYGSF 8
Db      75 RHNYGVF 81
||| ||| |
||| ||| |

RESULT  7
I47095
MHC class II OVAR-DR-beta-3 - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 23-Jul-1999
C:Accession: I47095
R:Rabb, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.
Anim. Genet. 24, 249-255, 1993
A:Title: Isolation, characterization and evolution of ovine major histocompatibility antigen (MHC) class II OVAR-DRB3
A:Reference number: I47075; MUID:94057592
A:Accession: I47095
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-225 <FAB>
A:Cross-references: GB:L04790; NID:g458880; PIDN:AAA16562.1; PID:g458881
C:Genetics:
A:Gene: OVAR-DRB3
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match      65.5%; Score 36; DB 2; Length 225;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 RHNYGSF 8
Db      68 RHNYGVF 74
||| ||| |
||| ||| |

RESULT  8
S00685
Hypothetical protein 3 - phage P1
C:Species: phage P1
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C:Accession: S00685
```

R:Eliason, J.L.; Sternberg, N.
J. Mol. Biol. 198, 281-293, 1987
A:Title: Characterization of the binding sites of c1 repressor of bacteriophage PL. Evid
A:Reference number: S00684; MUID:88118929
A:Accession: S00685
A>Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-31 <ELI>
A:Cross-references: EMBL:X06561; NID:gl5128; PIDN:CAA29805.1; PID:gi5130

Query Match 63.6%; Score 35; DB 2; Length 31;
Best Local Similarity 66.7%; Pred. No. 2.5;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAT 10
| | | | | : |
Db 18 RHNYGFHST 26

RESULT 9
S38725
multicatalytic endopeptidase complex chain RC7-I - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 08-Oct-1999
A:Accession: S38725; S38726
R:Nishimura, C.; Tamura, T.; Tokunaga, F.; Tanaka, K.; Ichihara, A.
FEBS Lett. 332, 52-56, 1993

A:Title: cDNA cloning of rat proteasome subunit RC7-I, a homologue of yeast PRE1 essential

A:Reference number: S38725; MUID:94009687
A:Accession: S38725
A:Molecule type: mRNA
A:Residues: 1-201 <NIS>

A:Cross-references: GB:D21799; NID:g436780; PIDN:BAA04823.1; PID:d1005357; PID:g436781
A:Accession: S38726
A:Molecule type: protein
A:Residues: 42-62; 69, 'L', 71-80, 'V', 82-90, 'P', 92-98, 'G', 100-119, 'X', 121-122, 'X', 124, 125, 1

Query Match 63.6%; Score 35; DB 2; Length 201;
Best Local Similarity 60.0%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFAT 10
| | | | | : |
Db 130 AAHGYGAFLT 139

RESULT 10
S55040
multicatalytic endopeptidase complex (EC 3.4.99.46) beta chain C7-I - human
N:Alternate names: proteasome beta-2; proteasome chain Hsc7-I
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 08-Oct-1999
A:Accession: S55040; S50148
R:Nottingham, H.G.; Tamura, T.; Tanaka, K.; Ichihara, A.
Biochim. Biophys. Acta 1219, 361-368, 1994
A:Title: Sequence analyses and inter-species comparisons of three novel human proteasoma

A:Reference number: S50147; MUID:95002149
A:Accession: S55040
A:Molecule type: mRNA

A:Residues: 1-201 <NOT>
A:Cross-references: GB:D26599; NID:g565648; PIDN:BAA05646.1; PID:d1006191; PID:g565649

C:Genetics:
A:Gene: GDB:PSMB2; HC7-I
A:Cross-references: GDB:567222
C:Keywords: hydrolase; proteinase

Query Match 63.6%; Score 35; DB 2; Length 201;
Best Local Similarity 60.0%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFAT 10
| | | | | : |
Db 130 AAHGYGAFLT 139

RESULT 11
G69040
translation initiation factor eIF-2, alpha subunit - Methanobacterium thermoautotroph
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 26-Aug-1999
A:Accession: G69040

R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.
Qiu, D.; Spadafora, R.; Vicair, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwanli,
K. S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: fu

A:Reference number: A69000; MUID:98037514

A:Accession: G69040

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-262 <MTH>

A:Cross-references: GB:AE000895; GB:AE000666; NID:g2622403; PIDN:AAB85786.1; PID:g2622

A:Experimental source: strain Delta H

C:Genetics:

A:Gene: MTH1308

A:Start codon: GTG

C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 63.6%; Score 35; DB 2; Length 262;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGGSFAT 10
| | | | | : |
Db 27 NYGAFAT 33

RESULT 12
S43771
phosphatidylcholine desaturase (EC 1.3.1.35) - Synecococcus sp. (strain PCC 7002)
N:Alternate names: Delta-12 desaturase; fatty acid desaturase (EC 1.14.99.-) (misiden
C:Species: Synecococcus sp.
A:Variety: PCC 7002

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 28-May-1999

C:Accession: S43771

R:Sakamoto, T.; Wada, H.; Nishida, I.; Ohmori, M.; Murata, N.

Plant Mol. Biol. 24, 643-650, 1994

A:Title: Identification of conserved domains in the Delta-12 desaturases of cyanobact
A:Reference number: S43770; MUID:94207189

A:Accession: S43771

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-347 <SAK>

A:Cross-references: GB:D13779; NID:9489510; PIDN:BAA02922.1; PID:d1003428; PID:g46851

C:Superfamily: omega-3 fatty acid desaturase

C:Keywords: oxidoreductase

Query Match 63.6%; Score 35; DB 2; Length 347;
Best Local Similarity 77.8%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
| | | | | : |
Db 334 AEHNYISFA 342

RESULT 13
T16840
hypothetical protein T10E10.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T16840
C:Geisel, C.
submitted to the EMBL Data Library, October 1995
A:Description: The sequence of C. elegans cosmid T10E10.
A:Reference number: Z18588
A:Accession: T16840
A>Status: preliminary; translated from CB/EMBL/DDEJ
A:Molecule type: DNA
A:Residues: 1-1101 <GEI>
A:Cross-references: EMBL:U39644; NID:g1049339; PID:g1049343; PIDN:AAA80360.1; CESP:T10E10
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP.T10E10.4
A:Introns: 93/2; 152/2; 191/3; 209/2; 283/3; 303/1; 399/3; 421/1; 440/1; 465/1; 547/3; 7

Query Match 63.6%; Score 35; DB 2; Length 1101;
Best Local Similarity 77.8%; Pred. No. 87;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 RHNYGSFAT 10
||| |
Db 32 RHNYPSTAT 40

RESULT 14
S26316
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26316
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
A:Reference number: S26309; MUID:91341421
A:Accession: S26316
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <STA>
A:Cross-references: EMBL:X59190; NID:g52066; PIDN:CAA41900.1; PID:e36170; PID:g1334035
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:2-85/Domain: immunoglobulin homology <IMM>

Query Match 61.8%; Score 34; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 ARHNYGSFA 9
|| |
Db 84 ARGNYGNYA 92

RESULT 15
S26317
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 17-Apr-1998
C:Accession: S26317
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
A:Reference number: S26309; MUID:91341421
A:Accession: S26317
A:Molecule type: mRNA
A:Residues: 1-110 <STA>
A:Cross-references: EMBL:X59186
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 61.8%; Score 34; DB 2; Length 110;

Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 ARHNYGSFA 9
|| |
Db 86 ARGNYGNYA 94
Search completed: May 27, 2000, 19:26:44
Job time: 1767 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 20:07:17 ; Search time 69.28 Seconds
(without alignments)
4.396 Million cell updates/sec

Title: US-09-016-061-70
Perfect score: 55
Sequence: 1 ARHNYGSFAT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	67.3	448	1 NCAP_CVHOC	P33469 human coron
2	35	63.6	201	1 PRCG_HUMAN	P49721 homo sapien
3	35	63.6	201	1 PRCG_RAT	P40307 rattus norv
4	35	63.6	262	1 IF2A_METTH	O27363 methanobact
5	34	61.8	275	1 IF2A_PVRHO	O58655 pyrococcus
6	34	61.8	284	1 IPVR_PICPA	O13505 pichia past
7	34	61.8	286	1 IPVR_KUOLA	P13998 kluyveromyc
8	34	61.8	286	1 IPVR_YEAST	P00817 saccharomyc
9	33	60.0	328	1 CCSA_PEA	P56770 arabidopsis
10	33	60.0	328	1 CCSA_ARATH	P31172 pisum sativ
11	33	60.0	467	1 VL2_HPV33	P06418 human papil
12	33	60.0	470	1 SYE2_RICPR	Q9ZCT8 rickettsia
13	33	60.0	473	1 SYE_AQUAE	O67271 aquifex aeo
14	33	60.0	512	1 PNTA_HAEIN	P43842 haemophilus
15	33	60.0	625	1 TRF5_YEAST	P48561 saccharomyc
16	33	60.0	682	1 VG50_BPML5	Q05262 mycobacteri
17	32	58.2	65	1 CCSA_ONBHE	P13155 oenothera b
18	32	58.2	98	1 VG7_BPPH2	P13848 bacterioph
19	32	58.2	98	1 VG7_BPPZA	P37750 escherichia
20	32	58.2	196	1 WBBJ_ECOLI	P01911 homo sapien
21	32	58.2	198	1 HB2G_HUMAN	P01913 homo sapien
22	32	58.2	266	1 HB2A_HUMAN	P01912 homo sapien
23	32	58.2	266	1 HB2B_HUMAN	P01914 homo sapien
24	32	58.2	266	1 HB2C_HUMAN	P18470 canis famil
25	32	58.2	266	1 HB2D_CANFA	P13759 homo sapien
26	32	58.2	266	1 HB2D_HUMAN	P04229 homo sapien
27	32	58.2	266	1 HB2E_HUMAN	P13758 homo sapien
28	32	58.2	266	1 HB2F_HUMAN	P13760 homo sapien
29	32	58.2	266	1 HB2H_HUMAN	P20039 homo sapien
30	32	58.2	266	1 HB2I_HUMAN	P12761 homo sapien
31	32	58.2	266	1 HB2J_HUMAN	P12216 nicotiana t
32	32	58.2	313	1 CCSA_TOBAC	P46659 zea mays (m
33	32	58.2	321	1 CCSA_MAZE	P12215 oryza sativ
34	32	58.2	321	1 CCSA_ORISA	

ALIGNMENTS

RESULT 1

NCAP_CVHOC
ID NCAP_CVHOC STANDARD; PRT; 448 AA.
AC P33469;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE NUCLEOCAPSID PROTEIN.
GN N.
OS Human coronavirus (strain OC43).
OC Viruses: ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89243809.
RA Kamahora T., Soe L.H., Lai M.M.C.;
RT "Sequence analysis of nucleocapsid gene and leader RNA of human coronavirus OC43.";
RL Virus Res. 12:1-9(1989).
DR PIR; A60003; A60003.
DR PFAM; PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 448 AA; 49316 MW; 5193AB1AE0D75626 CRC64;

Query Match 67.3%; Score 37; DB 1; Length 448;

Best Local Similarity 77.8%; Pred. No. 5.6;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAT 10
||| ||| |
Db 103 RHNRGSFAT 111

RESULT 2

PRCG_HUMAN
ID PRCG_HUMAN STANDARD; PRT; 201 AA.
AC P49721; P31145;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE PROTEASOME COMPONENT C7-I (EC 3.4.99.46) (MACROPAIN SUBUNIT C7-I)
DE (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C7-I).
GN PSMB2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Homnidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95002149.
RA Nothwang H.G., Tamura T., Tanaka K., Ichihara A.;
RT "Sequence analyses and inter-species comparisons of three novel human proteasomal subunits, HsN3, HsC7-I and HsC10-II, confine potential proteolytic active-site residues.";
RL Biochim. Biophys. Acta 1219:361-368(1994).
RN [2]
RP SEQUENCE OF 172-177 AND 186-193.


```

RC TISSUE-KERATINOCYTES;
RX MEDLINE; 93162043.
RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
RA Vandekerckhove J.;
RT "Microsequences of 145 proteins recorded in the two-dimensional gel
RL Electrophoresis 13:960-969(1992).
CC -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
CC WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH
CC ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT
CC NEUTRAL OR SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT
CC PROTEOLYTIC ACTIVITY. THIS SUBUNIT HAS A CHYMOTRYPSIN-LIKE
CC ACTIVITY.
CC -1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
CC SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.
CC -1- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND
CC ALSO IN THE NUCLEUS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1B; ALSO KNOWN AS THE
CC PROTEASOME B-TYPE FAMILY. C7-I SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; D26599; BAA05646.1; -.
DR AARHUS/GHENT-2DPAGE; 2120; IEF.
DR MIN; 602175; -.
DR PROSITE; PS00854; PROTEASOME_B; 1.
DR PFAM; PF00227; proteasome; 1.
KW Proteasome; Hydrolase; Protease.
SQ SEQUENCE 201 AA; 22836 MW; 04D085D7BAA76130 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 201;
Best Local Similarity 60.0%; Pred. No. 5.9;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ARHNGSFAT 10
| | | | |
Db 130 AAHGGAFLT 139

RESULT 3
PRCG_RAT PRCG_RAT STANDARD; PRT; 201 AA.
AC P40307;
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PROTEASOME COMPONENT C7-I (EC 3.4.99.46) (MACROPAIN SUBUNIT C7-I)
DE (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C7-I).
GN PSMB2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=LIVER;
RX MEDLINE; 94009687.
RA Nishimura C., Tamura T., Tokunaga F., Tanaka K., Ichihara A.;
RT "cDNA cloning of rat proteasome subunit RC7-I, a homologue of yeast
RT PRE1 essential for chymotrypsin-like activity.";
RL FEBS Lett. 332:52-56(1993).
CC -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
CC WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH
CC ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT
CC NEUTRAL OR SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT
CC PROTEOLYTIC ACTIVITY. THIS SUBUNIT HAS A CHYMOTRYPSIN-LIKE
CC ACTIVITY.

CC TISSUE-KERATINOCYTES;
CC MEDLINE; 93162043.
CC RA Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
CC RA Vandekerckhove J.;
CC RT "Microsequences of 145 proteins recorded in the two-dimensional gel
CC RL Electrophoresis 13:960-969(1992).
CC CC -1- FUNCTION: THE PROTEASOME IS A MULTICATALYTIC PROTEINASE COMPLEX
CC CC WHICH IS CHARACTERIZED BY ITS ABILITY TO CLEAVE PEPTIDES WITH
CC CC ARG, PHE, TYR, LEU, AND GLU ADJACENT TO THE LEAVING GROUP AT
CC CC NEUTRAL OR SLIGHTLY BASIC PH. THE PROTEASOME HAS AN ATP-DEPENDENT
CC CC PROTEOLYTIC ACTIVITY. THIS SUBUNIT HAS A CHYMOTRYPSIN-LIKE
CC CC ACTIVITY.
CC -1- SUBUNIT: THE PROTEASOME IS COMPOSED OF AT LEAST 15 NON IDENTICAL
CC SUBUNITS WHICH FORM A HIGHLY ORDERED RING-SHAPED STRUCTURE.
CC -1- SUBCELLULAR LOCATION: PROTEASOMES ARE FOUND IN THE CYTOPLASM AND
CC ALSO IN THE NUCLEUS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY T1B; ALSO KNOWN AS THE
CC PROTEASOME B-TYPE FAMILY. C7-I SUBFAMILY.
CC -----
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CC -----
DR EMBL; D21799; BAA04823.1; -.
DR PIR; S38725; S38725.
DR PROSITE; PS00854; PROTEASOME_B; 1.
DR PFAM; PF00227; proteasome; 1.
KW Proteasome; Hydrolase; Protease.
FT CONFLICT 70 70 R -> L (IN AA SEQUENCE).
FT CONFLICT 81 81 A -> V (IN AA SEQUENCE).
FT CONFLICT 91 91 C -> P (IN AA SEQUENCE).
SQ SEQUENCE 201 AA; 22912 MW; E9AC021972B76528 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 201;
Best Local Similarity 60.0%; Pred. No. 5.9;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 1 ARHNGSFAT 10
| | | | |
Db 130 AAHGGAFLT 139

RESULT 4
IF2A_METTH STANDARD; PRT; 262 AA.
ID IF2A_METTH STANDARD; PRT; 262 AA.
AC O27363;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
GN MTHL308.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteriales; Methanobacteriaceae;
OC Methanobacterium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DELTA H;
RX MEDLINE; 98037514.
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzadeh R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwnani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Nolling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155(1997).
CC -1- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
CC (BY SIMILARITY).
CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
CC CHAIN (BY SIMILARITY).
CC -----
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CC -----
DR EMBL; AF000895; AAB85786.1; -.
DR PFAM; PF00575; S1; 1.
KW Initiation factor; Protein biosynthesis.
SQ SEQUENCE 262 AA; 29780 MW; D7324B76DAFD5AA7 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 262;
Best Local Similarity 85.7%; Pred. No. 7.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NYGSPAT 10
Db 27 NYGAFAT 33

RESULT 5
ID IF2A_PYRHO STANDARD; PRT; 275 AA.
AC O58655;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
GN PH0961.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Pyrococcus.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-OT3;
RX MEDLINE; 98344137.
RA Kavarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
RL DNA Res. 5:55-76(1998).
CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
CC -!- FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
CC (BY SIMILARITY).
CC -!- SUBUNIT: HETEROPRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
CC CHAIN (BY SIMILARITY).
CC -----
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CC -----
DR EMBL; AP000004; BAA30058.1; -.
DR PFAM; PF00575; S1; 1.
KW Initiation factor; Protein biosynthesis.
SQ SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 275;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 23 HNYGAF 28

RESULT 6
ID IPYR_PICPA STANDARD; PRT; 284 AA.
IPYR_PICPA

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AC O13505;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
DE HYDROLASE) (PPASE).
GN IPPI.
OS Pichia pastoris (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Pichia.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-NRRL Y-11430;
RX MEDLINE; 99034033.
RA Cosano I.C., Alvarez P., Molina M., Nombela C.;
RT "Cloning and sequence analysis of the Pichia pastoris TRP1, IPPI and
RT HIS3 genes."
RL Yeast 14:861-867(1998).
CC -!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC -----
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CC -----
DR EMBL; AJ001000; CAA04453.1; -.
DR HSP; P00817; IWGI.
DR PRSITE; PS00387; PPASE; 1.
DR PFAM; PF00719; Pyrophosphatase; 1.
KW Hydrolase; Magnesium.
FT INIT_MET 0 BY SIMILARITY.
FT ACT_SITE 56 56 PROBABLE.
FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 284 AA; 31937 MW; 3DAD27970D775D6 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 284;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 91 HNYGAF 96

RESULT 7
ID IPYR_KLUJA STANDARD; PRT; 286 AA.
IPYR_KLUJA
AC PI3998;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
DE HYDROLASE) (PPASE).
GN IPPI OR IPP.
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Kluyveromyces.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89189093.
RA Stark M.J.R., Milner J.S.;
RT "Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a
RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
RT and histone H3."

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RL Yeast 5:35-50(1989).
RN [2]
RP SIMILARITY TO E.COLI AND YEAST PPASES.
RX MEDLINE; 90254161.
RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
RA Cooperman B.S.;
RT "Conservation of functional residues between yeast and E. coli
RT inorganic pyrophosphatases."
RL Biochim. Biophys. Acta 1038:338-345(1990).
CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC -----
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CC -----
DR EMBL; X14230; CRA32446.1;
DR PIR; S07894; PWVKL.
DR HSSP; P00817; LNCI.
DR PROSITE; PS00387; PPASE; 1.
DR PFAM; PF00719; Pyrophosphatase; 1.
KW Hydrolase; Magnesium.
FT INIT_MET 0 BY SIMILARITY.
FT ACT_SITE 56 56 PROBABLE.
FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 286 AA; 32034 MW; 11647F4ABD916A2F CRC64;

Query Match 61.8%; Score 34; DB 1; Length 286;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
Db 91 HNYGAF 96
||||:|

RESULT 8
IPYR_YEAST
ID IPYR_YEAST STANDARD; PRT; 286 AA.
AC P00817;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
DE HYDROLASE) (PPASE).
GN IPPI OR PPAL OR PPA OR YBR011C OR YBR0202.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-X2180.
RX MEDLINE; 89083474.
RA Kolakowski L.F. Jr., Schloesser M., Cooperman B.S.;
RT "Cloning, molecular characterization and chromosome localization of
RT the inorganic pyrophosphatase (PPA) gene from S. cerevisiae."
RL Nucleic Acids Res. 16:10441-10452(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN-S288C;
RA Entian K.-D., Koetter P., Rose M., Li Z., Thermann R., Brendel M.,
RA Baur A., Boles E., Miosga T., Schaaff-Gerstenschlaeger I.,
RA Zimmermann F.K.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.

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RN [3]
RP SEQUENCE.
RX MEDLINE; 78087552.
RA Cohen S.A., Sterner R., Keim P.S., Heinrichson R.L.;
RT "Covalent structural analysis of yeast inorganic pyrophosphatase."
RL J. Biol. Chem. 253:889-897(1978).
RN [4]
RP SEQUENCE OF 25-35 AND 239-251.
RX STRAIN-S288C;
RX MEDLINE; 95203288.
RA Garrels J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a Saccharomyces cerevisiae protein
RT database."
RL Electrophoresis 15:1466-1486(1994).
RN [5]
RP SEQUENCE OF 239-249.
RX STRAIN-ATCC 38531 / Y41;
RX MEDLINE; 97089742.
RA Norbeck J., Blomberg A.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
RT Saccharomyces cerevisiae."
RL FEMS Microbiol. Lett. 137:1-8(1996).
RN [6]
RP ACTIVE SITE.
RX MEDLINE; 80109718.
RA Bond M.W., Chiu N.Y., Cooperman B.S.;
RT "Identification of an arginine important for enzymatic activity
RT within the covalent structure of yeast inorganic pyrophosphatase."
RL Biochemistry 19:94-102(1980).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RA Arutiunian E.G., Terzian S.S., Voronova A.A., Kuranova I.P.,
RA Smirnova E.A., Vainstein B.K., Hohne W.E., Hansen G.;
RT "X-ray diffraction study of inorganic pyrophosphatase from baker's
RT yeast at the 3-A resolution."
RL Dokl. Akad. Nauk SSSR 258:1481-1492(1981).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE; 97148342.
RA Heikinheimo P., Lehtonen J., Baykov A., Lahti R., Cooperman B.S.,
RA Goldman A.;
RT "The structural basis for pyrophosphatase catalysis."
RL Structure 4:1491-1508(1996).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RA Swaminathan K., Cooperman B.S., Lahti R., Voet D.;
RL Submitted (DEC-1997) to the PDB data bank.
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF MUTANTS LYS-78 AND LYS-117.
RX MEDLINE; 99096888.
RA Tuominen V., Heikinheimo P., Kajander T., Torkkel T., Hyytiä T.,
RA Kapyla J., Lahti R., Cooperman B.S., Goldman A.;
RT "The R78K and D117E active-site variants of Saccharomyces cerevisiae
RT soluble inorganic pyrophosphatase: structural studies and mechanistic
RT implications."
RL J. Mol. Biol. 284:1565-1580(1998).
RN [11]
RP SIMILARITY TO E.COLI AND K.LACTIS PPASES.
RX MEDLINE; 90254161.
RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
RA Cooperman B.S.;
RT "Conservation of functional residues between yeast and E. coli
RT inorganic pyrophosphatases."
RL Biochim. Biophys. Acta 1038:338-345(1990).
CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY. IT BINDS UP TO 4 DIVALENT
CC CATIONS PER SUBUNIT, WITH THREE REQUIRED FOR ACTIVITY.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC -----

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EMBL; X13253; CAA31629.1; -;
DBL; 235880; CAA84949.1; -;
PIR; S45864; PWBY
PDB; 1YPY; 15-OCT-91.
PDB; 1YPP; 07-DEC-96.
PDB; 1WGI; 19-NOV-97.
PDB; 1WGT; 19-NOV-97.
PDB; 1HJG; 08-APR-98.
PDB; 1HJH; 08-APR-98.
PDB; 1HJL; 08-APR-98.
PDB; 1HJE; 23-DEC-98.
PDB; 8PRK; 23-DEC-98.
DR SWISS-2DPAGE; P00817; YEAST.
DR YEPD; 7305; -;
DR SGD; L0000872; IPPL
DR PROSITE; PS00387; PPASE; 1.
PFAM; PF00719; Pyrophosphatase; 1.
KW Hydrolase; Magnesium; 3D-structure.
FT INIT_MET 0
FT ACT_SITE 56 56 PROBABLE.
FT BINDING 78 78 INORGANIC PYROPHOSPHATE.
FT CONFLICT 40 40 N -> D (IN REF. 3).
FT CONFLICT 71 71 D -> N (IN REF. 3).
FT CONFLICT 74 74 MISSING (IN REF. 3).
FT CONFLICT 123 123 E -> Q (IN REF. 3).
FT CONFLICT 136 136 Q -> E (IN REF. 3).
FT CONFLICT 186 186 N -> D (IN REF. 3).
FT CONFLICT 224 224 D -> N (IN REF. 3).
FT CONFLICT 266 266 L -> P (IN REF. 2).
FT STRAND 4 7
FT STRAND 16 20
FT STRAND 25 25
FT TURN 28 30
FT TURN 38 41
FT STRAND 45 45
FT STRAND 55 55
FT STRAND 79 79
FT TURN 97 98
FT TURN 111 112
FT STRAND 121 123
FT TURN 131 132
FT STRAND 135 135
FT STRAND 138 146
FT STRAND 151 158
FT TURN 160 161
FT TURN 165 167
FT TURN 172 175
FT TURN 176 177
FT TURN 179 180
FT HELIX 182 197
FT STRAND 203 203
FT HELIX 205 207
FT STRAND 210 210
FT HELIX 212 230
FT TURN 231 231
FT TURN 245 246
FT TURN 248 249
FT TURN 251 252
FT TURN 255 260
FT TURN 274 275
SEQUENCE 286 AA; 32184 MW; F29390260B60C8B2 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 286;
Best Local Similarity 83.3%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
Db 91 HNYGAF 96
RESULT 9
CCSA_PEA
ID CCSA_PEA STANDARD; PRT; 65 AA.
AC P31172;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA (FRAGMENT).
GN CCSA.
OS Pisum sativum (Garden pea).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eukaryotes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
OC Pisum.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ALASKA;
RX MEDLINE; 91355950.
RA Nagano Y., Ishikawa H., Matsuno R., Sasaki Y.;
RT "Nucleotide sequence and expression of the ribosomal protein L2 gene
in pea chloroplasts.";
RL Plant Mol. Biol. 17:541-545(1991).
CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
HEME ATTACHMENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.
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Query Match 60.0%; Score 33; DB 1; Length 65;
Best Local Similarity 62.5%; Pred. No. 4.4;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNYGSFAT 10
Db 57 HSYGSFTS 64
RESULT 10
CCSA_ARATH
ID CCSA_ARATH STANDARD; PRT; 328 AA.
AC P56770;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA.
GN CCSA.
OS Arabidopsis thaliana (Mouse-ear cress).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eukaryotes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;
RT "Complete structure of the chloroplast genome of Arabidopsis
thaliana.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCLL/NRFE/CCSA FAMILY.
CC -----
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CC -----
DR EMBL; AP000423; BAA84436.1; -
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 328 AA; 37732 MW; C88D1508B2924D6F CRC64;

Query Match 60.0%; Score 33; DB 1; Length 328;
Best Local Similarity 62.5%; Pred. No. 25;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 RHYGSEAT 10
Db 320 HSYGSFTS 327

RESULT 11
VL2_HPV33
ID VL2_HPV33 STANDARD; PRT; 467 AA.
AC P06418;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-OCT-1986 (Rel. 34, Last annotation update)
DE MINOR CAPSID PROTEIN L2.
GN L2.
OS Human papillomavirus type 33.
OC Viruses; dsDNA viruses, no RNA stage; Papovaviridae; Papillomavirus.
RN [1]
RP SEQUENCE FROM N.A.
RX Cole S.T., Strecek R.E.;
RA "Genome organization and nucleotide sequence of human papillomavirus
type 33, which is associated with cervical cancer.";
RL J. Virol. 58:991-995(1986).
CC -----
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CC -----
DR EMBL; M12732; AAA46963.1; -
DR PIR; A03650; P2WL33.
DR PFAM; PF00513; late_protein_L2; 1.
KW Coat protein; Late protein.
SQ SEQUENCE 467 AA; 50595 MW; B70DC4ADFEB21957 CRC64;

Query Match 60.0%; Score 33; DB 1; Length 467;
Best Local Similarity 55.6%; Pred. No. 36;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHYGSEAT 10
Db 378 QHSYSTFAT 386

SEQUENCE FROM N.A.
SYE2_RICPR
ID SYE2_RICPR STANDARD; PRT; 470 AA.
AC Q9ZCT8;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE 2 (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE 2)
DE (GLURS 2).
DE GLTX2 OR RP623.
GN Rickettsia prowazekii.
OS Rickettsia prowazekii; alpha subdivision; Rickettsiales;
OC Bacteria; Proteobacteria; Rickettsiaceae; Rickettsia.
OC Rickettsiaceae; Rickettsia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E;
RX MEDLINE; 99039499.
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Scharitz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
mitochondria.";
RL Nature 396:133-140(1998).
CC -!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA (GLU) -> AMP +
PYROPHOSPHATE + L-GLUTAMYL-TRNA (GLU).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; AJ235272; CAA15066.1; -
DR HSSP; P27000; IGLN.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW Aminoacyl-TRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
RN SIMILAR 10 20 "HIGH" REGION.
FT SIMILAR 239 243 "KMSKS" REGION.
FT BINDING 242 242 ATP (BY SIMILARITY).
SQ SEQUENCE 470 AA; 53696 MW; DF1CE50A20B8A9FD CRC64;

Query Match 50.0%; Score 33; DB 1; Length 470;
Best Local Similarity 75.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSF 8
Db 31 ARHNNKRF 38

RESULT 13
SYE_AQUAE
ID SYE_AQUAE STANDARD; PRT; 473 AA.
AC O67271;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE)
DE (GLURS).
GN GLTX OR AQ_1221.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;

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RX MEDLINE; 98196666.
RA Decker G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., AuJay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus";
RL Nature 392:353-358(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) = AMP +
CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC
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CC
CC EMBL; AE000729; AAC07230.1; -.
DR PRINTS; PR00987; TRNASYNTHGLU.
DR PROSITE; PS00178; AA-TRNA-LIGASE_I; 1.
DR PFAM; PF00749; trna-synt_1c; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
FT SIMILAR 242 246 "KMSKS" REGION.
FT BINDING 245 245 ATP (BY SIMILARITY).
SQ SEQUENCE 473 AA; 55121 MW; 5CB4D1590973E07A CRC64;

Query Match 60.0%; Score 33; DB 1; Length 473;
Best Local Similarity 75.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
    |||||
DB 31 ARHNGGF 38

RESULT 14
ID PNTA_HAEIN STANDARD; PRT; 512 AA.
AC P43842;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE NAD(P) TRANSHYDROGENASE SUBUNIT ALPHA (EC 1.6.1.1) (PYRIDINE
DE NUCLEOTIDE TRANSHYDROGENASE SUBUNIT ALPHA) (NICOTINAMIDE NUCLEOTIDE
DE TRANSHYDROGENASE SUBUNIT ALPHA).
GN PNTA OR H1362.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellales;
OC Haemophilus.
[1]
SEQUENCE FROM N.A.
RP STRAIN=RD / KW20;
RX MEDLINE; 95350630.
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kervatage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA Mckenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.V., Geoghagen N.S.M.,
RA Gnehm C.D., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd.";
RL Science 269:496-512(1995).
CC -1- FUNCTION: THE TRANSHYDROGENATION BETWEEN NADH AND NADP IS COUPLED
CC TO RESPIRATION AND ATP HYDROLYSIS AND FUNCTIONS AS A PROTON PUMP

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CC ACROSS THE MEMBRANE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: NADPH + NAD(+) = NADP(+) + NADH.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
CC (BY SIMILARITY).
CC -1- SIMILARITY: TO THE N-TERMINAL PART OF THE EUKARYOTIC MITOCHONDRIAL
CC ENZYME AND TO ALANINE DEHYDROGENASES.
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CC
CC EMBL; U32816; AAC23009.1; -.
DR TIGR; H11362; -.
DR PROSITE; PS00837; ALADH_PNT_1; FALSE_NEG.
DR PROSITE; PS00837; ALADH_PNT_2; 1.
DR PFAM; PF01262; Aladh_PNT; 1.
KW Oxidoreductase; NAD; NADP; Transmembrane; Inner membrane.
FT NP_BIND 167 197 NAD (BY SIMILARITY).
FT TRANSMEM 401 421 POTENTIAL.
FT TRANSMEM 422 442 POTENTIAL.
FT TRANSMEM 452 472 POTENTIAL.
FT TRANSMEM 479 499 POTENTIAL.
SQ SEQUENCE 512 AA; 54972 MW; 50D63AD536E837EF CRC64;

Query Match 60.0%; Score 33; DB 1; Length 512;
Best Local Similarity 60.0%; Pred. No. 40;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFAT 10
    |||||
DB 145 AAHEFGSFFT 154

RESULT 15
ID TRF5_YEAST STANDARD; PRT; 625 AA.
AC P48561;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE TOPOISOMERASE I-RELATED PROTEIN TRF5.
GN TRF5 OR YNL299W OR NO440.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
[1]
SEQUENCE FROM N.A.
RP MEDLINE; 96279743.
RX Castano I.B., Heath-Pagliuso S., Sadoff B.U., Fitzhugh D.J.,
RA Christman M.F.;
RT "A novel family of TRF (DNA topoisomerase I-related function) genes
RT required for proper nuclear segregation.";
RL Nucleic Acids Res. 24:2404-2410(1996).
[2]
SEQUENCE FROM N.A.
RP STRAIN=S288C / FY1679;
RX MEDLINE; 96132033.
RA Maurer K.C.T., Urbanus J.H.M., Planta R.J.;
RT "Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV
RT carrying a ribosomal protein gene cluster, the genes encoding a
RT plasma membrane protein and a subunit of replication factor C, and a
RT novel putative serine/threonine protein kinase gene.";
RL Yeast 11:1303-1310(1995).
CC -1- FUNCTION: ESSENTIAL PROTEIN REQUIRED FOR PROPER NUCLEAR DIVISION
CC IN MITOSIS. MAY MEDIATE MITOTIC CHROMOSOME CONDENSATION.
CC -1- SIMILARITY: STRONG, TO YEAST TRF4 AND S.POMBE SPAC12G12.13C.
CC -1- SIMILARITY: SOME, TO TOPOISOMERASE 1.

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DR EMBL; U47282; AAC49397.1; -;
DR EMBL; U23084; AAC49099.1; -;
DR EMBL; Z71575; CAA96217.1; -;
DR SGD; L0003385; TRF5.
KW Mitosis.
FT CONFLICT 354 355 MH -> ID (IN REF. 2).
FT CONFLICT 612 613 LR -> PS (IN REF. 2).
SQ SEQUENCE 625 AA; 72591 MW; ASD6AF602EF7BD26 CRC64;

Query Match 60.0%; Score 33; DB 1; Length 625;
Best Local Similarity 75.0%; Pred. No. 49;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Oy 3 HNYGSFAT 10
| :|||||
Db 218 HVFGSFAT 225

Search completed: May 27, 2000, 20:07:17
Job time: 989 sec

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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:38:41 ; Search time 199.56 Seconds
(without alignments)
3.474 Million cell updates/sec

Title: US-09-016-061-70
Perfect score: 55
Sequence: 1 ARHNYGSPAT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

SPTREMBL12:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	39	70.9	446	5	O62086
2	38	69.1	89	7	O19495
3	36	65.5	39	7	P79474
4	36	65.5	39	7	P79477
5	36	65.5	39	7	P79478
6	36	65.5	39	7	P79479
7	36	65.5	78	6	O97835
8	36	65.5	78	6	O97839
9	36	65.5	78	6	O97844
10	36	65.5	78	6	O97968
11	36	65.5	79	7	O19191
12	36	65.5	79	7	O19192
13	36	65.5	79	7	O19380
14	36	65.5	79	7	O19381
15	36	65.5	79	7	O19382
16	36	65.5	79	7	O19396
17	36	65.5	79	7	O19397
18	36	65.5	79	7	O19405
19	36	65.5	79	7	O19406
20	36	65.5	79	7	O19407

```

21 36 65.5 79 7 O19408 019408 felis silve
22 36 65.5 79 7 O19435 019435 felis silve
23 36 65.5 81 7 O30568 030568 macaca fasc
24 36 65.5 81 7 O30571 030571 macaca fasc
25 36 65.5 81 7 O30737 030737 macaca neme
26 36 65.5 81 7 O30739 030739 macaca neme
27 36 65.5 81 7 O30563 030563 macaca fasc
28 36 65.5 81 7 O30740 030740 macaca neme
29 36 65.5 82 7 O95598 095598 phasianus c
30 36 65.5 82 7 O30606 030606 macaca mula
31 36 65.5 82 7 O30608 030608 macaca mula
32 36 65.5 82 7 O30637 030637 macaca mula
33 36 65.5 82 7 O30638 030638 macaca mula
34 36 65.5 82 7 O30658 030658 macaca mula
35 36 65.5 82 7 O30659 030659 macaca mula
36 36 65.5 82 7 O30666 030666 macaca mula
37 36 65.5 82 7 O30667 030667 macaca mula
38 36 65.5 82 7 O30668 030668 macaca mula
39 36 65.5 82 7 O19287 019287 macaca mula
40 36 65.5 82 7 O19288 019288 macaca mula
41 36 65.5 83 7 O98002 098002 ovis aries
42 36 65.5 83 7 O9XS06 09XS06 odocolleus
43 36 65.5 83 7 O9XR25 09XR25 odocolleus
44 36 65.5 83 7 O9XR24 09XR24 odocolleus
45 36 65.5 85 7 O30796 030796 ovis aries

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ALIGNMENTS

RESULT 1

```

O62086 PRELIMINARY; PRT; 446 AA.
ID O62086
AC O62086;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-JAN-1999 (Tremblrel. 09, Last annotation update)
DE C3IH5.6 PROTEIN.
GN C3IH5.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RA KERSHAW J.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94150718.
RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LATSTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL Nature 368:32-38(1994).
DR EMBL; 293778; CAB07846.1; -.
SQ SEQUENCE 446 AA; 50763 MW; B347C0C8 CRC32;

```

Query Match 70.9%; Score 39; DB 5; Length 446;
Best Local Similarity 87.5%; Pred. No. 7.9;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 RHNYGSA 9

|||||

Db 51 RHNYGSA 58

RA SHARBRICK P.A., CRAWFORD A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63082; AAB37782.1; -.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4806 MW; 4984754A CRC32;

Query Match 65.5%; Score 36; DB 7; Length 39;
 Best Local Similarity 85.7%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
 Db 25 RHNYGVF 31

RESULT 7
 O97835 PRELIMINARY; PRT; 78 AA.
 ID O97835
 AC O97835

DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
 GN OLA-DRB1*N20.2
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidæ;
 OC Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=7407; TISSUE=BLOOD;
 RA AIDA Y.;

RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017207; BAA36764.1; -.
 FT NON_TER 1 1
 FT NON_TER 78 78
 SQ SEQUENCE 78 AA; 9677 MW; D2252D9D CRC32;

Query Match 65.5%; Score 36; DB 6; Length 78;
 Best Local Similarity 85.7%; Pred. No. 4.9;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
 Db 72 RHNYGVF 78

RESULT 8
 O97839 PRELIMINARY; PRT; 78 AA.
 ID O97839
 AC O97839

DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
 GN OLA-DRB1*N2.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidæ;
 OC Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SUFFOLK BREED AND CORRIDAILE BREED; TISSUE=BLOOD;
 RA AIDA Y.;

RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017212; BAA36769.1; -.
 FT NON_TER 1 1

FT NON_TER 78 78
 SQ SEQUENCE 78 AA; 9430 MW; 2883C99C CRC32;

Query Match 65.5%; Score 36; DB 6; Length 78;
 Best Local Similarity 85.7%; Pred. No. 4.9;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
 Db 72 RHNYGVF 78

RESULT 9
 O97844 PRELIMINARY; PRT; 78 AA.
 ID O97844
 AC O97844;

DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
 GN OLA-DRB1*N8.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidæ;
 OC Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SUFFOLK BREED; TISSUE=BLOOD;
 RA AIDA Y.;

RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017220; BAA36777.1; -.
 FT NON_TER 1 1
 FT NON_TER 78 78
 SQ SEQUENCE 78 AA; 9645 MW; 0A246905 CRC32;

Query Match 65.5%; Score 36; DB 6; Length 78;
 Best Local Similarity 85.7%; Pred. No. 4.9;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
 Db 72 RHNYGVF 78

RESULT 10
 O97968 PRELIMINARY; PRT; 78 AA.
 ID O97968
 AC O97968;

DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
 GN OLA-DRB1*N21.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidæ;
 OC Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VARIOUS STRAINS;
 RA AIDA Y.;

RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017231; BAA36788.1; -.
 DR EMBL; AB017204; BAA36761.1; -.
 FT NON_TER 1 1
 FT NON_TER 78 78
 SQ SEQUENCE 78 AA; 9436 MW; 72250CEB CRC32;

Query Match 65.5%; Score 36; DB 6; Length 78;
 Best Local Similarity 85.7%; Pred. No. 4.9;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
 DB 72 RHNYGVF 78

RESULT 11
 O19191 ID O19191 PRELIMINARY; PRT; 79 AA.
 AC O19191;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
 GN MHCWAIR-DRB.
 OS Prionallurus bengalensis iriomotensis (Iriomote cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Carnivora; Fissipedia; Felidae; Prionallurus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97211851.
 RA YUHKI N., O'BRIEN S.J.;
 RT "Nature and origin of polymorphism in feline MHC class II DRB and DRB genes.";
 RL J. Immunol. 158:2822-2833(1997).
 DR EMBL; U51546; AAB65583.1; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 9582 MW; 8EEF2C7D CRC32;

Query Match 65.5%; Score 36; DB 7; Length 79;
 Best Local Similarity 85.7%; Pred. No. 5;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
 DB 72 RHNYGVF 78

RESULT 12
 O19192 ID O19192 PRELIMINARY; PRT; 79 AA.
 AC O19192;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
 GN MHCWAIR-DRB.
 OS Prionallurus bengalensis iriomotensis (Iriomote cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Carnivora; Fissipedia; Felidae; Prionallurus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97211851.
 RA YUHKI N., O'BRIEN S.J.;
 RT "Nature and origin of polymorphism in feline MHC class II DRB and DRB genes.";
 RL J. Immunol. 158:2822-2833(1997).
 DR EMBL; U51547; AAB65583.1; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 9582 MW; ED9F80F0 CRC32;

Query Match 65.5%; Score 36; DB 7; Length 79;

Best Local Similarity 85.7%; Pred. No. 5;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
 DB 72 RHNYGVF 78

RESULT 13
 O19380 ID O19380 PRELIMINARY; PRT; 79 AA.
 AC O19380;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
 GN MHCFECA-DRB.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97211851.
 RA YUHKI N., O'BRIEN S.J.;
 RT "Nature and origin of polymorphism in feline MHC class II DRB and DRB genes.";
 RL J. Immunol. 158:2822-2833(1997).
 DR EMBL; U51498; AAB65533.1; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 9659 MW; F352AD23 CRC32;

Query Match 65.5%; Score 36; DB 7; Length 79;
 Best Local Similarity 85.7%; Pred. No. 5;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
 DB 72 RHNYGVF 78

RESULT 14
 O19381 ID O19381 PRELIMINARY; PRT; 79 AA.
 AC O19381;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
 GN MHCFECA-DRB.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97211851.
 RA YUHKI N., O'BRIEN S.J.;
 RT "Nature and origin of polymorphism in feline MHC class II DRB and DRB genes.";
 RL J. Immunol. 158:2822-2833(1997).
 DR EMBL; U51499; AAB65534.1; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 9610 MW; 1F7FB873 CRC32;

Query Match 65.5%; Score 36; DB 7; Length 79;
 Best Local Similarity 85.7%; Pred. No. 5;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 72 RHNYGVF 78

RESULT 15
O19382
ID O19382 PRELIMINARY; PRT; 79 AA.
AC O19382;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
GN MHCFCFA-DRB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97211851.
RA YUHKI N., O'BRIEN S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
genes.";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51500; AAB65535.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 9421 MW; CB203F17 CRC32;

Query Match 65.5%; Score 36; DB 7; Length 79;
Best Local Similarity 85.7%; Pred. No. 5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 72 RHNYGVF 78

Search completed: May 27, 2000, 19:38:41
Job time: 2374 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2000, 19:21:36 ; Search time 148.45 Seconds
(without alignments)
1.596 Million cell updates/sec

Title: US-09-016-061-70
Perfect score: 55
Sequence: 1 ARHNYGSPAT 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	10	1 W76025	LM609 grafted anti
2	51	92.7	10	1 W76024	LM609 grafted anti
3	50	90.9	10	1 W76026	LM609 grafted anti
4	50	90.9	10	1 W76027	LM609 grafted anti
5	50	90.9	10	1 W76028	LM609 grafted anti
6	50	90.9	10	1 W76029	LM609 grafted anti
7	50	90.9	10	1 W76030	LM609 grafted anti
8	50	90.9	10	1 W76010	LM609 grafted anti
9	50	90.9	117	1 W76001	Vitaxin antibody h
10	50	90.9	117	1 W76003	LM609 antibody hea
11	47	85.5	10	1 W76021	LM609 grafted anti
12	46	83.6	10	1 W76037	LM609 grafted anti
13	46	83.6	10	1 W76039	LM609 grafted anti
14	46	83.6	10	1 W76040	LM609 grafted anti
15	46	83.6	10	1 W76022	LM609 grafted anti
16	46	83.6	10	1 W76023	LM609 grafted anti
17	45	81.8	10	1 W76020	LM609 grafted anti
18	42	76.4	110	1 W84099	Vitronectin alpha-
19	42	76.4	117	1 W84093	Murine vitronectin
20	42	76.4	117	1 W84097	Humanised anti-alp
21	41	74.5	10	1 W76038	LM609 grafted anti
22	36	65.5	117	1 R79157	Human IGE receptor
23	36	65.5	117	1 R79155	Human antiFc epsil
24	36	65.5	117	1 W27357	Heavy chain variab
25	36	65.5	117	1 W27526	Heavy chain variab
26	36	65.5	117	1 W27354	Heavy chain variab
27	36	65.5	119	1 W01578	Lead binding Mab 8
28	36	65.5	239	1 W73874	Human antiFc epsil
29	36	65.5	242	1 W73876	Human antiFc epsil
30	34	61.8	505	1 R47463	Ced-3. Isolated C
31	33	60.0	80	1 R13396	HLA-DRw12a antigen
32	33	60.0	80	1 R13397	HLA-DRw12b antigen
33	32	58.2	11	1 W22700	Peptide sequence #
34	32	58.2	15	1 W25799	Synthetic human S1

35 32 58.2 18 1 W27062 Chemically syntheses
36 32 58.2 25 1 R49334 DR1 beta chain pos
37 32 58.2 25 1 W41656 Immunomodulatory p
38 32 58.2 36 1 W03964 VDJ joint protein,
39 32 58.2 36 1 W41127 VH251 EXP-1 J6 mu
40 32 58.2 78 1 W71230 Major histocompata
41 32 58.2 80 1 R21415 Human leukocyte an
42 32 58.2 84 1 P90034 Peptide of human/m
43 32 58.2 89 1 R24276 DR1. Method and kl
44 32 58.2 89 1 W00380 HLA-DRB1*08 and *1
45 32 58.2 93 1 W10491 Beta1 region of Cl

ALIGNMENTS

RESULT 1

W76025
ID W76025 standard; Protein; 10 AA.
AC W76025;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #7.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis; primer; V-H region; CDR;
complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PE 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49862.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
integrin - and related grafted antibodies based on murine monoclonal
LM609, also related nucleic acid, used to treat, prevent or diagnose
angiogenesis or restenosis
Claim 62: Page 41: 129pp: English.
PS W76007-W76040 are protein fragments of the grafted monoclonal antibody
LM609 heavy and light chain variable region. LM609 and the antibody
vitaxin bind selectively to integrin alphavbeta3 and can be used to
inhibit binding of alphavbeta3 to a ligand and thus block
integrin-mediated signal transduction. This is useful in the treatment,
prevention and diagnosis of alphavbeta3-mediated disease, specifically
angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
arthritis, macular degeneration, osteoporosis etc.). The antibodies
contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSPAT 10

Db 1 ARHNYGSPAT 10

RESULT 2

W76024

ID W76024 standard; Protein; 10 AA.

AC W76024;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #6.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49861.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 CC Sequence 10 AA;

Query Match 92.7%; Score 51; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0033;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARHNYGSFAT 10
 |||||
 DB 1 ARHNYGSFAS 10

RESULT 3
 W76026
 ID W76026 standard; Protein; 10 AA.

AC W76026;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #8.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49863.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block

CC Integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 CC Sequence 10 AA;

Query Match 90.9%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0048;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARHNYGSFA 9
 |||||
 DB 1 ARHNYGSFA 9

RESULT 4
 W76027
 ID W76027 standard; Protein; 10 AA.

AC W76027;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #9.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49864.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 CC Sequence 10 AA;

Query Match 90.9%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0048;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARHNYGSFA 9
 |||||
 DB 1 ARHNYGSFA 9

RESULT 5
 W76028
 ID W76028 standard; Protein; 10 AA.

AC W76028;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #10.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; 001826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49865.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0048;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARHNYGSFA 9
 I|||||
 DB 1 ARHNYGSFA 9
 I|||||

RESULT 6
 ID W76029 standard; Protein; 10 AA.
 AC W76029;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #11.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; 001826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49867.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.

Query Match 90.9%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0048;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARHNYGSFA 9
 I|||||
 DB 1 ARHNYGSFA 9
 I|||||

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0048;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARHNYGSFA 9
 I|||||
 DB 1 ARHNYGSFA 9
 I|||||

RESULT 7
 ID W76030 standard; Protein; 10 AA.
 AC W76030;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #12.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; 001826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49867.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.

Query Match 90.9%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0048;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARHNYGSFA 9
 I|||||
 DB 1 ARHNYGSFA 9
 I|||||

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RESULT 8
W76010
ID W76010 standard; Protein; 10 AA.
AC W76010;
DE 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #1.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49847.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Disclosure: Page 40; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9
|||||||

RESULT 9
W76001
ID W76001 standard; Protein; 117 AA.
AC W76001;
DE 02-NOV-1998 (first entry)
DE Vitaxin antibody heavy chain variable region protein fragment.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49820.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 43; Fig 2a; 129pp; English.
CC This sequence represents the LM609 antibody variable heavy chain region.
CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC block integrin-mediated signal transduction. This is useful in the
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
SQ Sequence 117 AA;

Query Match 90.9%; Score 50; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 97 ARHNYGSFA 105
|||||||

PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 1; Fig 1a; 129pp; English.
CC This sequence represents a fragment of the vitaxin antibody variable
CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
CC to a ligand and thus block integrin-mediated signal transduction. This is
CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
CC disease, specifically angiogenesis and restenosis (but also e.g.
CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
CC osteoporosis etc.). The antibodies contain non-murine framework regions
CC so are suitable for use in humans. Enhanced types of LM609 have affinity
CC more than 90 times greater than that of parent the parent antibody.
SQ Sequence 117 AA;

Query Match 90.9%; Score 50; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 97 ARHNYGSFA 105
|||||||

ID W76003 standard; Protein; 117 AA.
AC W76003;
DE 02-NOV-1998 (first entry)
DE LM609 antibody heavy chain variable region protein fragment.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49822.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 43; Fig 2a; 129pp; English.
CC This sequence represents the LM609 antibody variable heavy chain region.
CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC block integrin-mediated signal transduction. This is useful in the
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
SQ Sequence 117 AA;

Query Match 90.9%; Score 50; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 97 ARHNYGSFA 105
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RESULT 11
W76021
ID W76021 standard; Protein; 10 AA.
AC W76021;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #3.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis; primer; V-H region; CDR;
complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49858.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62: Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
CC inhibit binding of alphaVbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 83.6%; Score 46; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.024;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAT 10
Dbbbbb|
Db 1 ARHNGSFAS 10
Dbbbbb|

RESULT 13
W76039
ID W76039 standard; Protein; 10 AA.
AC W76039;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #15.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis; primer; V-H region; CDR;
complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49876.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62: Page 43; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
CC inhibit binding of alphaVbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 85.5%; Score 47; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.016;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Dbbbbb|
Db 1 ARHNGSYA 9
Dbbbbb|

RESULT 12
W76037
ID W76037 standard; Protein; 10 AA.
AC W76037;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #13.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis; primer; V-H region; CDR;
complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49874.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

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PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62: Page 43; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
CC inhibit binding of alphaVbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 83.6%; Score 46; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.024;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAT 10
| | | | | | | | | |
Db 1 ARHNGSFAS 10
| | | | | | | | | |

RESULT 13
W76039
ID W76039 standard; Protein; 10 AA.
AC W76039;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #15.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis; primer; V-H region; CDR;
complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49876.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62: Page 43; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
CC inhibit binding of alphaVbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 85.5%; Score 47; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.016;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
| | | | | | | | | |
Db 1 ARHNGSYA 9
| | | | | | | | | |

RESULT 12
W76037
ID W76037 standard; Protein; 10 AA.
AC W76037;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #13.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis; primer; V-H region; CDR;
complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49874.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

Query Match 83.6%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
| | | | | | | |
Db 1 ARHNYGSF 8

RESULT 14

W76040
ID W76040 standard; Protein; 10 AA.
AC W76040;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #16.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis; primer; V-H region; CDR;
complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR N-PSDB; V49877.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
integrin - and related nucleic acid, used to treat, prevent or diagnose
LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 43; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
LM609 heavy and light chain variable region. LM609 and the antibody
vitaxin bind selectively to integrin alphavbeta3 and can be used to
inhibit binding of alphavbeta3 to a ligand and thus block
integrin-mediated signal transduction. This is useful in the treatment,
prevention and diagnosis of alphavbeta3-mediated disease, specifically
angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
arthritis, macular degeneration, osteoporosis etc.). The antibodies
contain non-murine framework regions so are suitable for use in humans.
Enhanced types of LM609 have affinity more than 90 times greater than
that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 83.6%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
| | | | | | | |
Db 1 ARHNYGSF 8

RESULT 15

W76022
ID W76022 standard; Protein; 10 AA.
AC W76022;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #4.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis; primer; V-H region; CDR;
complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
integrin - and related nucleic acid, used to treat, prevent or diagnose
LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
LM609 heavy and light chain variable region. LM609 and the antibody
vitaxin bind selectively to integrin alphavbeta3 and can be used to
inhibit binding of alphavbeta3 to a ligand and thus block
integrin-mediated signal transduction. This is useful in the treatment,
prevention and diagnosis of alphavbeta3-mediated disease, specifically
angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
arthritis, macular degeneration, osteoporosis etc.). The antibodies
contain non-murine framework regions so are suitable for use in humans.
Enhanced types of LM609 have affinity more than 90 times greater than
that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 83.6%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
| | | | | | | |
Db 1 ARHNYGSF 8

Search completed: May 27, 2000, 19:21:36
Job time: 1590 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:26:44 ; Search time 163.56 Seconds
(without alignments)
3.585 Million cell updates/sec

Title: US-09-016-061-72
Perfect score: 56
Sequence: 1 ARHNYGSFAD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_63:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	40	71.4	210	1	B69265	conserved hypothet
2	39	69.6	446	2	T19625	hypothetical prote
3	38	67.9	464	2	B70828	hypothetical prote
4	37	66.1	275	2	T04480	acyl-CoA oxidase h
5	36	64.3	82	2	I51106	Major Histocompati
6	36	64.3	89	2	S38688	MHC class II histo
7	36	64.3	89	2	S38683	MHC class II histo
8	36	64.3	89	2	S38684	MHC class II histo
9	36	64.3	225	2	I47095	MHC class II OVAR-
10	36	64.3	581	1	A37913	serine/threonine-s
11	36	64.3	731	1	JC2464	probable copper-tr
12	35	62.5	232	2	G69080	conserved hypothet
13	35	62.5	243	2	D72098	lysophospholipase
14	35	62.5	275	2	D71087	probable translati
15	35	62.5	275	2	G75130	translation initia
16	35	62.5	347	2	A34771	phosphatidylcholin
17	35	62.5	520	2	S78502	paired box transcr
18	35	62.5	538	2	T28874	hypothetical prote
19	35	62.5	682	2	JQ0420	beta-1,3-glucanase
20	35	62.5	743	2	T15062	hypothetical prote
21	34	60.7	108	2	S26316	Ig heavy chain v r
22	34	60.7	110	2	S26317	Ig heavy chain v r
23	34	60.7	287	1	PWBV	inorganic pyrophos
24	34	60.7	287	1	PWVKL	inorganic pyrophos
25	34	60.7	309	2	T41494	zinc finger, ADP-r
26	34	60.7	407	2	H71857	pyruvate ferredoxi
27	34	60.7	407	2	F64658	pyruvate synthase
28	34	60.7	418	2	A05139	serum albumin - mo
29	34	60.7	442	2	G69264	conserved hypothet
30	34	60.7	514	2	T10559	hypothetical prote

31	34	60.7	1263	2	T00649	hypothetical prote
32	33	58.9	80	2	S25050	Ig heavy chain v r
33	33	58.9	80	2	I54469	MHC HLA-DR-beta-1
34	33	58.9	80	2	I68777	MHC HLA-DR beta-1
35	33	58.9	81	2	I54550	HLA DRB1*1202 - hu
36	33	58.9	85	2	I59634	MHC class II DR-be
37	33	58.9	89	2	S38676	MHC class II histo
38	33	58.9	89	2	S38680	MHC class II histo
39	33	58.9	89	2	S57512	MHC class II histo
40	33	58.9	102	2	S25025	Ig heavy chain - m
41	33	58.9	106	2	S25036	Ig heavy chain v r
42	33	58.9	111	2	S25052	Ig heavy chain v r
43	33	58.9	111	2	S25055	Ig heavy chain v r
44	33	58.9	111	2	S25054	Ig heavy chain v r
45	33	58.9	111	2	S25031	Ig heavy chain v r

ALIGNMENTS

RESULT 1
B69265
conserved hypothetical protein AF0122 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: B69265
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artisch, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A:Reference number: A69250; MUID:98049343
A:Accession: B69265
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-210 <KLE>
A:Cross-references: GB:AE001098; GB:AE000782; NID:q2689421; PID:q2650532; TIGR:AF0122
C:Superfamily: conserved hypothetical protein AF0119

Query Match 71.4% Score 40; DB 1; Length 210;
Best Local Similarity 77.8%; Pred. No. 2.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 RHNYGSFAD 10
Db 128 RHAYGSFVD 136
II IIII I
RESULT 2
T19625
hypothetical protein C31H5.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19625
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19625
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-446 <WIL>
A:Cross-references: EMBL:Z93778; PIDN:CA807846.1; GSPDB:GN00019; CESP:C31H5.6
C:Genetics:
A:Experimental source: clone C31H5
A:Gene: CESP:C31H5.6
A:Map position: 1
A:Introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3
Query Match 69.6% Score 39; DB 2; Length 446;

```

Best Local Similarity 87.5%; Pred. No. 7.7;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFA 9
    ||||| |
Db 51 RHNYGSHA 58

RESULT 3
B70828
hypothetical protein Rv0462 - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: B70828
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.;
Rajandream, M.A.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.;
Nature 393, 537-544, 1998
A:Authors: Squires, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987
A:Accession: B70828
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-464 <COL>
A:Cross-references: GB:AL021933; GB:AL123456; NID:g3261529; PIDN:CAA17417.1; PID:el25253
C:Genetics:
A:Gene: Rv0462
C:Superfamily: dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase homology
F:7-450/Domain: dihydrolipoamide dehydrogenase homology <DLD>

Query Match 67.9%; Score 38; DB 2; Length 464;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAD 10
    ||||| |
Db 110 HGYGTFAD 117

RESULT 4
T04480
acyl-CoA oxidase homolog - barley (fragment)
C:Species: Hordeum vulgare (barley)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C:Accession: T04480
R:Grossi, M.; Gulli, M.; Stanca, A.M.; Cattivelli, L.
Plant Sci. 105, 71-80, 1995
A:Title: Characterization of two barley genes that respond rapidly to dehydration stress
A:Reference number: Z15371
A:Accession: T04480
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-275 <GRO>
A:Cross-references: EMBL:X84055; NID:g642243; PIDN:CAA58874.1; PID:g642244
A:Experimental source: cv. Arda, leaf
C:Genetics:
A:Gene: cdr29

Query Match 66.1%; Score 37; DB 2; Length 275;
Best Local Similarity 70.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFAD 10
    ||||| |
Db 1 ANHNSGSFLD 10

RESULT 5
151106

```

```

Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)
C:Species: Phasianus colchicus (ring-necked pheasant)
C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
C:Accession: I51106
R:Witzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.
Immunogenetics 39, 395-403, 1994
A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-necked pheasant
A:Reference number: I51103; MUID:94245280
A:Accession: I51106
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-82 <MIT>
A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.3%; Score 36; DB 2; Length 82;
Best Local Similarity 85.7%; Pred. No. 5.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
    ||||| |
Db 75 RHNYGVF 81

RESULT 6
S38688
MHC class II histocompatibility antigen HLA-DR-08 beta chain - Galago senegalensis (f
C:Species: Galago senegalensis
C>Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997
C:Accession: S38688
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduce
A:Reference number: S38676
A:Accession: S38688
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27158
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.3%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 5.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
    ||||| |
Db 75 RHNYGVF 81

RESULT 7
S38683
MHC class II histocompatibility antigen HLA-DR-03 beta chain - Galago senegalensis (f
C:Species: Galago senegalensis
C>Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997
C:Accession: S38683
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduce
A:Reference number: S38676
A:Accession: S38683
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27153
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.3%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 5.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
    ||||| |
Db 75 RHNYGVF 81

```

Db 75 RHNYGVF 81
|||||

RESULT 8

S38684

MHC class II histocompatibility antigen HLA-DR-04 beta chain - Galago senegalensis (frag

C:Species: Galago senegalensis

C>Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997

C:Accession: S38684

R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.

submitted to the EMBL Data Library, November 1993

A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced f

A:Reference number: S38676

A:Accession: S38684

A:Molecule type: DNA

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:Z27154

C:Superfamily: class II histocompatibility antigen; Immunoglobulin homology

Query Match 64.3%; Score 36; DB 2; Length 89;

Best Local Similarity 85.7%; Pred. No. 5.7;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

|||||

Db 75 RHNYGVF 81

RESULT 9

I47095

MHC class II OVAR-DR-beta-3 - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 13-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 23-Jul-1999

C:Accession: I47095

R:Fabb, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.

Anlm. Genet. 24, 249-255, 1993

A>Title: Isolation, characterization and evolution of ovine major histocompatibility com

A:Reference number: I47075; MUID:194057592

A:Accession: I47095

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-225 <FAB>

A:Cross-references: GB:I04790; NID:g458880; PIDN:AAA16562.1; PID:g458881

C:Genetics:

A:Gene: OVAR-DRB3

C:Superfamily: class II histocompatibility antigen; Immunoglobulin homology

Query Match 64.3%; Score 36; DB 2; Length 225;

Best Local Similarity 85.7%; Pred. No. 14;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

|||||

Db 68 RHNYGVF 74

RESULT 10

A37913

serine/threonine-specific protein kinase (EC 2.7.1.1-) mkl1 - fission yeast (Schizosaccha

N:Alternate names: mitosis inhibitor protein kinase

C:Species: Schizosaccharomyces pombe

C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Dec-1999

C:Accession: A37913; T40626

R:Lundgren, K.; Walworth, N.; Boother, R.; Dembski, M.; Kirschner, M.; Beach, D.

Cell 64, 1111-1122, 1991

A>Title: mkl1 and weel cooperate in the inhibitory tyrosine phosphorylation of cdc2.

A:Reference number: A37913; MUID:91168259

A:Accession: A37913

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-581 <LUN>

A:Cross-references: GB:MG0834; NID:g173413; PIDN:AAA91278.1; PID:g1213637

R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Rieger, M.

submitted to the EMBL Data Library, December 1998

A:Reference number: Z21941

A:Accession: T40626

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-581 <LYN>

A:Cross-references: EMBL:AL034563; PIDN:CAA22534.1; GSPDB:GN00067; SPDB:SPBC660.14

A:Experimental source: strain 972h-; cosmid c660

C:Genetics:

A:Gene: SPBC660.14

A:Map position: 2

A:Introns: 403/3

C:Superfamily: fission yeast mkl1 protein; protein kinase homology

C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase

F:287-558/Domain: protein kinase homology <KIN>

Query Match 64.3%; Score 36; DB 1; Length 581;

Best Local Similarity 70.0%; Pred. No. 37;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFAD 10

|||||

Db 463 ASHNYGKPAD 472

RESULT 11

JC2464

probable copper-transporting ATPase (EC 3.6.1.-) HRA-1 - Enterobacteriaceae spp.

C:Species: Enterobacteriaceae spp.

C>Date: 16-Oct-1998 #sequence_revision 16-Oct-1998 #text_change 18-Jun-1999

C:Accession: JC2464

R:Trenor III., C.; Lin, W.; Andrews, N.C.

Biochem. Biophys. Res. Commun. 205, 1644-1650, 1994

A>Title: Novel bacterial P-type ATPases with histidine-rich heavy-metal-associated se

A:Reference number: JC2464; MUID:95110304

A:Accession: JC2464

A:Molecule type: mRNA

A:Residues: 1-731 <TRE>

A:Cross-references: GB:U16658; NID:g643612; PIDN:AAA62113.1; PID:g643613

A:Experimental source: human small intestine cDNA library

A>Note: the source species is uncertain; the cloned sequence did not hybridize with h

C:Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-bindin

C:Keywords: ATP; copper transport; hydrolase; ion transport; phosphoprotein; transmem

F:7-92/Region: His-rich

F:135-477/Domain: ATPase transduction domain homology <ATT>

F:544-685/Domain: ATPase nucleotide-binding domain homology <ATN>

F:287/Active site: Glu #status predicted

F:431/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 64.3%; Score 36; DB 1; Length 731;

Best Local Similarity 60.0%; Pred. No. 47;

Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFAD 10

|||||

Db 88 AHHHGSFAD 97

RESULT 12

G69080

conserved hypothetical protein MTH1600 - Methanobacterium thermoautotrophicum (strain

C:Species: Methanobacterium thermoautotrophicum

C>Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 08-Oct-1999

C:Accession: G69080

R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T

; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani,

k1, S.; Church, G.M.; Daniels, C.J.; Mao, P.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997

A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funcd
A:Reference number: A69000; MUID:98037514
A:Accession: G69080
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-232 <MTH>
A:Cross-references: GB:AE000919; GB:AE000666; NID:g2622717; PIDN:AAB86073.1; PID:g262272
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH1600
C:Superfamily: Methanococcus jannaschii conserved hypothetical protein MJ1634

Query Match 62.5%; Score 35; DB 2; Length 232;
Best Local Similarity 62.5%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 HNYGSFAD 10
Db 154 HNYGGFTD 161
||| |

RESULT 13
D72098
lysophospholipase esterase - Chlamydia pneumoniae (strain CWL029)
C:Species: Chlamydia pneumoniae
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 08-Oct-1999
C:Accession: D72098
R:Kaiman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.; Grimwood, J.;
Nature Genet. 21, 385-389, 1999
A:Title: Comparative genomes of Chlamydia pneumoniae and C. trachomatis.
A:Reference number: A72000; MUID:99206606
A:Accession: D72098
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-243 <ARN>
A:Cross-references: GB:AE001612; GB:AE001363; NID:g4376541; PIDN:AAD18420.1; PID:g437654
A:Experimental source: strain CWL029
C:Genetics:
A:Gene: Cpn0271

Query Match 62.5%; Score 35; DB 2; Length 243;
Best Local Similarity 75.0%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 HNYGSFAD 10
Db 32 HNYGSLAD 39
||| |

RESULT 14
D71087
probable translation initiation factor eIF-2 alpha chain - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 26-Aug-1999
C:Accession: D71087
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137
A:Accession: D71087
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-275 <KAW>
A:Cross-references: GB:AF000004; NID:g3236131; PIDN:BAA30058.1; PID:d1031001; PID:g32573
A:Experimental source: strain OH3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0961
C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 62.5%; Score 35; DB 2; Length 275;
Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNYGSFAD 10
Db 23 HNYGAFLE 30
||||| :

RESULT 15
G75130
translation initiation factor aif-2, subun it alpha (aif2a) PAB0568 - Pyrococcus abys
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 24-Nov-1999
C:Accession: G75130
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s
A:Reference number: A75001
A:Accession: G75130
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-275 <KAW>
A:Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49760.1; PID:e151
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: aif2a; PAB0568
C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 62.5%; Score 35; DB 2; Length 275;
Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNYGSFAD 10
Db 23 HNYGAFLE 30
||||| :

Search completed: May 27, 2000, 19:26:45
Job time: 1768 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2000, 20:07:17 ; Search time 69.28 Seconds
(without alignments)
4.396 Million cell updates/sec

Title: US-09-016-061-72
Perfect score: 56
Sequence: 1 ARHNYGSPAD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	36	64.3	581	1 MIK1_SCHPO	P30290 schizosacch
2	35	62.5	275	1 IF2A_PYRHO	O58655 pyrococcus
3	35	62.5	467	1 PAX7_HUMAN	P23759 homo sapien
4	35	62.5	682	1 E13B_BACCI	P23903 bacillus ci
5	34	60.7	284	1 IPYR_PICPA	O13505 pichia past
6	34	60.7	286	1 IPYR_KLOLA	PI3998 kluyveromyc
7	34	60.7	286	1 IPYR_YEAST	P00817 saccharomyc
8	34	60.7	608	1 ALBU_MOUSE	P07724 mus musculu
9	33.5	59.8	587	1 COLA_VTBPA	Q56696 vibrio para
10	33	58.9	448	1 NCAP_CVROC	P33469 human coron
11	33	58.9	470	1 SYE2_RICPR	Q9ZC18 rickettsia
12	33	58.9	473	1 SYE_AQUAE	O67271 aquifex aeo
13	33	58.9	608	1 ALBU_RAT	P02770 rattus norv
14	33	58.9	682	1 VG50_BPML5	Q05262 mycobacteri
15	32	57.1	65	1 CCSA_OENBE	P31565 oenothera b
16	32	57.1	65	1 CCSA_PEA	P31172 pisum sativ
17	32	57.1	196	1 WBBJ_ECOLI	P37750 escherichia
18	32	57.1	198	1 HB2G_HUMAN	P01911 homo sapien
19	32	57.1	227	1 PRRA_RAT	P09320 rattus norv
20	32	57.1	246	1 YAFK_ECOLI	Q47148 escherichia
21	32	57.1	255	1 CBPM_STRAL	P00733 streptomyce
22	32	57.1	266	1 HB2A_HUMAN	P01913 homo sapien
23	32	57.1	266	1 HB2B_HUMAN	P01912 homo sapien
24	32	57.1	266	1 HB2C_HUMAN	P01914 homo sapien
25	32	57.1	266	1 HB2D_CANFA	PI8470 canis famil
26	32	57.1	266	1 HB2D_HUMAN	PI3759 homo sapien
27	32	57.1	266	1 HB2E_HUMAN	P04229 homo sapien
28	32	57.1	266	1 HB2F_HUMAN	PI3758 homo sapien
29	32	57.1	266	1 HB2H_HUMAN	PI3760 homo sapien
30	32	57.1	266	1 HB2I_HUMAN	P20039 homo sapien
31	32	57.1	266	1 HB2J_HUMAN	PI3761 homo sapien
32	32	57.1	298	1 MTRC_METKA	O49606 methanopyru
33	32	57.1	313	1 CCSA_TOBAC	PI2216 nicotiana t
34	32	57.1	315	1 VC04_VACCV	PI7370 vaccinia vi

35	32	57.1	316	1 VC04_VACCC	P21038 vaccinia v1
36	32	57.1	321	1 CGSA_MAIZE	P46659 zea mays (m
37	32	57.1	321	1 CGSA_ORYSA	PI2215 oryza sativ
38	32	57.1	328	1 CGSA_ATH	P56770 arabidopsis
39	32	57.1	349	1 Y3Y9_YEAST	P41903 saccharomyc
40	32	57.1	466	1 GSHR_MOUSE	P47791 mus musculu
41	32	57.1	502	1 YM40_MARPO	P20457 saccharomyc
42	32	57.1	528	1 PRI2_YEAST	P38478 marchantia
43	32	57.1	561	1 DIM_ATH	Q39085 arabidopsis
44	32	57.1	567	1 DIM_PEA	P93472 pisum sativ
45	32	57.1	629	1 KSYK_RAT	O64725 rattus norv

ALIGNMENTS

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RESULT 1
MIK1_SCHPO
ID MIK1_SCHPO STANDARD; PRT; 581 AA.
AC P30290;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE MITOSIS INHIBITOR PROTEIN KINASE MIK1 (EC 2.7.1.-).
GN MIK1.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetales;
OC Schizosaccharomycetaceae; Schizosaccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 91168259.
RA Lundgren K., Walworth N., Boohar R., Dembski M., Kirschner M.,
RA Beach D.;
RT "mik1 and weel cooperate in the inhibitory tyrosine phosphorylation
RT of cdc2."
RL Cell 64:1111-1122(1991).
CC -!- FUNCTION: PROTEIN KINASE THAT ACTS BOTH ON SERINES AND ON
CC TYROSINES. IT ACTS AS A NEGATIVE REGULATOR OF ENTRY INTO MITOSIS
CC (G2 TO M TRANSITION). PHOSPHORYLATES AND INHIBITS CDC2.
CC -!- SIMILARITY: WITH THE CONSERVED CATALYTIC DOMAINS OF SER/THR-
CC PROTEIN KINASES. HIGHLY SIMILAR TO S.POMBE WEE1.
CC -----
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CC -----
CC EMBL; M60834; AAA91278.1; -.
CC PIR; A37913; A37913.
CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
CC DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1
CC DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC DR PFAM; PF00069; PKinase; 1.
CC KW Mitosis; Transference; Serine/threonine-protein kinase;
CC Tyrosine-protein kinase; ATP-binding.
CC FT DOMAIN 289 561 PROTEIN KINASE.
CC FT NP_BIND 295 303 ATP (BY SIMILARITY).
CC FT BINDING 320 320 ATP (BY SIMILARITY).
CC FT ACT_SITE 417 417 BY SIMILARITY.
CC SQ SEQUENCE 581 AA; 65933 MW; 371E0CEDB2CAICE3 CRC64;
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Query Match 64.3%; Score 36; DB 1; Length 581;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ARHNYGSPAD 10
Db 463 ASHNYGKPAD 472

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RESULT 2
IP2A_PYRHO
ID AC O58655; STANDARD; PRT; 275 AA.
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
GN PH0961.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Pyrococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OT3;
RX MEDLINE: 98344137.
RA Kawarabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo H. Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3."
RL DNA Res. 5:55-76(1998).
CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
CC (BY SIMILARITY)
CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
CC CHAIN (BY SIMILARITY).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AP000004; BAA30058.1; -.
CC PFAM: PF00575; SI; 1.
CC KW Initiation factor; Protein biosynthesis.
CC SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;

Query Match 62.5%; Score 35; DB 1; Length 275;
Best Local Similarity 62.5%; Pred. No. 9.4;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGFSAD 10
DB 23 HNYGAFLE 30
|||||:|

RESULT 3
PAX7_HUMAN
ID PAX7_HUMAN STANDARD; PRT; 467 AA.
AC P23759;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PAIRED BOX PROTEIN PAX-7 (HUP1).
GN PAX7 OR HUP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 95075634.
RA Schaffer B.W., Czerny T., Bernasconi M., Genini M., Busslinger M.;
RT "Molecular cloning and characterization of a human PAX-7 cDNA
RT expressed in normal and neoplastic myocytes."
RL Nucleic Acids Res. 22:4574-4582(1994).

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[2]
RN SEQUENCE OF 30-195 FROM N.A.
RX MEDLINE: 89305521.
RA Burri M., Tromvoukis Y., Bopp D., Frigerio G., Noll M.;
RT "Conservation of the paired domain in metazoans and its structure in
RT three isolated human genes."
RL EMBO J. 8:1183-1190(1989).
CC -!- FUNCTION: PROBABLE TRANSCRIPTION FACTOR. IT MAY HAVE A ROLE IN
CC MYOGENESIS.
CC -!- SUBUNIT: CAN BIND AS A HETERODIMER WITH PAX3.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- DISEASE: IN SOME TUMORS, PAX7 BECOMES JOINED TO FKBP.
CC -!- SIMILARITY: BELONGS TO THE PAIRED FAMILY OF HOMEBOX PROTEINS.
CC -!- SIMILARITY: CONTAINS A PAIRED BOX DOMAIN.
CC -----
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CC -----
CC EMBL: Z35141; CAA84513.1; -.
CC EMBL: X15042; E14747; -.
CC EMBL: X15250; E14749; -.
CC EMBL: X15251; E14751; -.
CC PIR: S06959; S06959.
CC HSP: P06601; IFJL.
CC TRANSFAC: T003996; -.
CC MIM: 167410; -.
CC PRINTS: PR00027; PAIREDBOX.
CC PROSITE: PS00027; HOMEBOX_1; 1.
CC PROSITE: PS00071; HOMEBOX_2; 1.
CC PROSITE: PS00034; PAIRED_BOX; 1.
CC PFAM: PF00046; homeobox; 1.
CC PFAM: PF00292; PAX; 1.
CC KW Transcription regulation; Homeobox; DNA-binding; Nuclear protein;
CC Developmental protein; Paired box.
FT DOMAIN 34 161 PAIRED BOX.
FT DNA_BIND 217 276 HOMEBOX.
FT DOMAIN 340 346 POLY-ALA.
FT CONFLICT 151 152 MISSING (IN REF. 2).
SQ SEQUENCE 467 AA; 51019 MW; 99FED562CCEC45A CRC64;

Query Match 62.5%; Score 35; DB 1; Length 467;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFAD 10
DB 354 ARHSFSSYSD 363
|||||:|:|

RESULT 4
E13B_BACCI
ID E13B_BACCI STANDARD; PRT; 682 AA.
AC P23903;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A1 PRECURSOR (EC 3.2.1.39) ((1->3)-
DE BETA-GLUCAN ENDOHYDROLASE) ((1->3)-BETA-GLUCANASE A1).
GN GLCA.
OS Bacillus circulans.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 39-52.
RC STRAIN-WL-12;
RX MEDLINE: 90185240.
RA Yahata N., Watanabe T., Nakamura Y., Yamamoto Y., Kamimiya S.,

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RA Tanaka H.;
RT "Structure of the gene encoding beta-1,3-glucanase A1 of Bacillus
RL cireulans WL-12.";
RL Gene 86:113-117(1990).
CC -1- FUNCTION: LYSIS OF CELLULAR WALLS CONTAINING BETA-1,3-GLUCANS.
CC IMPLICATED IN THE DEFENSE AGAINST FUNGAL PATHOGENS.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF 1,3-BETA-D-GLUCOSIDIC LINKAGES
CC IN 1,3-BETA-D-GLUCANS.
CC -1- SIMILARITY: BELONGS TO FAMILY 16 OF GLYCOSYL HYDROLASES.
CC -----
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CC -----
DR EMBL; M34503; AAA22474.1; -.
DR PIR; JQ0420; JQ0420.
DR HSSP; P23904; LAJO.
DR PROSITE; PS01034; GLYCOSYL_HYDROL_F16; 1.
KW Cell wall; Hydrolase; Glycosidase; Signal.
FT SIGNAL 1 38
FT CHAIN 39 682 GLUCAN ENDO-1,3-BETA-GLUCOSIDASE A1.
FT ACT_SITE 552 552 NUCLEOPHILE (BY SIMILARITY).
FT ACT_SITE 557 557 PROTON DONOR (BY SIMILARITY).
SQ SEQUENCE 682 AA; 75465 MW; 8C4F407E34D4ADD5 CRC64;

Query Match 62.5%; Score 35; DB 1; Length 682;
Best Local Similarity 62.5%; Pred. No. 25;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSPAD 10
Db 227 HNYGQFTD 234

RESULT 5
ID IPYR_PICPA STANDARD; PRT; 284 AA.
AC O13505;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
DE HYDROLASE) (PPASE).
GN IPP1.
OS Pichia pastoris (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Pichia.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-NRRL Y-11430;
RX MEDLINE; 99034033.
RA Cosano I.C., Alvarez P., Molina M., Nombela C.;
RT "Cloning and sequence analysis of the Pichia pastoris TRP1 and
RT HIS3 genes.";
RL Yeast 14:861-867(1998).
CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O -> 2 ORTHOPHOSPHATE.
CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC -----
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CC -----
DR EMBL; AJ001000; CAA04453.1; -.
DR HSSP; P00817; 1WGI.
DR PROSITE; PS00387; PPASE; 1.
DR PFAM; PF00719; Pyrophosphatase; 1.
KW Hydrolase; Magnesium.
FT INIT_MET 0 0 BY SIMILARITY.
FT ACT_SITE 56 56 PROBABLE.
FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 284 AA; 31937 MW; 3DAD27970D7775D6 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 284;
Best Local Similarity 83.3%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 91 HNYGAF 96

RESULT 6
ID IPYR_KLULA STANDARD; PRT; 286 AA.
AC P13998;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
DE HYDROLASE) (PPASE).
GN IPP1 OR Ipp.
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Kluyveromyces.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89189093.
RA Stark M.J.R., Milner J.S.;
RT "Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a
RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
RT and histone H3.";
RL Yeast 5:35-50(1989).
RN [2]
RP SIMILARITY TO E.COLI AND YEAST PPASES.
RX MEDLINE; 90254161.
RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
RA Cooperman B.S.;
RT "Conservation of functional residues between yeast and E. coli
RT inorganic pyrophosphatases.";
RL Biochim. Biophys. Acta 1038:338-345(1990).
CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O -> 2 ORTHOPHOSPHATE.
CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC -----
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CC -----
DR EMBL; X14230; CAA32446.1; -.
DR PIR; S07894; PWVKL.
DR HSSP; P00817; 1WGI.
DR PROSITE; PS00387; PPASE; 1.
DR PFAM; PF00719; Pyrophosphatase; 1.
KW Hydrolase; Magnesium.
FT INIT_MET 0 0 BY SIMILARITY.

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FT ACT_SITE 56 56 PROBABLE.
FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 286 AA; 32034 MW; 11647F4ABD916A2F CRC64;

Query Match 60.7%; Score 34; DB 1; Length 286;
Best Local Similarity 83.3%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
Db 91 HNYGAF 96

RESULT 7
IPYR_YEAST
ID IPYR_YEAST STANDARD; PRT; 286 AA.
AC P00817;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
DE HYDROLASE) (PPASE).
GN IPPI OR PPAL OR PPA OR YBR011C OR YBR0202.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=X2180;
RX MEDLINE; 89083474.
RA Kolakowski L.F. Jr., Schloesser M., Cooperman B.S.;
RT "Cloning, molecular characterization and chromosome localization of
RT the inorganic pyrophosphatase (PPA) gene from S. cerevisiae."
RL Nucleic Acids Res. 16:10441-10452(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Entian K.-D., Koetter P., Rose M., Li Z., Thermann R., Brendel M.,
RA Baur A., Boles E., Miosga T., Schaeff-Gerstenschlaeger I.,
RA Zimmermann F.K.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE.
RX MEDLINE; 78087552.
RA Cohen S.A., Sterner R., Keim P.S., Henrikson R.L.;
RT "Covalent structural analysis of yeast inorganic pyrophosphatase."
RT J. Biol. Chem. 253:889-897(1978).
RN [4]
RP SEQUENCE OF 25-35 AND 239-251.
RC STRAIN=S288C;
RX MEDLINE; 95203288.
RA Gareis J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a Saccharomyces cerevisiae protein
RT database."
RL Electrophoresis 15:1466-1486(1994).
RN [5]
RP SEQUENCE OF 239-249.
RC STRAIN=ATCC 38531 / Y41;
RX MEDLINE; 97089742.
RA Norbeck J., Blomberg A.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
RT Saccharomyces cerevisiae."
RL FEMS Microbiol. Lett. 137:1-8(1996).
RN [6]
RP ACTIVE SITE.
RX MEDLINE; 80109718.
RA Bond M.W., Chiu N.Y., Cooperman B.S.;
RT "Identification of an arginine important for enzymatic activity
RT within the covalent structure of yeast inorganic pyrophosphatase."
RL Biochemistry 19:94-102(1980).
RN [7]

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RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RA Arutunian E.G., Terrian S.S., Voronova A.A., Kuranova I.P.,
RA Smirnova E.A., Vainstein B.K., Hohne W.E., Hansen G.;
RT "X-ray diffraction study of inorganic pyrophosphatase from baker's
RT yeast at the 3-A resolution."
RL Dokl. Akad. Nauk SSSR 258:1481-1492(1981).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE; 97148342.
RA Heikinheimo P., Lehtonen J., Baykov A., Lahti R., Cooperman B.S.,
RA Goldman A.;
RT "The structural basis for pyrophosphatase catalysis."
RL Structure 4:1491-1508(1996).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RA Swaminathan K., Cooperman B.S., Lahti R., Voet D.;
RL Submitted (DEC-1997) to the PDB data bank.
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF MUTANTS LYS-78 AND LYS-117.
RX MEDLINE; 99096888.
RA Tuominen V., Heikinheimo P., Kajander T., Torkkel T., Hyytiä T.,
RA Kapyla J., Lahti R., Cooperman B.S., Goldman A.;
RT "The R78K and D117E active-site variants of Saccharomyces cerevisiae
RT soluble inorganic pyrophosphatase: structural studies and mechanistic
RT implications."
RL J. Mol. Biol. 284:1565-1580(1998).
RN [11]
RP SIMILARITY TO E.COLI AND K.LACTIS PPASES.
RX MEDLINE; 90254161.
RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
RA Cooperman B.S.;
RT "Conservation of functional residues between yeast and E. coli
RT inorganic pyrophosphatases."
RL Biochim. Biophys. Acta 1038:338-345(1990).
CC -!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O -> 2 ORTHOPHOSPHATE.
CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC -!- MAGNESIUM CONFERS THE HIGHEST ACTIVITY. IT BINDS UP TO 4 DIVALENT
CC CATIONS PER SUBUNIT, WITH THREE REQUIRED FOR ACTIVITY.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC -----
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CC -----
CC EMBL; X13253; CAA31629.1; -.
CC DDB; 235880; CAA84949.1; -.
CC PIR; S45864; PWBY.
CC PDB; 1PYP; 15-OCT-91.
CC PDB; 1YPP; 07-DEC-96.
CC PDB; 1WGI; 19-NOV-97.
CC PDB; 1WGS; 19-NOV-97.
CC PDB; 1HUJ; 08-APR-98.
CC PDB; 1HUK; 08-APR-98.
CC PDB; 117E; 23-DEC-98.
CC PDB; 8PRK; 23-DEC-98.
CC SWISS-2DPAGE; P00817; YEAST.
CC YEPD; 7305; -.
CC SGD; L0000872; IPP1.
CC PROSITE; PS00387; PPASE; 1.
CC PFAM; PF00719; Pyrophosphatase; 1.
KW Hydrolase; Magnesium; 3D-structure.
FT INIT_MET 0
FT ACT_SITE 56 56 PROBABLE.
FT BINDING 78 78 INORGANIC PYROPHOSPHATE.
FT CONFLICT 40 40 N -> D (IN REF. 3).
FT CONFLICT 71 71 D -> N (IN REF. 3).
FT CONFLICT 74 74 MISSING (IN REF. 3).

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FT CONFLICT 123 123 E -> Q (IN REF. 3).
FT CONFLICT 136 136 Q -> E (IN REF. 3).
FT CONFLICT 186 186 N -> D (IN REF. 3).
FT CONFLICT 224 224 D -> N (IN REF. 3).
FT CONFLICT 266 266 L -> P (IN REF. 2).
FT STRAND 4 7
FT STRAND 16 20
FT STRAND 25 25
FT TURN 28 30
FT TURN 38 41
FT TURN 45 45
FT STRAND 55 55
FT STRAND 79 79
FT TURN 97 98
FT TURN 111 112
FT STRAND 121 123
FT TURN 131 132
FT STRAND 135 135
FT STRAND 138 146
FT STRAND 151 158
FT TURN 160 161
FT TURN 165 167
FT HELIX 172 175
FT TURN 176 177
FT TURN 179 180
FT HELIX 182 197
FT STRAND 203 203
FT HELIX 205 207
FT STRAND 210 210
FT HELIX 212 230
FT TURN 231 231
FT TURN 245 246
FT TURN 248 249
FT TURN 251 252
FT TURN 255 260
FT TURN 274 275
SQ SEQUENCE 286 AA; 32184 MW; F29390260B60C8B2 CRC64;
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Query Match 60.7%; Score 34; DB 1; Length 286;

Best Local Similarity 83.3%; Pred. No. 15;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 3 HNYGSF 8
Db 91 HNYGAF 96
|||||
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RESULT 8
ALBU_MOUSE STANDARD; PRT; 608 AA.
AC P07724; Q61802;
DT 01-APR-1988 (Rel. 07, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE SERUM ALBUMIN PRECURSOR.
GN ALB OR ALBI.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA van Reeth T., Gabant P., Dreze P., Szpirer J., Szpirer C.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 99-516 FROM N.A.
RX MEDLINE; 88216123.
RA Minghetti P.P., Law S.W., Dugaiczak A.;
RT "The rate of molecular evolution of alpha-fetoprotein approaches that
of pseudogenes.";
RL Mol. Biol. Evol. 2:347-358(1985).
RN [3]
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RP SEQUENCE OF 477-551 FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE; 90269606.
RA Boccaccio C., Deschatrette J., Meunier-Rotival M.;
RT "Empty and occupied insertion site of the truncated LINE-1 repeat
located in the mouse serum albumin-encoding gene.";
RL Gene 88:181-186(1990).
RN [4]
RP SEQUENCE OF 25-44.
RC TISSUE=LIVER;
RX MEDLINE; 93162044.
RA Giometti C.S., Taylor J., Tollaksen S.L.;
RT "Mouse liver protein database: a catalog of proteins detected by two-
dimensional gel electrophoresis.";
RL Electrophoresis 13:970-991(1992).
CC -1- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
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-----
CC EMBL; AJ011413; CAA09617.1; -.
DR EMBL; M16111; AAA37190.1; -.
DR EMBL; X13060; CAA31458.1; -.
DR PIR; A05139; A05139.
DR HSP; P02768; LUOR.
DR SWISS-2DPAGE; P07724; MOUSE.
DR MGD; MGI:87991; ALBI.
DR PROSITE; PS00212; ALBUMIN; 3.
DR PFAM; PF00273; transport_prot; 1.
KW Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
KW Copper.
FT SIGNAL 1 18 BY SIMILARITY.
FT PROPEP 19 24
FT CHAIN 25 608 SERUM ALBUMIN.
FT REPEAT 28 202 1.
FT REPEAT 221 394 2.
FT REPEAT 413 592 3.
FT METAL 27 27 COPPER.
FT DISULFID 77 86 BY SIMILARITY.
FT DISULFID 99 115 BY SIMILARITY.
FT DISULFID 114 125 BY SIMILARITY.
FT DISULFID 148 193 BY SIMILARITY.
FT DISULFID 192 201 BY SIMILARITY.
FT DISULFID 224 270 BY SIMILARITY.
FT DISULFID 269 277 BY SIMILARITY.
FT DISULFID 289 303 BY SIMILARITY.
FT DISULFID 302 313 BY SIMILARITY.
FT DISULFID 340 385 BY SIMILARITY.
FT DISULFID 384 393 BY SIMILARITY.
FT DISULFID 416 462 BY SIMILARITY.
FT DISULFID 461 472 BY SIMILARITY.
FT DISULFID 485 501 BY SIMILARITY.
FT DISULFID 500 511 BY SIMILARITY.
FT DISULFID 538 583 BY SIMILARITY.
FT DISULFID 582 591 BY SIMILARITY.
FT CONFLICT 27 27 H -> D (IN REF. 4).
FT CONFLICT 33 33 H -> D (IN REF. 4).
FT CONFLICT 41 41 Q -> I (IN REF. 4).
SQ SEQUENCE 608 AA; 68692 MW; 292F7C7EED3A61B4 CRC64;
```

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Query Match          60.7%; Score 34; DB 1; Length 608;
Best Local Similarity 66.7%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYGSFAD 10
DB 105 RENYGLAD 113

RESULT 9
COLA_VIBPA
ID COLA_VIBPA STANDARD; PRT; 587 AA.
AC Q56696;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE MICROBIAL COLLAGENASE PRECURSOR (EC 3.4.24.3).
GN PRTPV.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-93;
RX MEDLINE; 96036215.
RA Lee C., Su S., Liaw R.;
RT "Molecular analysis of an extracellular protease gene from Vibrio
parahaemolyticus";
RL Microbiology 141:2569-2576(1995).
CC -!- CATALYTIC ACTIVITY: DIGESTION OF NATIVE COLLAGEN IN THE TRIPLE
HELICAL REGION AT XAA-1-GLY BONDS. WITH SYNTHETIC PEPTIDES, A
PREFERENCE IS SHOWN FOR GLY AT P3 AND P1'; PRO AND ALA AT P2 AND
P2'; AND HYDROXYPROLINE, ALA OR ARG AT P3'.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M9 (ZINC METALLOPROTEASE).
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CC -----
DR EMBL; 246782; CAA86734.1; -.
DR PRINTS; PR00931; MICOLLPASE.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Hydrolase; Metalloprotease; Zinc; Zymogen; Signal.
FT SIGNAL 1 25
FT CHAIN 26 587 MICROBIAL COLLAGENASE.
FT METAL 435 435 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 436 436 BY SIMILARITY.
FT METAL 439 439 ZINC (CATALYTIC) (BY SIMILARITY).
SQ SEQUENCE 587 AA; 66003 MW; 8A94D83E3D2A2BD1 CRC64;

Query Match          59.8%; Score 33.5; DB 1; Length 587;
Best Local Similarity 72.7%; Pred. No. 42;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 ARHN-YGSFAD 10
DB 443 ARFNQYGSFSD 453

RESULT 10
NCAP_CVHOC
ID NCAP_CVHOC STANDARD; PRT; 448 AA.
AC P33469;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE NUCLEOCAPSID PROTEIN.
GN N.

Query Match          58.9%; Score 33; DB 1; Length 470;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OS Human coronavirus (strain OC43).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89243809.
RA Kamahora T., Soe L.H., Lai M.M.C.;
RT "Sequence analysis of nucleocapsid gene and leader RNA of human
coronavirus OC43";
RL Virus Res. 12:1-9(1989).
DR PIR; A60003; A60003.
DR PFAM; PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 448 AA; 49316 MW; 5193AB1AE0D75626 CRC64;

Query Match          58.9%; Score 33; DB 1; Length 448;
Best Local Similarity 85.7%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
DB 103 RHNKGSF 109

RESULT 11
SYE2_RICPR
ID SYE2_RICPR STANDARD; PRT; 470 AA.
AC Q9ZCT8;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE 2 (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE 2)
DE (GLURS 2).
GN GLTX2 OR RP623.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MADRID E;
RX MEDLINE; 99039499.
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sichteritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
mitochondria";
RL Nature 396:133-140(1998).
CC -!- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) -> AMP +
PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -!- SUBUNIT: MONOMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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CC -----
DR EMBL; AJ235272; CAA15066.1; -.
DR HSP; P27000; IGLN.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW Aminoacyl-TRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
FT SIMILAR 239 243 "KMSKS" REGION.
FT BINDING 242 242 ATP (BY SIMILARITY).
SQ SEQUENCE 470 AA; 53696 MW; DF1CE50A20B8A9FD CRC64;

Query Match          58.9%; Score 33; DB 1; Length 470;
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Best Local Similarity 75.08; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSF 8
   |||||
Db 31 ARHNGKF 38

RESULT 12
SYE_AQAE
ID SYE_AQAE STANDARD; PRT; 473 AA.
AC 067271; 2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE)
DE (GLURS).
GN GLTX OR AQ_1221.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VF5;
RX MEDLINE; 98196666.
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus."
RL Nature 392:353-358(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) -> AMP +
CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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DR EMBL; AE000729; AAC07230.1; -
DR PRINTS; PR00987; TRNASYNTHGLU.
DR PROSITE; PS00178; AA-TRNA_LIGASE_I; 1.
DR PFAM; PF00749; trna-synt_1c; 1.
KW Aminoacyl-trna synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
FT SIMILAR 242 246 "KMSKS" REGION.
FT BINDING 245 245 ATP (BY SIMILARITY).
SQ SEQUENCE 473 AA; 55121 MW; 5CB4D1590973E07A CRC64;

Query Match 58.98; Score 33; DB 1; Length 473;
Best Local Similarity 75.08; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSF 8
   |||||
Db 31 ARHNGKF 38

RESULT 13
ALBU_RAT
ID ALBU_RAT STANDARD; PRT; 608 AA.
AC P02770;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE SERUM ALBUMIN PRECURSOR.
GN ALB.

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OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81223722.
RA Sargent T.D., Yang M., Bonner J.;
RT "Nucleotide sequence of cloned rat serum albumin messenger RNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:243-246(1981).
RN [2]
RP SEQUENCE OF 1-38, AND PROCESSING.
RX MEDLINE; 77249657.
RA Strauss A.W., Bennett C.D., Donohue A.M., Rodkey J.A., Alberts A.W.;
RT "Rat liver pre-proalbumin: complete amino acid sequence of the pre-
RT piece. Analysis of the direct translation product of albumin
RT messenger RNA.";
RL J. Biol. Chem. 252:6846-6855(1977).
RN [3]
RP SEQUENCE OF 25-222.
RX MEDLINE; 78109429.
RA Isemura S., Ikenaka T.;
RT "Amino acid sequences of fragments I and II obtained by cyanogen
RT bromide cleavage of rat serum albumin.";
RL J. Biochem. 83:35-48(1978).
RN [4]
RP SEQUENCE OF 223-288 AND 572-608.
RX MEDLINE; 76260153.
RA Isemura S., Ikenaka T.;
RT "Fragmentation of rat serum albumin by cyanogen bromide cleavage and
RT the amino acid sequences of four fragments.";
RL J. Biochem. 79:1183-1196(1976).
RN [5]
RP COPPER BINDING.
RX MEDLINE; 79001617.
RA Aoyagi Y., Ikenaka T., Ichida F.;
RT "Copper(II)-binding ability of human alpha-fetoprotein.";
RL Cancer Res. 38:3483-3486(1978).
CC -1- FUNCTION: SERUM ALBUMIN, THE MAIN PROTEIN OF PLASMA, HAS A GOOD
CC BINDING CAPACITY FOR WATER, CA++, NA+, K+, FATTY ACIDS, HORMONES,
CC BILIRUBIN AND DRUGS. ITS MAIN FUNCTION IS THE REGULATION OF THE
CC COLLOIDAL OSMOTIC PRESSURE OF BLOOD.
CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -1- TISSUE SPECIFICITY: PLASMA.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE ALB/AFP/VDB FAMILY.
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DR EMBL; V01222; CAA24532.1; -
DR PIR; A03233; ABRTS.
DR HSP; P02768; IUOR.
DR PRINTS; PR00802; SERUMALBUMIN.
DR PROSITE; PS00212; ALBUMIN; 3.
DR PFAM; PF00273; transport_prot; 1.
KW Plasma; Metal-binding; Lipid-binding; Albumin; Repeat; Signal;
KW Copper.
FT SIGNAL 1 18
FT PROPEP 19 24
FT CHAIN 25 608 SERUM ALBUMIN.
FT REPEAT 28 202 1.
FT REPEAT 221 394 2.
FT REPEAT 413 592 3.
FT METAL 27 27 COPPER.
FT DISULFID 77 86 BY SIMILARITY.
FT DISULFID 99 115 BY SIMILARITY.
FT DISULFID 114 125 BY SIMILARITY.
FT DISULFID 148 193 BY SIMILARITY.

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FT DISULFID 192 201 BY SIMILARITY.
FT DISULFID 224 270 BY SIMILARITY.
FT DISULFID 269 277 BY SIMILARITY.
FT DISULFID 289 303 BY SIMILARITY.
FT DISULFID 302 313 BY SIMILARITY.
FT DISULFID 340 385 BY SIMILARITY.
FT DISULFID 384 393 BY SIMILARITY.
FT DISULFID 416 462 BY SIMILARITY.
FT DISULFID 461 472 BY SIMILARITY.
FT DISULFID 485 501 BY SIMILARITY.
FT DISULFID 500 511 BY SIMILARITY.
FT DISULFID 538 583 BY SIMILARITY.
FT DISULFID 582 591 BY SIMILARITY.
FT VARIANT 262 262 V -> L.
SQ SEQUENCE 608 AA; 68718 MW; 5BB497A282411AB7 CRC64;

Query Match 58.9%; Score 33; DB 1; Length 608;
Best Local Similarity 66.7%; Pred. No. 54;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHYGSGFAD 10
Db 105 RDNYGELAD 113

RESULT 14
VG50_BPML5 STANDARD; PRT; 682 AA.
AC Q05262;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PUTATIVE ADENOSYLCOBALAMIN-DEPENDENT RIBONUCLEOTIDE REDUCTASE
DE (EC 1.17.4.2) (GP50).
GN 50.
OS Mycobacteriophage L5.
OC Viruses.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93211282.
RA Hatfull G.F., Sarkis G.J.;
RT "DNA sequence, structure and gene expression of mycobacteriophage L5:
a phage system for mycobacterial genetics.";
RL Mol. Microbiol. 7:395-405(1993).
CC -|- CATALYTIC ACTIVITY: 2'-DEOXYRIBONUCLEOSIDE TRIPHOSPHATE +
OXIDIZED THIOREDUXIN + H(2)O -> RIBONUCLEOSIDE TRIPHOSPHATE +
REDUCED THIOREDUXIN.
CC -----
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CC -----
CC EMBL; Z18946; CAA79426.1; -.
DR PIR; S30995; S30995.
KW Oxidoreductase; DNA replication.
SQ SEQUENCE 682 AA; 76331 MW; 8D2A71B873BC04A8 CRC64;
```

```
Query Match 58.9%; Score 33; DB 1; Length 682;
Best Local Similarity 66.7%; Pred. No. 61;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 311 AKEGYGSFA 319
```

RESULT 15

```
CCSA_OENBE STANDARD; PRT; 65 AA.
ID AC P31565;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA (FRAGMENT).
GN CCSA.
OS Oenothera bertiana (Bertero's evening primrose).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; euroids II; Myrtales; Onagraceae; Oenothera.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93169690.
RA Nimzyk R., Schoendorf T., Hachtel W.;
RT "In-frame length mutations associated with short tandem repeats are
located in unassigned open reading frames of Oenothera chloroplast
DNA.";
RL Curr. Genet. 23:265-270(1993).
CC -|- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
HEME ATTACHMENT (BY SIMILARITY).
CC -|- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X64617; CAA45900.1; -.
DR PIR; S19981; S19981.
DR PIR; S19988; S19988.
KW Cytochrome c-type biogenesis; Chloroplast.
FT NON_TER 1
SQ SEQUENCE 65 AA; 7441 MW; 343E66DDA1492C0C CRC64;

Query Match 57.1%; Score 32; DB 1; Length 65;
Best Local Similarity 83.3%; Pred. No. 7.9;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 57 HSYGSF 62

Search completed: May 27, 2000, 20:07:18
Job time: 990 sec
```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2000, 19:38:41 ; Search time 199.56 Seconds
(without alignments)
3.474 Million cell updates/sec

Title: US-09-016-061-72
Perfect score: 56
Sequence: 1 ARHNYGSFAD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225978

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SPTREMBL12:*
1: sp-archaea:*
2: sp-bacteria:*
3: sp-fungi:*
4: sp-human:*
5: sp-invertebrate:*
6: sp-mammal:*
7: sp-mhc:*
8: sp-organelle:*
9: sp-phage:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-invertebrate:*
14: sp-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	71.4	210	1 O30115	O30115 archaeoglob
2	39	69.6	162	2 O08236	O08236 ixodes scap
3	39	68.6	162	2 O52253	O52253 rickettsia
4	39	69.6	446	5 O62086	O62086 caenorhabdi
5	39	69.6	707	2 Q52307	Q52307 prevotella
6	38	67.9	89	7 O19495	O19495 gallus gall
7	38	67.9	464	2 O53747	O53747 mycobacteri
8	37	66.1	275	10 Q43476	Q43476 hordeum vul
9	36	64.3	39	7 P79474	P79474 cervus elap
10	36	64.3	39	7 P79477	P79477 cervus elap
11	36	64.3	39	7 P79478	P79478 cervus elap
12	36	64.3	39	7 P79479	P79479 cervus elap
13	36	64.3	38	6 O97835	O97835 ovis aries
14	36	64.3	78	6 O97839	O97839 ovis aries
15	36	64.3	78	6 O97844	O97844 ovis aries
16	36	64.3	78	6 O97968	O97968 ovis aries
17	36	64.3	79	7 O19191	O19191 prionailuru
18	36	64.3	79	7 O19192	O19192 prionailuru
19	36	64.3	79	7 O19380	O19380 felis silve
20	36	64.3	79	7 O19381	O19381 felis silve

21	36	64.3	79	7	O19382	O19382 felis silve
22	36	64.3	79	7	O19396	O19396 felis silve
23	36	64.3	79	7	O19397	O19397 felis silve
24	36	64.3	79	7	O19405	O19405 felis silve
25	36	64.3	79	7	O19406	O19406 felis silve
26	36	64.3	79	7	O19407	O19407 felis silve
27	36	64.3	79	7	O19408	O19408 felis silve
28	36	64.3	79	7	O19435	O19435 felis silve
29	36	64.3	81	7	O30568	O30568 macaca fasc
30	36	64.3	81	7	O30571	O30571 macaca fasc
31	36	64.3	81	7	O30737	O30737 macaca neme
32	36	64.3	81	7	O30739	O30739 macaca neme
33	36	64.3	81	7	O30563	O30563 macaca fasc
34	36	64.3	81	7	O30740	O30740 macaca neme
35	36	64.3	82	7	O95598	O95598 phasianus c
36	36	64.3	82	7	O30606	O30606 macaca mula
37	36	64.3	82	7	O30608	O30608 macaca mula
38	36	64.3	82	7	O30637	O30637 macaca mula
39	36	64.3	82	7	O30638	O30638 macaca mula
40	36	64.3	82	7	O30658	O30658 macaca mula
41	36	64.3	82	7	O30659	O30659 macaca mula
42	36	64.3	82	7	O30666	O30666 macaca mula
43	36	64.3	82	7	O30667	O30667 macaca mula
44	36	64.3	82	7	O30668	O30668 macaca mula
45	36	64.3	82	7	O19287	O19287 macaca mula

ALIGNMENTS

RESULT 1
O30115 PRELIMINARY; PRT; 210 AA.
AC O30115;
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-NOV-1999 (Tremblrel. 12, Last annotation update)
DE CONSERVED HYPOTHETICAL PROTEIN.
GN AF0122.
OS Archaeoglobus fulgidus.
OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OC Archaeoglobus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE; 98049343.
RA KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,
RA KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
RA RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRIDES N.C.,
RA FLEISCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
RA KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
RA PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,
RA OVERBECK R., GOCAYNE J.D., WEIDMAN J.F., McDONALD L., UTTERBACK T.,
RA COTTON M.D., SPRIGGS T., ARTIACH P., KAINE B.P., SYKES S.M.,
RA SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
RA MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
RA VENTER J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
DR EMBL; AE001098; AAB91117.1; -.
DR TIGR; AF0122; -.
DR PFAM; PF01629; DUF22; 1.
KW Hypothetical protein.
SQ SEQUENCE 210 AA; 24129 MW; 5DD4973D CRC32;

Query Match 71.4%; Score 40; DB 1; Length 210;
Best Local Similarity 77.8%; Pred. No. 2.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAD 10
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Db 128 RHAYGSFVD 136

RESULT 2
O08236 PRELIMINARY; PRT; 162 AA.
AC O08236;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE ROMPA (FRAGMENT).
OS Bacterioides scapularis endosymbiont.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae.
RN [1]
RP SEQUENCE FROM N.A.
RA WELLER S.J., BALDRIDGE G., MUNDERLOH U.G., NODA H., SIMSER J.,
RA KURTTI T.J.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB002268; BAA19525.1; -.
FT NON_TER 1
FT NON_TER 162
SQ SEQUENCE 162 AA; 16211 MW; 58EF1F0E CRC32;

Query Match 69.6%; Score 39; DB 2; Length 162;
Best Local Similarity 60.0%; Pred. No. 3.5;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAD 10
|:::|:|
Db 144 AHDFGAFAD 153

RESULT 3
O52253 PRELIMINARY; PRT; 162 AA.
AC O52253;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE 190 KDA ANTIGEN (FRAGMENT).
OS Rickettsia cooleyi.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
RN [1]
RP SEQUENCE FROM N.A.
RA BILLINGS A.N., TELTOW G.J., WALKER D.H.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF031535; AAB95268.1; -.
FT NON_TER 1
FT NON_TER 162
SQ SEQUENCE 162 AA; 16230 MW; 9E553932 CRC32;

Query Match 69.6%; Score 39; DB 2; Length 162;
Best Local Similarity 60.0%; Pred. No. 3.5;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAD 10
|:::|:|
Db 144 AHDFGAFAD 153

RESULT 4
O62086 PRELIMINARY; PRT; 446 AA.
AC O62086;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
DE C3IH5.6 PROTEIN.
GN C3IH5.6.

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OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RA KERSHAW J.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., CORSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., McMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON J., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans;
RL Nature 368:32-38(1994).
DR EMBL; Z93778; CAB07846.1; -.
SQ SEQUENCE 446 AA; 50763 MW; B347C0C8 CRC32;

Query Match 69.6%; Score 39; DB 5; Length 446;
Best Local Similarity 87.5%; Pred. No. 10;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSFA 9
|:|:|:|
Db 51 RHNYGSHA 58

RESULT 5
O52307 PRELIMINARY; PRT; 707 AA.
AC O52307;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE XYLANASE.
OS Prevotella ruminicola (Bacteroides ruminicola).
OC Bacteria; Cytophagales; Bacteroidaceae; Prevotella.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D31D;
RA WHITEHEAD T.R.;
RT "Cloning and comparison of xylanase genes from ruminal and colonic
RT Bacteroides species.";
RL Curr. Microbiol. 23:15-19(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=D31D;
RX MEDLINE; 97201063.
RA FLINT H.J., WHITEHEAD T.R., MARTIN J.C., GASPARIC A.;
RT "Interrupted catalytic domain structures in xylanases from two
RT distantly related strains of Prevotella ruminicola.";
RL Biochim. Biophys. Acta 1337:161-165(1997).
DR EMBL; U53926; AAB81559.1; -.
DR HSSP; P56588; 1B3V.
DR PFAM; PF00331; GLHYDRLASE10.
DR PRINTS; PR00134; GLHYDRLASE.
KW Xylan degradation; Hydrolase; Glycosidase.
SQ SEQUENCE 707 AA; 78252 MW; B998FDD7 CRC32;

Query Match 69.6%; Score 39; DB 2; Length 707;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY      2 RHNYGSPAD 10
Db      694 KHTYGGFAD 702

RESULT 6
O19495 PRELIMINARY; PRT; 89 AA.
AC O19495;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS II BETA 1 DOMAIN (FRAGMENT).
GN B-LBI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=15.151-5; TISSUE=BURSA;
RA PHARR G.T., DODGSON J.B., HUNT H.D., BACON L.D.;
RL Immunogenetics 47:350-354(1998).
DR EMBL; U91532; AAC15813.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 89 89
SQ SEQUENCE 89 AA; 10724 MW; FDAC6024 CRC32;

Query Match 67.9%; Score 38; DB 7; Length 89;
Best Local Similarity 85.7%; Pred. No. 2.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 RHNYGSF 8
Db      75 RHNYGDF 81

RESULT 7
O53747 PRELIMINARY; PRT; 464 AA.
AC O53747;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE PUTATIVE DIHYDROLIPOAMIDE DEHYDROGENASE.
GN MPO38.06.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RA BROWN D., CHURCHER C.M.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RA COLE S.T., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=H37RV;
RX MEDLINE; 96181548.
RA PHILIPP W.J., POULET S., EIGLMETER K., PASCOPELLA L.,
RA BALASUBRAMANIAN V., HEYM B., BERGH S., BLOOM B.R., JACOBS W.R. JR.,
RA COLE S.T.;
RT "An integrated map of the genome of the tubercle bacillus,
RT Mycobacterium tuberculosis H37Rv, and comparison with Mycobacterium
RT leprae."
RL Proc. Natl. Acad. Sci. U.S.A. 93:3132-3137(1996).
CC -1- COFACTOR: FAD FLAVOPROTEIN (BY SIMILARITY).

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CC      -1- SIMILARITY: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULPHIDE
CC      OXIDOREDUCTASES CLASS-I.
DR      EMBL; AL021933; CAA17417.1; -.
DR      HSSP; P11959; 1EBD.
DR      PROSITE; PS00076; PYRIDINE_REDOX_1; 1.
DR      PFAM; PF00070; pyr_redox; 1.
DR      PRINTS; PR00368; FADPNR.
DR      PRINTS; PR00411; PNRDRTASEI.
KW      Redox-active center; Oxidoreductase; Flavoprotein; FAD.
SQ      SEQUENCE 464 AA; 49239 MW; 6FF92403 CRC32;

Query Match 67.9%; Score 38; DB 2; Length 464;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 HNYGSPAD 10
Db      110 HGYGTFFAD 117

RESULT 8
Q43476 PRELIMINARY; PRT; 275 AA.
AC Q43476;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE MAMMALIAN ACYL COA OXIDASE HOMOLOGOUS (FRAGMENT).
GN CDR29.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eubryophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
OC Poaceae; Hordeum.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ARDA; TISSUE=GREEN LEAF;
RA GROSSI M., GULLI M., STANCA A.M., CATTIVELLI L.;
RL Plant Sci. 105:71-80(1995).
DR EMBL; X84055; CAA58874.1; -.
DR MENDEL; 12863; Horvu; 2063; 12863.
FT NON_TER 1 1
SQ SEQUENCE 275 AA; 30689 MW; 803E811E CRC32;

Query Match 66.1%; Score 37; DB 10; Length 275;
Best Local Similarity 70.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      1 ARHNYGSPAD 10
Db      1 ANHNSGSFELD 10

RESULT 9
P79474 PRELIMINARY; PRT; 39 AA.
AC P79474;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae; Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.
RA SWARBRICK P.A., CRAWFORD A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63077; AAB37777.1; -.
KW MHC.
FT NON_TER 1 1

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FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4767 MW; E01AA287 CRC32;

Query Match
Best Local Similarity 64.3%; Score 36; DB 7; Length 39;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 10
P79477
ID P79477 PRELIMINARY; PRT; 39 AA.
AC P79477;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
OC Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.
RA SWARBRICK P.A., CRAWFORD A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63080; AAB37780.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match
Best Local Similarity 64.3%; Score 36; DB 7; Length 39;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 11
P79478
ID P79478 PRELIMINARY; PRT; 39 AA.
AC P79478;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
OC Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.
RA SWARBRICK P.A., CRAWFORD A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63081; AAB37781.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match
Best Local Similarity 64.3%; Score 36; DB 7; Length 39;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 12
P79479
ID P79479 PRELIMINARY; PRT; 39 AA.
AC P79479;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
OC Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.
RA SWARBRICK P.A., CRAWFORD A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63082; AAB37782.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match
Best Local Similarity 64.3%; Score 36; DB 7; Length 39;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 13
O97835
ID O97835 PRELIMINARY; PRT; 78 AA.
AC O97835;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLA-DRB1*N20.2.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae; Bovidae;
OC Caprinae; Ovis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=7407; TISSUE=BLOOD;
RA AIDA Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017207; BAA36764.1; -.
FT NON_TER 1 1
FT NON_TER 78 78
SQ SEQUENCE 78 AA; 9677 MW; D2252D9D CRC32;

Query Match
Best Local Similarity 64.3%; Score 36; DB 6; Length 78;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
Db 72 RHNYGVF 78

RESULT 14
O97839
ID O97839 PRELIMINARY; PRT; 78 AA.

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AC O97839;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLA-DRB1*N2.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
OC Caprinae; Ovis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SUFFOLK BREED AND CORRIDALE BREED; TISSUE=BLOOD;
RA AIDA Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017212; BAA36769.1; -.
FT NON_TER 1
FT NON_TER 78
SQ SEQUENCE 78 AA; 9430 MW; 2883C99C CRC32;

Query Match 64.3%; Score 36; DB 6; Length 78;
Best Local Similarity 85.7%; Pred. No. 5.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 72 RHNYGVF 78

RESULT 15
OS7844
ID O97844 PRELIMINARY; PRT; 78 AA.
AC O97844;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TReMBLrel. 10, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLA-DRB1*N8.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
OC Caprinae; Ovis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-SUFFOLK BREED; TISSUE=BLOOD;
RA AIDA Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017220; BAA36777.1; -.
FT NON_TER 1
FT NON_TER 78
SQ SEQUENCE 78 AA; 9645 MW; 0A246905 CRC32;

Query Match 64.3%; Score 36; DB 6; Length 78;
Best Local Similarity 85.7%; Pred. No. 5.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 72 RHNYGVF 78

Search completed: May 27, 2000, 19:38:41
Job time: 2374 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:21:36 ; Search time 148.45 Seconds
(without alignments)
1.596 Million cell updates/sec

Title: US-09-016-061-72
Perfect score: 56
Sequence: 1 ARHNYGSPAD 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues
Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	56	100.0	10	W76026	LM609 grafted anti
2	52	92.9	10	W76027	LM609 grafted anti
3	50	89.3	10	W76024	LM609 grafted anti
4	50	89.3	10	W76025	LM609 grafted anti
5	50	89.3	10	W76028	LM609 grafted anti
6	50	89.3	10	W76029	LM609 grafted anti
7	50	89.3	10	W76030	LM609 grafted anti
8	50	89.3	10	W76010	LM609 grafted anti
9	50	89.3	117	W76001	Vitaxin antibody h
10	50	89.3	117	W76003	LM609 antibody hea
11	47	83.9	10	W76021	LM609 grafted anti
12	46	82.1	10	W76039	LM609 grafted anti
13	46	82.1	10	W76040	LM609 grafted anti
14	46	82.1	10	W76022	LM609 grafted anti
15	46	82.1	10	W76023	LM609 grafted anti
16	45	80.4	10	W76037	LM609 grafted anti
17	45	80.4	10	W76020	LM609 grafted anti
18	42	75.0	110	W84099	Vitronectin alpha-
19	42	75.0	117	W84093	Murine vitronectin
20	42	75.0	117	W84097	Humanised anti-alp
21	41	73.2	10	W76038	LM609 grafted anti
22	38	67.9	464	W72907	Mycobacterium tube
23	36	64.3	117	R79157	Human Ige receptor
24	36	64.3	117	R79155	Human Ige receptor
25	36	64.3	117	W27357	Heavy chain variab
26	36	64.3	117	W27526	Heavy chain variab
27	36	64.3	117	W27354	Heavy chain variab
28	36	64.3	119	W01578	Lead binding MAb 8
29	36	64.3	239	W73874	Human antiFc epsil
30	36	64.3	242	W73876	Human antiFc epsil
31	34	60.7	33	W45312	Glucagon-like pept
32	34	60.7	165	W38713	S. pneumoniae glut
33	34	60.7	407	W98453	H. pylori GHPO 639
34	34	60.7	408	W19760	Pyruvate:ferredoxi

ALIGNMENTS

RESULT 1

W76026
ID W76026 standard; Protein; 10 AA.
AC W76026;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #8.
KW Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB: V49863.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation, toid
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 100.0%; Score 56; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00052;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSPAD 10
| | | | | | | | | |
Db 1 ARHNYGSPAD 10

RESULT 2

W76027
ID W76027 standard; Protein; 10 AA.
AC W76027;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #9.
KW Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 PT N-PSDB; V49864.
 DT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 92.9%; Score 52; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0025;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSPAD 10
 | | | | | | | | | |
 Db 1 ARHNYGSFAE 10

RESULT 3
 W76024
 ID W76024 standard; Protein; 10 AA.

AC W76024;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #6.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 PT N-PSDB; V49861.
 DT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 89.3%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0055;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 | | | | | | | | | |
 Db 1 ARHNYGSFA 9

RESULT 4
 W76025
 ID W76025 standard; Protein; 10 AA.

AC W76025;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #7.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 PT N-PSDB; V49862.
 DT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 89.3%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0055;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 | | | | | | | | | |
 Db 1 ARHNYGSFA 9

RESULT 5
 W76028
 ID W76028 standard; Protein; 10 AA.


```

AC W76028;
-DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #10.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB; V49865.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 89.3%; Score 50; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
| | | | |
DB 1 ARHNYGSFA 9

RESULT 7
W76030
ID W76030 standard; Protein; 10 AA.
AC W76030;
DE 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #12.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB; V49867.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 89.3%; Score 50; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
| | | | |
DB 1 ARHNYGSFA 9

RESULT 6
W76029
ID W76029 standard; Protein; 10 AA.
AC W76029;
DE 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #11.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB; V49866.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.

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RESULT 8
W76010
ID W76010 standard; Protein; 10 AA.
AC W76010:
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #1.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementary determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1997; US-791391.
PR (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB; V49847.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Disclosure: Page 40; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
CC inhibit binding of alphaVbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
CC Sequence 10 AA;

Query Match 89.3%; Score 50; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9
|||||||

RESULT 9
W76001
ID W76001 standard; Protein; 117 AA.
AC W76001:
DT 02-NOV-1998 (first entry)
DE Vitaxin antibody heavy chain variable region protein fragment.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1997; US-791391.
PR (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB; V49820.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 43; Fig 2a; 129pp; English.
CC This sequence represents the LM609 antibody variable heavy chain region.
CC LM609 and the antibody vitaxin bind selectively to integrin alphaVbeta3
CC and can be used to inhibit binding of alphaVbeta3 to a ligand and thus
CC block integrin-mediated signal transduction. This is useful in the
CC treatment, prevention and diagnosis of alphaVbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
CC Sequence 117 AA;

Query Match 89.3%; Score 50; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 97 ARHNYGSFA 105
|||||||

PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 1; Fig 1a; 129pp; English.
CC This sequence represents a fragment of the vitaxin antibody variable
CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
CC integrin alphaVbeta3 and can be used to inhibit binding of alphaVbeta3
CC to a ligand and thus block integrin-mediated signal transduction. This is
CC useful in the treatment, prevention and diagnosis of alphaVbeta3-mediated
CC disease, specifically angiogenesis and restenosis (but also e.g.
CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
CC osteoporosis etc.). The antibodies contain non-murine framework regions
CC so are suitable for use in humans. Enhanced types of LM609 have affinity
CC more than 90 times greater than that of parent the parent antibody.
CC Sequence 117 AA;

Query Match 89.3%; Score 50; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 97 ARHNYGSFA 105
|||||||

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```

RESULT 11
W76021
ID W76021 standard; Protein; 10 AA.
AC W76021;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #3.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49858.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC LM609 heavy and light chain fragments of the grafted monoclonal antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 82.1%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSF 8
Db 1 ARHNYGSF 8
|||||||

RESULT 13
W76040
ID W76040 standard; Protein; 10 AA.
AC W76040;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #16.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49877.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 43; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 83.9%; Score 47; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.018;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSYA 9
|||||||

RESULT 12
W76039
ID W76039 standard; Protein; 10 AA.
AC W76039;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #15.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49876.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

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Query Match 82.1%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 82.1%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ARHNYGSF 8
 Db 1 ARHNYGSF 8

RESULT 14

W76022
 ID W76022 standard; Protein; 10 AA.
 AC W76022;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #4.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DT N-PSDB: V49859.
 PR Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related nucleic acid, used to treat, prevent or diagnose
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 82.1%; Score 46; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.027;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
 Db 1 ARHNYGSF 8

RESULT 15

W76023
 ID W76023 standard; Protein; 10 AA.
 AC W76023;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #5.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DT N-PSDB: V49860.
 PR Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related nucleic acid, used to treat, prevent or diagnose
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 82.1%; Score 46; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.027;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
 Db 1 ARHNYGSF 8

Search completed: May 27, 2000, 19:21:37
 Job time: 1591 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2000, 19:26:45 ; Search time 163.56 Seconds
(without alignments)
3.585 Million cell updates/sec

Title: US-09-016-061-74
Perfect score: 55
Sequence: 1 ARHNYGSFAE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_63:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	70.9	446	2 T19625	hypothetical prote
2	38	69.1	275	2 D71087	probable translati
3	38	69.1	275	2 G75130	translation initia
4	37	67.3	347	2 S43771	phosphatidylcholin
5	36	65.5	82	2 I51106	Major Histocompati
6	36	65.5	89	2 S38688	MHC class II histo
7	36	65.5	89	2 S38683	MHC class II histo
8	36	65.5	89	2 S38684	MHC class II histo
9	36	65.5	210	1 B69265	conserved hypothet
10	36	65.5	225	2 I47095	MHC class II OVAR-
11	36	65.5	326	2 S47248	site-specific DNA-
12	35	63.6	287	1 PWBX	inorganic pyrophos
13	35	63.6	287	1 PWBKL	inorganic pyrophos
14	34	61.8	108	2 S26316	Ig heavy chain V r
15	34	61.8	110	2 S26317	Ig heavy chain V r
16	34	61.8	189	2 D75026	hypothetical prote
17	34	61.8	192	2 D71211	hypothetical prote
18	34	61.8	364	2 C64326	succinyl-CoA synth
19	34	61.8	464	2 B70828	hypothetical prote
20	34	61.8	484	2 G72395	alpha-L-arabinofur
21	33	60.0	80	2 I54469	MHC HLA-DR-beta-1
22	33	60.0	80	2 I68777	MHC HLA-DR beta-1
23	33	60.0	81	2 I54550	HLA DRB1*1202 - hu
24	33	60.0	85	2 I59634	MHC class II DR-be
25	33	60.0	89	2 S38676	MHC class II histo
26	33	60.0	89	2 S38680	MHC class II histo
27	33	60.0	89	2 S57512	MHC class II histo
28	33	60.0	123	2 C25239	MHC class II histo
29	33	60.0	127	2 G70105	conserved hypothet
30	33	60.0	167	2 T16454	hypothetical prote

31	33	60.0	200	2 D32526	class II histocomp
32	33	60.0	237	2 C27060	class II histocomp
33	33	60.0	266	2 I54287	gene HLA-DRB1 prot
34	33	60.0	266	2 A27618	class II histocomp
35	33	60.0	266	2 I54295	lymphocyte antigen
36	33	60.0	275	2 T04480	acyl-CoA oxidase h
37	33	60.0	279	2 T05421	hypothetical prote
38	33	60.0	302	2 T26540	hypothetical prote
39	33	60.0	383	2 S56179	secreted glycoprot
40	33	60.0	395	2 G75587	hypothetical prote
41	33	60.0	448	1 A60003	nucleocapsid prote
42	33	60.0	470	2 H71667	glutamate--trna li
43	33	60.0	473	2 D70405	glutamate--trna li
44	33	60.0	682	2 S30995	gene 50 protein -
45	33	60.0	688	2 T33708	hypothetical prote

ALIGNMENTS

RESULT 1

T19625

hypothetical protein C31H5.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T19625

R:Kershaw, J.

submitted to the EMBL Data Library, April 1997

A:Reference number: Z19153

A:Accession: T19625

A>Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-446 <WILL>

A:Cross-references: EMBL:293778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6

A:Experimental source: clone C31H5

C:Genetics:

A:Gene: CESP:C31H5.6

A:Map position: 1

A:Introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3

Query Match 70.9%; Score 39; DB 2; Length 446;
Best Local Similarity 87.5%; Pred No. 7;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSFA 9
| | | | |
Db 51 RHNYGSHA 58

RESULT 2

D71087

probable translation initiation factor eIF-2 alpha chain - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 26-Aug-1999

C:Accession: D71087

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hainaka, Y.; Hino, Y.; Yamamoto, S.; Se

M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu

DNA Res. 5, 55-76, 1998

A>Title: Complete sequence and gene organization of the genome of a hyper-thermophilic

A:Reference number: AY1000; MUID:98344137

A:Accession: D71087

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-275 <KAW>

A:Cross-references: GB:AF000004; NID:92326131; PIDN:BAA30058.1; PID:dl031001; PID:g32

A:Experimental source: strain OF3

A>Note: this accession replaces an interim accession for a sequence replaced by GenBa

C:Genetics:

A:Gene: PH0961

C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 69.1%; Score 38; DB 2; Length 275;
 Best Local Similarity 75.0%; Pred. No. 6.7;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAE 10
 Db 23 HNYGAFLE 30
 |||||
 |||||

RESULT 3
 G751130
 translation initiation factor aif-2, subunit alpha (aif2a) PAB0568 - Pyrococcus abyssi
 C:Species: Pyrococcus abyssi
 C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 24-Nov-1999
 C:Accession: G75130
 R:anonymous, Genoscope
 submitted to the EMBL Data Library, July 1999
 A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
 A:Reference number: A75001
 A:Accession: G75130
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-275 <KAN>
 A:Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49760.1; PID:e151569
 A:Experimental source: strain Orsay
 C:Genetics:
 A:Gene: aif2A; PAB0568
 C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 69.1%; Score 38; DB 2; Length 275;
 Best Local Similarity 75.0%; Pred. No. 6.7;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAE 10
 Db 23 HNYGAFLE 30
 |||||
 |||||

RESULT 4
 S43771
 phosphatidylcholine desaturase (EC 1.3.1.35) - Synecococcus sp. (strain PCC 7002)
 N:Alternate names: Delta-12 desaturase; fatty acid desaturase (EC 1.14.99.-) (misidentified)
 C:Species: Synecococcus sp.
 A:Variety: PCC 7002
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 28-May-1999
 C:Accession: S43771
 R:Sakamoto, T.; Wada, H.; Nishida, I.; Ohmori, M.; Murata, N.
 Plant Mol. Biol. 24, 643-650, 1994
 A:Title: Identification of conserved domains in the Delta-12 desaturases of cyanobacteria
 A:Reference number: S43770; MUID:94207189
 A:Accession: S43771
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-347 <SAK>
 A:Cross-references: GB:D13779; NID:g488510; PIDN:BA02922.1; PID:d1003428; PID:g488511
 C:Superfamily: omega-3 fatty acid desaturase
 C:Keywords: oxidoreductase

Query Match 67.3%; Score 37; DB 2; Length 347;
 Best Local Similarity 70.0%; Pred. No. 13;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFAE 10
 Db 334 ARHNYISFAQ 343
 |||||
 |||||

RESULT 5
 151106
 Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)
 C:Species: Phasianus colchicus (ring-necked pheasant)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
 C:Accession: I51106
 R:Witzell, H.; von Schantz, T.; Zorrob, R.; Auffray, C.
 Immunogenetics 39, 395-403, 1994
 A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-necked pheasant
 A:Reference number: I51103; MUID:94245280
 A:Accession: I51106
 A:Status: preliminary; translated from GB/EMBL/DBDJ
 A:Molecule type: DNA
 A:Residues: 1-82 <WIT>
 A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 82;
 Best Local Similarity 85.7%; Pred. No. 4.8;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 Db 75 RHNYGVF 81
 |||||
 |||||

RESULT 6
 S38688
 MHC class II histocompatibility antigen HLA-DR-08 beta chain - Galago senegalensis (f
 C:Species: Galago senegalensis
 C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997
 C:Accession: S38688
 R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
 submitted to the EMBL Data Library, November 1993
 A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduce
 A:Reference number: S38676
 A:Accession: S38688
 A:Molecule type: DNA
 A:Residues: 1-89 <FIG>
 A:Cross-references: EMBL:Z27158
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 89;
 Best Local Similarity 85.7%; Pred. No. 5.2;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 Db 75 RHNYGVF 81
 |||||
 |||||

RESULT 7
 S38683
 MHC class II histocompatibility antigen HLA-DR-03 beta chain - Galago senegalensis (f
 C:Species: Galago senegalensis
 C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997
 C:Accession: S38683
 R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
 submitted to the EMBL Data Library, November 1993
 A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduce
 A:Reference number: S38676
 A:Accession: S38683
 A:Molecule type: DNA
 A:Residues: 1-89 <FIG>
 A:Cross-references: EMBL:Z27153
 C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 89;
 Best Local Similarity 85.7%; Pred. No. 5.2;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 Db 75 RHNYGVF 81
 |||||
 |||||

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RESULT 8
S38684
MHC class II histocompatibility antigen HLA-DR-04 beta chain - Galago senegalensis (frag
C;Species: Galago senegalensis
C;Date: 23-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997
C;Accession: S38684
R;Figueras, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A;Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced f
A;Reference number: S38676
A;Accession: S38684
A;Molecule type: DNA
A;Residues: 1-89 <FIG>
A;Cross-references: EMBL:Z27154
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 5.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 75 RHNYGVF 81

RESULT 9
B69265
conserved hypothetical protein AF0122 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: B69265
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343
A;Accession: B69265
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-210 <KLE>
A;Cross-references: GB:AE001098; GB:AE000782; NID:Q2689421; PID:g2650532; TIGR:AF0122
C;Superfamily: conserved hypothetical protein AF0119

Query Match 65.5%; Score 36; DB 1; Length 210;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAE 10
|||||
Db 128 RHAYGSEVD 136

RESULT 10
I47095
MHC class II OVAR-DR-beta-3 - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 23-Jul-1999
C;Accession: I47095
R;Fabb, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.
AnIm. Genet. 24, 249-255, 1993
A;Title: Isolation, characterization and evolution of ovine major histocompatibility com
A;Reference number: I47075; MUID:94057592
A;Accession: I47095
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-225 <FAB>
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A;Cross-references: GB:L04790; NID:g458880; PIDN:AAAL6562.1; PID:g458881
C;Genetics:
A;Gene: OVAR-DRB3
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 225;
Best Local Similarity 85.7%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 68 RHNYGVF 74

RESULT 11
S47248
site-specific DNA-methyltransferase (cytosine-specific) (EC 2.1.1.73) phi3TII - phage
C;Species: phage phi-3T
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 08-Oct-1999
C;Accession: S47248; S50099
R;Noyer-Weidner, M.; Walter, J.; Terschueren, P.A.; Chai, S.; Trautner, T.A.
submitted to the EMBL Data Library, August 1994
A;Description: M.phi3TII: a new monospecific C5-DNA-methyltransferase with pronounced
A;Reference number: S47248
A;Accession: S47248
A;Molecule type: DNA
A;Residues: 1-326 <NOY>
A;Cross-references: EMBL:X80202; NID:g535136; PIDN:CAA56493.1; PID:g535137
R;Noyer-Weidner, M.; Walter, J.; Terschueren, P.A.; Chai, S.; Trautner, T.A.
Nucleic Acids Res. 22, 4066-4072, 1994
A;Title: M.phi3TII: a new monospecific DNA (cytosine-C5) methyltransferase with pron
A;Reference number: S50099; MUID:95023172
A;Accession: S50099
A;Molecule type: DNA
A;Residues: 1-90,120-130,177-237 <NOW>
A;Cross-references: EMBL:X80202
C;Genetics:
A;Gene: M.phi3TII
C;Superfamily: site-specific methyltransferase (cytosine-specific) EcoRII
C;Keywords: methyltransferase

Query Match 65.5%; Score 36; DB 2; Length 326;
Best Local Similarity 55.6%; Pred. No. 19;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAE 10
|||||
Db 52 RHNFGDYE 60

RESULT 12
PWB9
inorganic pyrophosphatase (EC 3.6.1.1) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein YBR011c; protein YBR0202; pyrophosphate phosphohydrolase
C;Species: Saccharomyces cerevisiae
C;Date: 30-Nov-1980 #sequence_revision 09-Sep-1994 #text_change 05-Nov-1999
C;Accession: S45864; S07679; A01014; S29189
R;Entian, K.D.; Koetter, P.; Rose, M.; Li, Z.; Thermann, R.; Brendel, M.; Baur, A.; B
submitted to the Protein Sequence Database, August 1994
A;Reference number: S45862
A;Accession: S45864
A;Molecule type: DNA
A;Residues: 1-287 <ENT>
A;Cross-references: EMBL:Z35880; NID:g536205; PIDN:CAA84949.1; PID:g536206; CSPDB:GMO
R;Experimental source: strain S288C
R;Kolakowski Jr., L.F.; Schloesser, M.; Cooperman, B.S.
Nucleic Acids Res. 16, 10441-10452, 1988
A;Title: Cloning, molecular characterization and chromosome localization of the inorg
A;Reference number: S07679; MUID:89083474
A;Accession: S07679
A;Molecule type: DNA
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A;Residues: 1-266,'L',268-287 <KOL>
A;Cross-references: EMBL:X13253; NID:g4198; PIDN:CAA31629.1; PID:g4199
R;Cohen, S.A.; Sterner, R.; Keim, P.S.; Heinrikson, R.L.
J. Biol. Chem. 253, 889-897, 1978
A;Title: Covalent structural analysis of yeast inorganic pyrophosphatase.
A;Reference number: A92241; MUID:78087552
A;Accession: A01014
A;Molecule type: protein
A;Residues: 2-40,'D',42-71,'N',73,75-117,'N',119-123,'Q',125-136,'E',138-186,'D',188-224
A;Note: this is the final paper in a series
A;Note: no disulfide bonds are present
R;Razinkov, A.V.; Sklyankina, V.A.; Aveeva, S.M.
FEBS Lett. 308, 62-64, 1992
A;Title: Tyrosine-89 is important for enzymatic activity of *S. cerevisiae* inorganic pyrophosphatase
A;Reference number: S29189; MUID:92354770
A;Accession: S29189
A;Molecule type: protein
A;Residues: 83-105,'E',107-112 <RAZ>
R;Bond, M.W.; Chiu, N.Y.; Cooperman, B.S.
Biochemistry 19, 94-102, 1980
A;Title: Identification of an arginine important for enzymatic activity within the covalent binding site of inorganic pyrophosphatase
A;Reference number: A90443
A;Contents: annotation; active site
C;Genetics:
A;Gene: SGD:IPP1; PPA; MIPS:YBR011c
A;Cross-references: SGD:S0000215; MIPS:YBR011c
A;Map position: 2R
C;Function:
A;Description: catalyzes hydrolysis of pyrophosphate to orthophosphate
A;Note: requires divalent metal cation
C;Superfamily: inorganic pyrophosphatase
C;Keywords: homodimer; hydrolase
F:2-287/Product: inorganic pyrophosphate #status experimental <MAT>
F:79/Binding site: pyrophosphate (Arg) #status experimental

Query Match 63.6%; Score 35; DB 1; Length 287;
Best Local Similarity 62.5%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAE 10
|||||:
Db 92 HNYGAPQ 99

RESULT 13
PMVKL
Inorganic pyrophosphatase (EC 3.6.1.1) - yeast (*Kluyveromyces marxianus* var. *lactis*)
C;Species: *Kluyveromyces marxianus* var. *lactis*, *Candida sphaerica*
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Jun-1999
C;Accession: S07894
R;Stark, M.J.R.; Milner, J.S.
Yeast 5, 35-50, 1989
A;Title: Cloning and analysis of the *Kluyveromyces lactis* TRP1 gene: a chromosomal locus
A;Reference number: S07892; MUID:89189093
A;Accession: S07894
A;Molecule type: DNA
A;Residues: 1-287 <STA>
A;Cross-references: EMBL:X14230; NID:g2900; PIDN:CAA32446.1; PID:g2903
C;Genetics:
A;Gene: IPP
C;Superfamily: inorganic pyrophosphatase
C;Keywords: hydrolase
F:79,151/Active site: Arg, Glu #status predicted

Query Match 63.6%; Score 35; DB 1; Length 287;
Best Local Similarity 62.5%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAE 10
|||||:
Db 92 HNYGAPQ 99

RESULT 14

S26316
Ig heavy chain V region - mouse
C;Species: *Mus musculus* (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S26316
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein
A;Reference number: S26309; MUID:91341421
A;Accession: S26316
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 <STA>
A;Cross-references: EMBL:X59190; NID:g52066; PIDN:CAA41900.1; PID:e36170; PID:g133403
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F:2-85/Domain: immunoglobulin homology <IMM>

Query Match 61.8%; Score 34; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|||||:
Db 84 ARGNYGNYA 92

RESULT 15

S26317
Ig heavy chain V region - mouse (fragment)
C;Species: *Mus musculus* (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 17-Apr-1998
C;Accession: S26317
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein
A;Reference number: S26317
A;Accession: S26317
A;Molecule type: mRNA
A;Residues: 1-110 <STA>
A;Cross-references: EMBL:X59186
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 61.8%; Score 34; DB 2; Length 110;
Best Local Similarity 66.7%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|||||:
Db 86 ARGNYGNYA 94

Search completed: May 27, 2000, 19:26:45
Job time: 1768 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 20:07:18 ; Search time 69.28 seconds
(without alignments)
4.396 Million cell updates/sec

Title: US-09-016-061-74
Perfect score: 55
Sequence: 1 ARHNYGSPAE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	69.1	275	1 IF2A_PYRHO	O58655 pyrococcus
2	35	63.6	284	1 IPYR_PICPA	O13505 pichia past
3	35	63.6	286	1 IPYR_KIULA	P13998 kluyveromyc
4	35	63.6	286	1 IPYR_YEAST	P00817 saccharomyc
5	34	61.8	364	1 SUCC_METJA	Q57663 methanococ
6	33	60.0	448	1 NCAP_CVHOC	P33469 human coron
7	33	60.0	470	1 SYE2_RICPR	Q9ZCT8 rickettsia
8	33	60.0	473	1 SYE_AQUAE	O67271 aquifex aeo
9	33	60.0	682	1 VG50_BPWL5	Q05262 mycobacteri
10	33	60.0	1267	1 VL3_REOVL	P17376 reovirus (t
11	33	60.0	1267	1 VL3_REOVL	P17376 reovirus (t
12	32	58.2	65	1 CCSA_OENBE	P31565 oenothera b
13	32	58.2	65	1 CCSA_PEA	P31172 pisum sativ
14	32	58.2	196	1 WBBJ_ECOLI	P37750 escherichia
15	32	58.2	198	1 HB2G_HUMAN	P01911 homo sapien
16	32	58.2	220	1 SDHB_BAGSU	O34635 bacillus su
17	32	58.2	262	1 VP2_BPCHP	P19193 bacterioph
18	32	58.2	266	1 HB2A_HUMAN	P01913 homo sapien
19	32	58.2	266	1 HB2B_HUMAN	P01912 homo sapien
20	32	58.2	266	1 HB2C_HUMAN	P01914 homo sapien
21	32	58.2	266	1 HB2D_CANFA	P18470 canis fami
22	32	58.2	266	1 HB2D_HUMAN	P13759 homo sapien
23	32	58.2	266	1 HB2E_HUMAN	P04229 homo sapien
24	32	58.2	266	1 HB2F_HUMAN	P13758 homo sapien
25	32	58.2	266	1 HB2H_HUMAN	P13760 homo sapien
26	32	58.2	266	1 HB2I_HUMAN	P20039 homo sapien
27	32	58.2	266	1 HB2J_HUMAN	P13761 homo sapien
28	32	58.2	310	1 APBA_AQUAE	O67619 aquifex aeo
29	32	58.2	313	1 CCSA_TOBAC	P12216 nicotiana t
30	32	58.2	321	1 CCSA_MAIZE	P46659 zea mays (m
31	32	58.2	321	1 CCSA_ORYSA	P12215 oryza sativ
32	32	58.2	328	1 CCSA_ARATH	P56770 arabidopsis
33	32	58.2	349	1 YJY9_YEAST	P41903 saccharomyc
34	32	58.2	480	1 VP5_BRD	P21230 broadhaven

```
RESULT 1
IF2A_PYRHO
ID IF2A_PYRHO STANDARD; PRT; 275 AA.
AC O58655;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
GN PH0961.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OT3;
RX MEDLINE: 98344137;
RA Kawarabayasi Y., Savada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
CC (BY SIMILARITY)
CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
CC CHAIN (BY SIMILARITY).
CC -----
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CC -----
DR EMBL; AP000004; BAA30056.1; -.
DR PFAM; PF00575; SI; 1.
DR KJW
KW Initiation factor; Protein biosynthesis.
SQ SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;

Query Match 69.1%; Score 38; DB 1; Length 275;
Best Local Similarity 75.0%; Pred. No. 2;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSPAE 10
Db 23 HNYGAFLE 30

RESULT 2
IPYR_PICPA STANDARD; PRT; 284 AA.
ID IPYR_PICPA
AC O13505;
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DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI.
 OS Pichia pastoris (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 RC Saccharomycetaceae; Pichia.
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NRRL Y-11430;
 RX MEDLINE; 99034033.
 RA Cosano I.C., Alvarez P., Molina M., Nombela C.;
 RT "Cloning and sequence analysis of the Pichia pastoris TRP1, IPPI and
 RT HIS3 genes.";
 RL Yeast 14:861-867(1998).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC
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 CC
 CC
 DR EMBL; AJ001000; CAA04453.1; -.
 DR HSP; P00817; 1WG1.
 DR PROSITE; PS00387; PPASE; 1.
 DR PFAM; PF00719; Pyrophosphatase; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 284 AA; 31937 MW; 3DAD2970D775D6 CRC64;

 Query Match 63.6%; Score 35; DB 1; Length 284;
 Best Local Similarity 62.5%; Pred. No. 8.2;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3 HNYGSFAE 10
 Db 91 HNYGAFFQ 98
 ||||| :
 RESULT 3
 IPYR_KLUJIA
 ID IPYR_KLUJIA STANDARD; PRT; 286 AA.
 AC P13998;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI OR IPP.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 RC Saccharomycetaceae; Kluyveromyces.
 [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89180993.
 RA Stark M.J.R., Milner J.S.;
 RT "Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a
 RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
 RT and -histone H3.";
 RL Yeast 5:35-50(1989).

[2]
 RN SIMILARITY TO E-COLI AND YEAST PPASES.
 RX MEDLINE; 90254161.
 RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RT "Conservation of functional residues between yeast and E. coli
 RT inorganic pyrophosphatases.";
 RL Biochim. Biophys. Acta 1038:338-345(1990).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC
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 CC
 CC
 DR EMBL; X14230; CAA32446.1; -.
 DR PIR; S07894; PWVKL.
 DR HSP; P00817; 1WG1.
 DR PROSITE; PS00387; PPASE; 1.
 DR PFAM; PF00719; Pyrophosphatase; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 286 AA; 32034 MW; 11647F4ABD916A2F CRC64;

 Query Match 63.6%; Score 35; DB 1; Length 286;
 Best Local Similarity 62.5%; Pred. No. 8.3;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3 HNYGSFAE 10
 Db 91 HNYGAFFQ 98
 ||||| :
 RESULT 4
 IPYR_YEAST
 ID IPYR_YEAST STANDARD; PRT; 286 AA.
 AC P00817;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI OR PPAL OR PPA OR YBR011C OR YBR0202.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomyces.
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=X2180;
 RX MEDLINE; 89083474.
 RA Kolakowski L.F. Jr., Schloesser M., Cooperman B.S.;
 RT "Cloning, molecular characterization and chromosome localization of
 RT the inorganic pyrophosphatase (PPA) gene from S. cerevisiae.";
 RL Nucleic Acids Res. 16:10441-10452(1988).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=S288C;
 RC Entian K.-D., Koetter P., Rose M., Li Z., Thermann R., Brendel M.,
 RA Baur A., Boles E., Miosga T., Schaaff-Gerstenschlaeger I.,
 RA Zimmermann F.K.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 [3]

RP SEQUENCE.
RX MEDLINE; 78087552.
RA Cohen S.A., Sterner R., Keim P.S., Heinrikson R.L.;
RT "Covalent structural analysis of yeast inorganic pyrophosphatase.";
RL J. Biol. Chem. 253:889-897(1978).
RN [4]
RP SEQUENCE OF 25-35 AND 239-251.
RC STRAIN=9288C;
RX MEDLINE; 95203288.
RA Garrels J.I., Fletcher B., Kobayashi R., Latter G.I., Schwender B.,
RV Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a Saccharomyces cerevisiae protein
database.";
RL Electrophoresis 15:1466-1486(1994).
RN [5]
RP SEQUENCE OF 239-249.
RC STRAIN=ATCC 38531 / Y41;
RX MEDLINE; 97089742.
RA Norbeck J., Blomberg A.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
Saccharomyces cerevisiae";
RL FEMS Microbiol. Lett. 137:1-8(1996).
RN [6]
RP ACTIVE SITE.
RX MEDLINE; 80109718.
RA Bond M.W., Chiu N.Y., Cooperman B.S.;
RT "Identification of an arginine important for enzymatic activity
within the covalent structure of yeast inorganic pyrophosphatase.";
RL Biochemistry 19:94-102(1980).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RA Arutiunian E.G., Terzian S.S., Voronova A.A., Kuranova I.P.,
RV Smirnova E.A., Vainstein B.K., Hohne W.E., Hansen G.;
RT "A-ray diffraction study of inorganic pyrophosphatase from baker's
yeast at the 3-A resolution.";
RL Dokl. Akad. Nauk SSSR 258:1481-1492(1981).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE; 97148342.
RA Heikinheimo P., Lehtonen J., Baykov A., Lahti R., Cooperman B.S.,
RV Goldman A.;
RT "The structural basis for pyrophosphatase catalysis.";
RL Structure 4:1491-1508(1996).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RA Swaminathan K., Cooperman B.S., Lahti R., Voet D.;
RT Submitted (DEC-1997) to the PDB data bank.
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF MUTANTS LYS-78 AND LYS-117.
RX MEDLINE; 99096888.
RA Tuominen V., Heikinheimo P., Kajander T., Torkkel T., Hyttia T.,
RV Kapyla J., Lahti R., Cooperman B.S., Goldman A.;
RT "The R78K and D117E active-site variants of Saccharomyces cerevisiae
soluble inorganic pyrophosphatase: structural studies and mechanistic
implications.";
RL J. Mol. Biol. 284:1565-1580(1998).
RN [11]
RP SIMILARITY TO E.COLI AND K.LACTIS PPASES.
RX MEDLINE; 90254161.
RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
RV Cooperman B.S.;
RT "Conservation of functional residues between yeast and E. coli
inorganic pyrophosphatases.";
RL Biochim. Biophys. Acta 1038:338-345(1990).
CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY. IT BINDS UP TO 4 DIVALENT
CC CATIONS PER SUBUNIT, WITH THREE REQUIRED FOR ACTIVITY.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC -----
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CC -----
CC EMBL; X13253; CAA31629.1; -;
DR EMBL; Z35880; CAA84949.1; -;
DR PIR; S45864; PNBV.
DR PDB; 1EYP; 15-OCT-91.
DR PDB; 1YPP; 07-DEC-96.
DR PDB; 1WGI; 19-NOV-97.
DR PDB; 1WJG; 19-NOV-97.
DR PDB; 1HJG; 08-APR-98.
DR PDB; 1HUK; 08-APR-98.
DR PDB; 117E; 23-DEC-98.
DR PDB; 8PRK; 23-DEC-98.
DR SWISS-2DPAGE; P00817; YEAST.
DR YEPD; 7305; -;
DR SGD; L0000872; IPP1.
DR PROSITE; PS00387; PPASE; 1.
DR PFAM; PF00719; Pyrophosphatase; 1.
KW Hydrolase; Magnesium; 3D-structure.
FT INIT_MET 0
FT ACT_SITE 56 56 PROBABLE.
FT BINDING 78 78 INORGANIC PYROPHOSPHATE.
FT CONFLICT 40 40 N -> D (IN REF. 3).
FT CONFLICT 71 71 D -> N (IN REF. 3).
FT CONFLICT 74 74 MISSING (IN REF. 3).
FT CONFLICT 123 123 E -> Q (IN REF. 3).
FT CONFLICT 136 136 Q -> E (IN REF. 3).
FT CONFLICT 186 186 N -> D (IN REF. 3).
FT CONFLICT 224 224 D -> N (IN REF. 3).
FT CONFLICT 266 266 L -> P (IN REF. 2).
FT STRAND 4 7
FT STRAND 16 20
FT STRAND 25 25
FT TURN 28 30
FT TURN 38 41
FT STRAND 45 45
FT STRAND 55 55
FT STRAND 79 79
FT TURN 97 98
FT TURN 111 112
FT STRAND 121 123
FT TURN 131 132
FT STRAND 135 135
FT STRAND 138 146
FT STRAND 151 158
FT TURN 160 161
FT TURN 165 167
FT HELIX 172 175
FT TURN 176 177
FT TURN 179 180
FT STRAND 182 197
FT STRAND 203 203
FT HELIX 205 207
FT STRAND 210 210
FT HELIX 212 230
FT TURN 231 231
FT TURN 245 246
FT TURN 248 249
FT TURN 251 252
FT TURN 255 260
FT TURN 274 275
SQ SEQUENCE 286 AA; 32184 MW; F29390260B60C8B2 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 286;
Best Local Similarity 62.5%; Pred. No. 8.3;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;


```
QY 1 ARHNGSF 8
DB 31 ARHNGKF 38

RESULT 8
SYE_AQUAE
ID SYE_AQUAE STANDARD; PRT; 473 AA.
AC O67271;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE)
DE (GLURS).
GN GLTX OR AQ.1221.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VF5;
RX MEDLINE; 98196666.
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aulay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus."
RL Nature 392:353-358(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) = AMP +
CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; AE000729; AAC07230.1; -.
DR PRINTS; PR00987; TRNASYNTHGLU.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
DR PFWA; PF00749; trna-synt_lc; 1.
KW Aminoacyl-trna synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
FT SIMILAR 242 246 "KMSKS" REGION.
FT BINDING 245 245 ATP (BY SIMILARITY).
SQ SEQUENCE 473 AA; 55121 MW; 5CB4D1590973E07A CRC64;

Query Match 60.0%; Score 33; DB 1; Length 473;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNGSF 8
DB 31 ARHNGKF 38

RESULT 9
VG50_BPML5
ID VG50_BPML5 STANDARD; PRT; 682 AA.
AC Q05262;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PUTATIVE ADENOSYLCOBALAMIN-DEPENDENT RIBONUCLEOTIDE REDUCTASE
DE (EC 1.17.4.2) (GP50).
GN 50.
OS Mycobacteriophage L5.

Query Match 60.0%; Score 33; DB 1; Length 473;
Best Local Similarity 75.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNGSF 8
DB 31 ARHNGKF 38
```

```
OC Viruses.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93211282.
RA Hatfull G.F., Sarkis G.J.;
RT "DNA sequence, structure and gene expression of mycobacteriophage L5:
RT a phage system for mycobacterial genetics.";
RL Mol. Microbiol. 7:395-405(1993).
CC -1- CATALYTIC ACTIVITY: 2'-DEOXYRIBONUCLEOSIDE TRIPHOSPHATE +
CC OXIDIZED THIOREDOXIN + H(2)O = RIBONUCLEOSIDE TRIPHOSPHATE +
CC REDUCED THIOREDOXIN.
CC -----
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CC -----
DR EMBL; Z18946; CAA79426.1; -.
DR PIR; S30995; S30995.
KW Oxidoreductase; DNA replication.
SQ SEQUENCE 682 AA; 76331 MW; 8D2A71B873BC04A8 CRC64;

Query Match 60.0%; Score 33; DB 1; Length 682;
Best Local Similarity 66.7%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNGSFA 9
DB 311 AKEGYGSPA 319

RESULT 10
VL3_REOVD
ID VL3_REOVD STANDARD; PRT; 1267 AA.
AC P17378;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE MINOR CORE PROTEIN LAMBDA 3.
GN L1.
OS Reovirus (type 3 / strain Dearing).
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89163254.
RA Wiener J.R., Joklik W.K.;
RT "The sequences of the reovirus serotype 1, 2, and 3 L1 genome
RT segments and analysis of the mode of divergence of the reovirus
RT serotypes."
RL Virology 169:194-203(1989).
CC -1- MISCELLANEOUS: IT IS UNLIKELY THAT CORES CONTAIN MORE THAN 12
CC MOLECULES OF PROTEIN LAMBDA 3.
CC -1- SIMILARITY: VERY HIGH WITH OTHER REOVIRUS TYPES.
CC -----
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CC -----
DR EMBL; M24734; AAA47234.1; -.
DR PIR; C30121; MWXR33.
KW Core protein.
SQ SEQUENCE 1267 AA; 142269 MW; FC9FD43CEF527148 CRC64;

Query Match 60.0%; Score 33; DB 1; Length 1267;
```

```

Best Local Similarity 55.6%; Pred. No. 1e+02; Mismatches 1; Indels 0; Gaps 0;
Matches 5; Conservative 3;

QY 2 RHNYGSFAE 10
Db 1043 RHYSSFSK 1051
||:| ||:|
-----
RESULT 11
VL3_REOVL STANDARD; PRT; 1267 AA.
AC P17376;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE MINOR CORE PROTEIN LAMBDA 3.
GN L1.
OS Reovirus (type 1 / strain Lang).
OC Viruses; dsRNA viruses; Reoviridae; Orthoreovirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89163254.
RA Wiener J.R., Joklik W.K.;
RT "The sequences of the reovirus serotype 1, 2, and 3 L1 genome
RT segments and analysis of the mode of divergence of the reovirus
RT serotypes."
RL Virology 169:194-203(1989).
CC -1- MISCELLANEOUS: IT IS UNLIKELY THAT CORES CONTAIN MORE THAN 12
CC MOLECULES OF PROTEIN LAMBDA 3.
CC -1- SIMILARITY: VERY HIGH WITH OTHER REOVIRUS TYPES.
DR PIR: A30121; MWXR31.
KW Core protein.
SQ SEQUENCE 1267 AA; 142354 MW; 157EBFDAD664FCDB CRC64;

Query Match 60.0%; Score 33; DB 1; Length 1267;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFAE 10
Db 1043 RHYSSFSK 1051
||:| ||:|
-----
RESULT 12
ID CCSA_OENBE STANDARD; PRT; 65 AA.
AC P31565;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA (FRAGMENT).
GN CCSA.
OS Oenothera bertiana (Bertero's evening primrose).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Myrtales; Onagraceae; Oenothera.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93169690.
RA Nimzyk R., Schoendorf T., Hachtel W.;
RT "In-frame length mutations associated with short tandem repeats are
RT located in unassigned open reading frames of Oenothera chloroplast
RT DNA."
RL Curr. Genet. 23:265-270(1993).
CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCCL/NRFE/CCSA FAMILY.
-----
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between the Swiss Institute of Bioinformatics and the EMBL outstation -
located in unassigned open reading frames of Oenothera chloroplast
DNA."

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-----
DR EMBL; X64617; CAA45900.1; -.
DR EMBL; X64614; CAA45894.1; -.
DR PIR; S19981; S19981.
DR PIR; S19988; S19988.
KW Cytochrome c-type biogenesis; Chloroplast.
FT NON_TER 1
SQ SEQUENCE 65 AA; 7441 MW; 343E66DDA1492C0C CRC64;

Query Match 58.2%; Score 32; DB 1; Length 65;
Best Local Similarity 83.3%; Pred. No. 6.8;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 57 HSYGSF 62
|:||||
-----
RESULT 13
ID CCSA_PEA STANDARD; PRT; 65 AA.
AC P31172;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA (FRAGMENT).
GN CCSA.
OS Pisum sativum (Garden pea).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
OC Pisum.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ALASKA;
RX MEDLINE: 91359590.
RA Nagano Y., Ishikawa H., Matsuno R., Sasaki Y.;
RT "Nucleotide sequence and expression of the ribosomal protein L2 gene
RT in pea chloroplasts."
RL Plant Mol. Biol. 17:541-545(1991).
CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCCL/NRFE/CCSA FAMILY.
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-----
DR EMBL; X59015; CAA41754.1; -.
DR PIR; S17441; S17441.
KW Cytochrome c-type biogenesis; Chloroplast.
FT NON_TER 1
SQ SEQUENCE 65 AA; 7396 MW; 9E523E0C70B102AA CRC64;

Query Match 58.2%; Score 32; DB 1; Length 65;
Best Local Similarity 83.3%; Pred. No. 6.8;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 57 HSYGSF 62
|:||||
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RESULT 14
WBBJ_ECOLI
AC WBBJ_ECOLI STANDARD; PRT; 196 AA.
ID P3750; P76375;
DT 01-OCT-1994 (Rel. 30, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE PUTATIVE LIPOPOLYSACCHARIDE BIOSYNTHESIS O-ACETYL TRANSFERASE WBBJ
  (EC 2.3.1.-).
GN WBBJ
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / W3110;
RX MEDLINE; 94292434.
RA Yao Z., Valvano M.A.;
RT "Genetic analysis of the O-specific lipopolysaccharide biosynthesis
RT region (rfb) of Escherichia coli K-12 W3110: identification of genes
RT that confer group 6 specificity to Shigella flexneri serotypes Y and
RT 4a";
RL J. Bacteriol. 176:4144-4156(1994).
RN [3]
RP REVISIONS TO 168-176 AND 187-189.
RC STRAIN-K12 / W3110;
RX Stevenson G.;
RA Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE; 97426617.
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glaesner F.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE; 97251358.
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sampei G., Seki Y., Sivasubraman S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [6]
RP FUNCTION: PUTATIVE O-ACETYLTRANSFERASE THAT TRANSFERS AN O-ACETYL
  ON THE O ANTIGEN.
CC -1- PATHWAY: LIPOPOLYSACCHARIDE BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NOBL FAMILY OF
CC ACETYLTTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
-----
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CC -----
CC EMBL; U03041; AAC31635.1; -.
DR EMBL; U09876; AAB88406.1; -.
DR EMBL; AE000294; AAC75094.1; -.
DR EMBL; D90841; CAB21803.1; -.
DR EMBL; D90842; CAB21811.1; -.
DR ECOGENE; EG11984; WBBJ.
DR PROSITE; PS00101; HEXAPEP_TRANSFERASES; FALSE_NEG.
DR PFAM; PF00132; hexapep; 1
KW Lipopolysaccharide biosynthesis; Transferase; Acyltransferase; Repeat.
FT CONFLICT 168 176 SIPENTVIA -> LFRKYCHC (IN REF. 1).
FT CONFLICT 187 189 NHE -> IMR (IN REF. 1).
SQ SEQUENCE 196 AA; 21675 MW; D1C2FA7D3B29A1B1 CRC64;

Query Match 58.2%; Score 32; DB 1; Length 196;
Best Local Similarity 83.3%; Pred. No. 22;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
Db 105 HHGGSF 110
|||||

RESULT 15
HB2G_HUMAN
ID HB2G_HUMAN STANDARD; PRT; 198 AA.
AC P01911;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JAN-1990 (Rel. 13, Last annotation update)
DE HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DW2.2/DR2.2 BETA CHAIN
  (FRAGMENT).
DE Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE; 82096757.
RA Kratzin H., Yang C.-Y., Gotz H., Pauly E., Kolbel S., Egert G.,
RA Thinnies F.P., Wernet P., Altevogt P., Hilschmann N.;
RT "Primary structure of class II human histocompatibility antigens. 1st
RT communication. Amino acid sequence of the N-terminal 198 residues of
RT the beta chain of a HLA-DW2,2/DR2,2-alloantigen.";
RL Hoppe-Seyler's Z. Physiol. Chem. 362:1665-1669(1981).
CC -1- MISCELLANEOUS: THE CHAIN SHOWN CONSTITUTED ABOUT 70% OF A POOL OF
  AT LEAST SEVEN SIMILAR BETA CHAINS.
DR PIR; A02220; HLHUB.
DR HSSP; P13758; IDUH.
DR PROSITE; PS00290; IG_MHC; 1.
DR PFAM; PF00047; Ig; 1.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC II; Transmembrane; Glycoprotein.
FT DOMAIN 1 94 EXTRACELLULAR BETA-1.
FT DOMAIN 95 187 EXTRACELLULAR BETA-2.
FT DOMAIN 188 197 CONNECTING PEPTIDE.
FT TRANSMEM 198 >198
FT DISULFID 15 79 BY SIMILARITY.
FT DISULFID 117 172 BY SIMILARITY.
FT CARBOHYD 19 19
FT NON_TER 198 198
SQ SEQUENCE 198 AA; 22965 MW; 18199D91A4D737EC CRC64;

Query Match 58.2%; Score 32; DB 1; Length 198;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNYG 6
Db 80 RHNYG 84
|||||

```

Search completed: May 27, 2000, 20:07:18
Job time: 990 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:38:41 ; Search time 199.56 Seconds
(without alignments)
3.474 Million cell updates/sec

Title: US-09-016-061-74
Perfect score: 55
Sequence: 1 ARHNYGSPAE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 segs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL12:**

- 1: sp_archaea:**
- 2: sp_bacteria:**
- 3: sp_fungi:**
- 4: sp_human:**
- 5: sp_invertebrate:**
- 6: sp_mammal:**
- 7: sp_mhc:**
- 8: sp_Organelle:**
- 9: sp_phase:**
- 10: sp_plant:**
- 11: sp_rodent:**
- 12: sp_virus:**
- 13: sp_vertebrate:**
- 14: sp_unclassified:**

Pred, No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	39	70.9	446	5	O62086
2	39	70.9	723	7	P72121
3	38	69.1	89	7	O19495
4	37	67.3	347	2	Q55231
5	36	65.5	39	7	P79474
6	36	65.5	39	7	P79477
7	36	65.5	39	7	P79478
8	36	65.5	39	7	P79479
9	36	65.5	78	6	O97835
10	36	65.5	78	6	O97839
11	36	65.5	78	6	O97844
12	36	65.5	78	6	O97968
13	36	65.5	79	7	O19191
14	36	65.5	79	7	O19192
15	36	65.5	79	7	O19380
16	36	65.5	79	7	O19381
17	36	65.5	79	7	O19382
18	36	65.5	79	7	O19396
19	36	65.5	79	7	O19397
20	36	65.5	79	7	O19405

21	36	65.5	79	7	O19406
22	36	65.5	79	7	O19407
23	36	65.5	79	7	O19408
24	36	65.5	79	7	O19435
25	36	65.5	81	7	O30568
26	36	65.5	81	7	O30571
27	36	65.5	81	7	O30737
28	36	65.5	81	7	O30739
29	36	65.5	81	7	O30563
30	36	65.5	81	7	O30740
31	36	65.5	82	7	O95598
32	36	65.5	82	7	O30606
33	36	65.5	82	7	O30608
34	36	65.5	82	7	O30637
35	36	65.5	82	7	O30638
36	36	65.5	82	7	O30658
37	36	65.5	82	7	O30659
38	36	65.5	82	7	O30666
39	36	65.5	82	7	O30667
40	36	65.5	82	7	O30668
41	36	65.5	82	7	O19287
42	36	65.5	82	7	O19288
43	36	65.5	83	7	O98002
44	36	65.5	83	7	O9XS06
45	36	65.5	83	7	O9XR24

ALIGNMENTS

RESULT 1

O62086
ID O62086 PRELIMINARY; PRT; 446 AA.
AC O62086;
DC 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)
DE C3IH5.6 PROTEIN.
GN C3IH5.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RA KERSHAW J.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RX MEDLINE: 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAYSTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
RL Nature 368:32-38(1994).
DR EMBL; 293778; CAB07846.1; -;
SQ SEQUENCE 446 AA; 50763 MW; B347C0C8 CRC32;

Query Match 70.9%; Score 39; DB 5; Length 446;
Best Local Similarity 87.5%; Pred. No. 8.6;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 RHNYGSFA 9

Db 51 RHNYGSHA 58

```

RESULT 2
P72121 ID P72121 PRELIMINARY; PRT; 723 AA.
AC P72121;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)
DE OUTER MEMBRANE PROTEIN C PRECURSOR.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
OC Pseudomonas.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PAOI;
RX MEDLINE; 96349120.
RA YONEYAMA H., NAKAE T.;
RT "Protein C (OprC) of the outer membrane of Pseudomonas aeruginosa is a
copper-regulated channel protein.";
RL Microbiology 142:2137-2144(1996).
DR EMBL; D28119; BAA05664.1; -.
DR PFAM; PF00593; TonB_boxC; 1.
KW Signal.
FT SIGNAL. 1 55 POTENTIAL.
FT CHAIN 56 723 MATURE PROTEIN C.
SQ SEQUENCE 723 AA; 79303 MW; AFD6C0D CRC32;

Query Match 70.9%; Score 39; DB 2; Length 723;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAE 10
DB 407 HNYGAFGE 414

RESULT 3
O19495 ID O19495 PRELIMINARY; PRT; 89 AA.
AC O19495;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE MHC CLASS II BETA 1 DOMAIN (FRAGMENT).
GN B-LBI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=15.151-5; TISSUE=BURSA;
RA PHARR G.T., DODGSON J.B., HUNT H.D., BACON L.D.;
RL Immunogenetics 47:350-354(1998).
DR EMBL; U91532; AAC15813.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 89 89
SQ SEQUENCE 89 AA; 10724 MW; FDAC6024 CRC32;

Query Match 69.1%; Score 38; DB 7; Length 89;
Best Local Similarity 85.7%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
DB 75 RHNYGDF 81

RESULT 4

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Q55231 ID Q55231 PRELIMINARY; PRT; 347 AA.
AC Q55231;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)
DE DELTA 12 DESATURASE.
GN DESA.
OS Synechococcus sp. (strain PCC 6301).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC7002;
RX MEDLINE; 94207189.
RA SAKAMOTO T., WADA H., NISHIDA I., OHMORI M., MURATA N.;
RT "Identification of conserved domains in the delta 12 desaturases of
cyanobacteria.";
RL Plant Mol. Biol. 24:643-650(1994).
DR EMBL; D13779; BAA02922.1; -.
DR PFAM; PF00487; FA_desaturase; 1.
SQ SEQUENCE 347 AA; 40655 MW; A8518F91 CRC32;

Query Match 67.3%; Score 37; DB 2; Length 347;
Best Local Similarity 70.0%; Pred. No. 16;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFAE 10
DB 334 AEHNYISFAQ 343

RESULT 5
P79474 ID P79474 PRELIMINARY; PRT; 39 AA.
AC P79474;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
OC Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.
RA SWARBRICK P.A., CRAWFORD A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63077; AAB37777.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4767 MW; E01AA287 CRC32;

Query Match 65.5%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
DB 25 RHNYGVF 31

RESULT 6
P79477 ID P79477 PRELIMINARY; PRT; 39 AA.
AC P79477;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
OC Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.
RA SWARRICK P.A., CRAWFORD A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63080; AAB37780.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match 65.5%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 7
P79478 PRELIMINARY; PRT; 39 AA.
ID AC P79478;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
OC Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.
RA SWARRICK P.A., CRAWFORD A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63081; AAB37781.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match 65.5%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 8
P79479 PRELIMINARY; PRT; 39 AA.
ID AC P79479;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
OC Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.
RA SWARRICK P.A., CRAWFORD A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63082; AAB37782.1; -.
KW MHC.

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FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match 65.5%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 9
O97835 PRELIMINARY; PRT; 78 AA.
ID AC O97835;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLA-DRB1*N20.2.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae; Bovidae;
OC Caprinae; Ovis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=7407; TISSUE=BLOOD;
RA AIDA Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017207; BAA36764.1; -.
FT NON_TER 1 1
FT NON_TER 78 78
SQ SEQUENCE 78 AA; 9677 MW; D2252D9D CRC32;

Query Match 65.5%; Score 36; DB 6; Length 78;
Best Local Similarity 85.7%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 2 RHNYGSF 8
Db 72 RHNYGVF 78

RESULT 10
O97839 PRELIMINARY; PRT; 78 AA.
ID AC O97839;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLA-DRB1*N2.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae; Bovidae;
OC Caprinae; Ovis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SUFFOLK BREED AND CORRIDAILE BREED; TISSUE=BLOOD;
RA AIDA Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017212; BAA36769.1; -.
FT NON_TER 1 1
FT NON_TER 78 78
SQ SEQUENCE 78 AA; 9430 MW; 2883C99C CRC32;

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Query Match 65.5%; Score 36; DB 6; Length 78;
 Best Local Similarity 85.7%; Pred. No. 5.1;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
 Db 72 RHNYGVF 78

RESULT 11
 O97844 PRELIMINARY; PRT; 78 AA.
 AC O97844;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
 GN OLA-DRB1*N8.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
 OC Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SUFFOLK BREED; TISSUE=BLOOD;
 RA AIDA Y.;
 RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017220; BAA36777.1; -.
 FT NON_TER 1 1
 FT NON_TER 78 78
 SQ SEQUENCE 78 AA; 9645 MW; 0A246905 CRC32;

Query Match 65.5%; Score 36; DB 6; Length 78;
 Best Local Similarity 85.7%; Pred. No. 5.1;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
 Db 72 RHNYGVF 78

RESULT 12
 O97968 PRELIMINARY; PRT; 78 AA.
 AC O97968;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
 GN OLA-DRB1*N21.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea; Bovidae;
 OC Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VARIOUS STRAINS;
 RA AIDA Y.;
 RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017231; BAA36788.1; -.
 DR EMBL; AB017204; BAA36761.1; -.
 FT NON_TER 1 1
 FT NON_TER 78 78
 SQ SEQUENCE 78 AA; 9436 MW; 72250CEB CRC32;

Query Match 65.5%; Score 36; DB 6; Length 78;
 Best Local Similarity 85.7%; Pred. No. 5.1;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
 Db 72 RHNYGVF 78

RESULT 13
 O19191 PRELIMINARY; PRT; 79 AA.
 AC O19191;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
 GN MHCMAIR-DRB.
 OS Prionailurus bengalensis iriomotensis (Iriomote cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Carnivora; Fissipedia; Felidae; Prionailurus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97211851.
 RA YUHKI N., O'BRIEN S.J.;
 RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB genes.";
 RL J. Immunol. 158:2822-2833(1997).
 DR EMBL; U51546; AAB65582.1; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 9582 MW; 8EEF2C7D CRC32;

Query Match 65.5%; Score 36; DB 7; Length 79;
 Best Local Similarity 85.7%; Pred. No. 5.1;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
 Db 72 RHNYGVF 78

RESULT 14
 O19192 PRELIMINARY; PRT; 79 AA.
 AC O19192;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
 GN MHCMAIR-DRB.
 OS Prionailurus bengalensis iriomotensis (Iriomote cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Carnivora; Fissipedia; Felidae; Prionailurus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97211851.
 RA YUHKI N., O'BRIEN S.J.;
 RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB genes.";
 RL J. Immunol. 158:2822-2833(1997).
 DR EMBL; U51547; AAB65583.1; -.
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 9582 MW; ED9F80F0 CRC32;

Query Match 65.5%; Score 36; DB 7; Length 79;
 Best Local Similarity 85.7%; Pred. No. 5.1;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

Db 72 RHNYGVF 78
|||||

RESULT 15
O19380
ID O19380 PRELIMINARY; PRT; 79 AA.
AC O19380;
DT 01-JAN-1998 (TReMBLrel. 05, Created)
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
GN MHCPECA-DRB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97211851.
RA YUHKI N., O'BRIEN S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
genes.";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51498; AAB65533.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 9659 MW; F352AD23 CRC32;

Query Match 65.5%; Score 36; DB 7; Length 79;
Best Local Similarity 85.7%; Pred. No. 5.1;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 72 RHNYGVF 78

Search completed: May 27, 2000, 19:38:42
Job time: 2375 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:21:37 ; Search time 148.45 Seconds
(without alignments)
1.596 Million cell updates/sec

Title: US-09-016-061-74
Perfect score: 55
Sequence: 1 ARHNYGSPAE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	55	100.0	10	1 W76027	LM609 grafted anti
2	52	94.5	10	1 W76026	LM609 grafted anti
3	50	90.9	10	1 W76024	LM609 grafted anti
4	50	90.9	10	1 W76025	LM609 grafted anti
5	50	90.9	10	1 W76028	LM609 grafted anti
6	50	90.9	10	1 W76029	LM609 grafted anti
7	50	90.9	10	1 W76030	LM609 grafted anti
8	50	90.9	10	1 W76010	LM609 grafted anti
9	50	90.9	117	1 W76001	Vitaxin antibody h
10	50	90.9	117	1 W76003	LM609 antibody hea
11	49	89.1	10	1 W76039	LM609 grafted anti
12	47	85.5	10	1 W76021	LM609 grafted anti
13	46	83.6	10	1 W76040	LM609 grafted anti
14	46	83.6	10	1 W76022	LM609 grafted anti
15	46	83.6	10	1 W76023	LM609 grafted anti
16	45	81.8	10	1 W76037	LM609 grafted anti
17	45	81.8	10	1 W76020	LM609 grafted anti
18	42	76.4	110	1 W84099	Vitronectin alpha-
19	42	76.4	117	1 W84093	Murine vitronectin
20	42	76.4	117	1 W84097	Humanised anti-alp
21	41	74.5	10	1 W76038	LM609 grafted anti
22	36	65.5	117	1 R79157	Human IGE receptor
23	36	65.5	117	1 R79155	Human IGE receptor
24	36	65.5	117	1 W27357	Heavy chain variab
25	36	65.5	117	1 W27526	Heavy chain variab
26	36	65.5	117	1 W27354	Heavy chain variab
27	36	65.5	119	1 W01578	Lead binding Mab 8
28	36	65.5	239	1 W73874	Human antiFc epsil
29	36	65.5	242	1 W73876	Human antiFc epsil
30	34	61.8	464	1 W72907	Mycobacterium tube
31	33	60.0	80	1 R13396	HLA-DRw12a antigen
32	33	60.0	80	1 R13397	HLA-DRw12b antigen
33	32	58.2	11	1 W22700	Peptide sequence #
34	32	58.2	15	1 W25799	Synthetic human S1

35 32 58.2 18 1 W27062 Chemically syntheses
36 32 58.2 25 1 R49334 DRI beta chain pos
37 32 58.2 25 1 W41656 Immunomodulatory p
38 32 58.2 36 1 W03964 VDJ joint protein,
39 32 58.2 36 1 W41127 VH251 DXP 1 J6 mu
40 32 58.2 78 1 W71230 Major histocompata
41 32 58.2 80 1 R21415 Human leukocyte an
42 32 58.2 84 1 P00034 Peptide of human/m
43 32 58.2 89 1 R24276 DRI. Method and k1
44 32 58.2 89 1 W00380 HLA-DRb1*08 and *1
45 32 58.2 93 1 W10491 Beta1 region of C1

ALIGNMENTS

RESULT 1

W76027
ID W76027 standard; Protein; 10 AA.
AC W76027;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #9.
KW Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PE 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49864.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
Integrin - and related grafted antibodies based on murine monoclonal
LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angio genesis or restenosis
PS Claim 62: Page 41: 129pp: English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
LM609 heavy and light chain variable region. LM609 and the antibody
vitaxin bind selectively to integrin alphavbeta3 and can be used to
inhibit binding of alphavbeta3 to a ligand and thus block
integrin-mediated signal transduction. This is useful in the treatment,
prevention and diagnosis of alphavbeta3-mediated disease, specifically
angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
arthritis, macular degeneration, osteoporosis etc.). The antibodies
contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00077;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ARHNYGSPAE 10
Db 1 ARHNYGSPAE 10
|||||

RESULT 2

W76026
ID W76026 standard; Protein; 10 AA.
AC W76026;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #8.
KW Vitaxin; antibody; variable region; heavy chain; Integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DT N-PSDB; V49863.
 PR Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 94.5%; Score 52; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0025;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAE 10
 | | | | | | | | | |
 Db 1 ARHNYGSFAD 10

RESULT 3
 W76024
 ID W76024 standard; Protein; 10 AA.

AC W76024;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #6.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DT N-PSDB; V49861.
 PR Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0055;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 | | | | | | | | | |
 Db 1 ARHNYGSFA 9

RESULT 4
 W76025
 ID W76025 standard; Protein; 10 AA.

AC W76025;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #7.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DT N-PSDB; V49862.
 PR Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0055;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 | | | | | | | | | |
 Db 1 ARHNYGSFA 9

RESULT 5
 W76028
 ID W76028 standard; Protein; 10 AA.

W76028;
 CC 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #10.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49865.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT Integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;
 Query Match 90.9%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0055;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFA 9
 Db ||||||||
 Db 1 ARHNYGSFA 9
 RESULT 6
 ID W76029 standard; Protein; 10 AA.
 AC W76029;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #11.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49866.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT Integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.

W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;
 Query Match 90.9%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0055;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFA 9
 Db ||||||||
 Db 1 ARHNYGSFA 9
 RESULT 7
 ID W76030 standard; Protein; 10 AA.
 AC W76030;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #12.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49867.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT Integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;
 Query Match 90.9%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0055;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFA 9
 Db ||||||||
 Db 1 ARHNYGSFA 9

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RESULT 8
ID W76010
AC W76010 standard; Protein; 10 AA.
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #1.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49847.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Disclosure: Page 40; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
CC Sequence 10 AA;
SQ

Query Match 90.9%; Score 50; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0055;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSEA 9
Db 1 ARHNYGSEA 9

RESULT 9
ID W76001
AC W76001 standard; Protein; 117 AA.
DT 02-NOV-1998 (first entry)
DE Vitaxin antibody heavy chain variable region protein fragment.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49820.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal

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PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 1; Fig 1a; 129pp; English.
CC This sequence represents a fragment of the vitaxin antibody variable
CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
CC to a ligand and thus block integrin-mediated signal transduction. This is
CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
CC disease, specifically angiogenesis and restenosis (but also e.g.
CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
CC osteoporosis etc.). The antibodies contain non-murine framework regions
CC so are suitable for use in humans. Enhanced types of LM609 have affinity
CC more than 90 times greater than that of parent the parent antibody.
CC Sequence 117 AA;
SQ

Query Match 90.9%; Score 50; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSEA 9
Db 97 ARHNYGSEA 105

RESULT 10
ID W76003
AC W76003 standard; Protein; 117 AA.
DT 02-NOV-1998 (first entry)
DE LM609 antibody heavy chain variable region protein fragment.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49822.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 43; Fig 2a; 129pp; English.
CC This sequence represents the LM609 antibody variable heavy chain region.
CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC block integrin-mediated signal transduction. This is useful in the
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
CC Sequence 117 AA;
SQ

Query Match 90.9%; Score 50; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSEA 9
Db 97 ARHNYGSEA 105

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RESULT 11
W76039
ID W76039 standard; Protein; 10 AA.
AC W76039;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #15.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49876.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62: Page 43; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 85.5%; Score 47; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.018;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 1 ARHNYGSVA 9
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RESULT 13
W76040
ID W76040 standard; Protein; 10 AA.
AC W76040;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #16.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49877.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62: Page 43; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 83.6%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAE 10
Db 1 ARHNYGSFYE 10
|||||||:|

RESULT 12
W76021
ID W76021 standard; Protein; 10 AA.
AC W76021;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #3.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49858.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

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QY 1 ARHNYGSF 8
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Db 1 ARHNYGSF 8

RESULT 14

W76022 ID W76022 standard; Protein; 10 AA.

AC W76022; 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #4.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49859.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 83.6%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
| | | | | | | |
Db 1 ARHNYGSF 8

RESULT 15

W76023 ID W76023 standard; Protein; 10 AA.

AC W76023; 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #5.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49860.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 83.6%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.026;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
| | | | | | | |
Db 1 ARHNYGSF 8

Search completed: May 27, 2000, 19:21:37
Job time: 1591 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:26:45 ; Search time 163.56 Seconds
(without alignments)
3.585 Million cell updates/sec

Title: US-09-016-061-76

Perfect score: 55

Sequence: 1 ARHNYGSFAM 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_63.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	70.9	446	2 T19625	hypothetical prote
2	36	65.5	82	2 I51106	Major Histocompat
3	36	65.5	89	2 S38688	MHC class II histo
4	36	65.5	89	2 S38683	MHC class II histo
5	36	65.5	89	2 S38684	MHC class II histo
6	36	65.5	225	2 I47095	MHC class II OVAR-
7	35	63.6	347	2 S43771	phosphatidylcholin
8	35	63.6	383	2 S56179	secreted glycoprot
9	35	63.6	473	2 D70405	glutamate--tRNA l1
10	34	61.8	108	2 S26316	Ig heavy chain V r
11	34	61.8	110	2 S26317	Ig heavy chain V r
12	34	61.8	210	1 B69265	conserved hypothet
13	34	61.8	275	2 D71087	probable translati
14	34	61.8	275	2 G75130	translation initia
15	34	61.8	287	1 PWBY	inorganic pyrophos
16	34	61.8	287	1 PWVKL	inorganic pyrophos
17	34	61.8	321	1 S58614	cytochrome c-type
18	34	61.8	321	1 JQ0288	cytochrome c-type
19	34	61.8	628	1 A56707	protein-tyrosine k
20	34	61.8	682	2 S30995	gene 50 protein -
21	33	60.0	80	2 I54469	MHC HLA-DR-beta-1
22	33	60.0	80	2 I68777	MHC HLA-DR-beta-1
23	33	60.0	81	2 I54550	HLA DRB1*1202 - hu
24	33	60.0	85	2 I58634	MHC class II DR-be
25	33	60.0	89	2 S38676	MHC class II histo
26	33	60.0	89	2 S38680	MHC class II histo
27	33	60.0	89	2 S57512	MHC class II histo
28	33	60.0	123	2 C25239	MHC class II histo
29	33	60.0	167	2 T16454	hypothetical prote
30	33	60.0	200	2 D32526	class II histocomp

31 33 60.0 237 2 C27060 class II histocomp
32 33 60.0 266 2 I54287 gene HLA-DRB1 prot
33 33 60.0 266 2 A27618 class II histocomp
34 33 60.0 266 2 I54295 lymphocyte antigen
35 33 60.0 279 2 T05421 hypothetical prote
36 33 60.0 405 2 D75441 fennA-related prote
37 33 60.0 448 1 A50003 nucleocapsid prote
38 33 60.0 470 2 H71667 glutamate--tRNA l1
39 33 60.0 548 2 T25424 hypothetical prote
40 33 60.0 582 1 S51945 ferredoxin--nitrit
41 33 60.0 583 1 S20495 ferredoxin--nitrit
42 33 60.0 594 1 S16603 ferredoxin--nitrit
43 33 60.0 694 2 T07638 SWH1 protein homol
44 32.5 59.1 232 2 B48381 MHC class II histo
45 32 58.2 9 2 S36850 Ig heavy chain V r

ALIGNMENTS

RESULT 1

T19625

hypothetical protein C31H5.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T19625

R:Kershaw, J.

submitted to the EMBL Data Library, April 1997

A:Reference number: Z19153.

A:Accession: T19625

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-446 <WIL>

A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6

A:Experimental source: clone C31H5

C:Genetics:

A:Gene: CESP:C31H5.6

A:Map position: 1

A:Introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3

Query Match

Best Local Similarity 70.9%; Score 39; DB 2; Length 446;

Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFA 9

Db 51 RHNYGSHA 58

RESULT 2

I51106

Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)

C:Species: Phasianus colchicus (ring-necked pheasant)

C>Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999

C:Accession: I51106

R:Wittzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.

Immunogenetics 39, 395-403, 1994

A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-ne

A:Reference number: I51103; MUID:94245280

A:Accession: I51106

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-82 <WIT>

A:Cross-references: EMBL:X75406; NID:q496926; PIDN:CAA53160.1; PID:q496927

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match

Best Local Similarity 65.5%; Score 36; DB 2; Length 82;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

Db 75 RHNYGVF 81
|||||

RESULT 3

S38688
MHC class II histocompatibility antigen HLA-DR-08 beta chain - Galago senegalensis (frag
C:Species: Galago senegalensis
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997
C:Accession: S38688
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced f
A:Reference number: S38676
A:Accession: S38688
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:227158
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 89;

Best Local Similarity 85.7%; Pred. No. 4.1;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||

Db 75 RHNYGVF 81
|||||

RESULT 4

S38683
MHC class II histocompatibility antigen HLA-DR-03 beta chain - Galago senegalensis (frag
C:Species: Galago senegalensis
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997
C:Accession: S38683
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced f
A:Reference number: S38676
A:Accession: S38683
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:227153
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 89;

Best Local Similarity 85.7%; Pred. No. 4.1;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||

Db 75 RHNYGVF 81
|||||

RESULT 5

S38684
MHC class II histocompatibility antigen HLA-DR-04 beta chain - Galago senegalensis (frag
C:Species: Galago senegalensis
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997
C:Accession: S38684
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced f
A:Reference number: S38676
A:Accession: S38684
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:227154
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 4.1;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||

Db 75 RHNYGVF 81
|||||

RESULT 6

I47095
MHC class II OVAR-DR-beta-3 - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 23-Jul-1999
C:Accession: I47095
R:Pabb, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.
Anim. Genet. 24, 249-255, 1993
A:Title: Isolation, characterization and evolution of ovine major histocompatibility
A:Reference number: I47075; MUID:94057592
A:Accession: I47095
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-225 <PAB>
A:Cross-references: GB:L04790; NID:g458880; PIDN:AAA16562.1; PID:g458881
C:Genetics:
A:Gene: OVAR-DRB3
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 65.5%; Score 36; DB 2; Length 225;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||

Db 68 RHNYGVF 74
|||||

RESULT 7

S43771
phosphatidylcholine desaturase (EC 1.3.1.35) - Synecococcus sp. (strain PCC 7002)
N:Alternate names: Delta-12 desaturase; fatty acid desaturase (EC 1.14.99.-) (misiden
C:Species: Synecococcus sp.
A:Variety: PCC 7002
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 28-May-1999
C:Accession: S43771
R:Sakamoto, T.; Wada, H.; Nishida, I.; Ohmori, M.; Murata, N.
Plant Mol. Biol. 24, 643-650, 1994
A:Title: Identification of conserved domains in the Delta-12 desaturases of cyanobact
A:Reference number: S43770; MUID:94207189
A:Accession: S43771
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-347 <SAK>
A:Cross-references: GB:D13779; NID:g488510; PIDN:BAA02922.1; PID:d1003428; PID:g48851
C:Superfamily: omega-3 fatty acid desaturase
C:Keywords: oxidoreductase

Query Match 63.6%; Score 35; DB 2; Length 347;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
|||||

Db 334 AEHNYISFA 342
|||||

RESULT 8

S56179
secreted glycoprotein Ep4, 47K, precursor - carrot (fragment)
C:Species: Daucus carota (carrot)
C:Date: 27-Oct-1995 #sequence_revision 26-Jul-1996 #text_change 17-Mar-1999

C;Accession: S56179; S56180
R;van Engelen, F.A.; de Jong, A.J.; Meijer, E.A.; Kuil, C.W.; Meyboom, J.K.; Dirkse, W.G.
Plant Mol. Biol. 27, 901-910, 1995
A;Title: Purification, immunological characterization and cDNA cloning of a 47 kDa glyco-
A;Reference number: S56179; MUID:95284347
A;Accession: S56179
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-383 <VAN>
A;Cross-references: EMBL:L36956; NID:g886222; PID:g886223
A;Accession: S56180
A;Molecule type: protein
A;Residues: 121-133;272-276;281-284 <VAN>
C;Keywords: glycoprotein
F;1-15/Domain: signal sequence (fragment) #status predicted <SIG>
F;16-383/Product: secreted glycoprotein Ep4, 47K #status predicted <MAT>

Query Match 63.6%; Score 35; DB 2; Length 383;
Best Local Similarity 55.6%; Pred. No. 27;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFAM 10
Db 305 RYNYGEFSL 313
||||| |::

RESULT 9
D70405
glutamate--tRNA ligase (EC 6.1.1.17) - Aquifex aeolicus
C;Species: Aquifex aeolicus
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C;Accession: D70405
R;Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ovi-
V.
Nature 392, 353-358, 1998
A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666
A;Accession: D70405
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-473 <AQF>
A;Cross-references: GB:AE000729; NID:g2983659; PIDN:AAC07230.1; PID:g2983664; GB:AE00065
A;Experimental source: strain VF5
C;Genetics:
A;Gene: gltx
C;Superfamily: glutamate--tRNA ligase; glutamine--tRNA ligase homology
C;Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 63.6%; Score 35; DB 2; Length 473;
Best Local Similarity 60.0%; Pred. No. 34;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFAM 10
Db 31 ARHNGGFVL 40
||||| |::

RESULT 10
S26316
Ig heavy chain V region - mouse
C;Species: Mus musculus (house mouse)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C;Accession: S26316
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protein e
A;Reference number: S26309; MUID:91341421
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-108 <STA>

A;Cross-references: EMBL:X59190; NID:g52056; PIDN:CAM41900.1; PID:e36170; PID:g133403
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;2-85/Domain: immunoglobulin homology <IMM>

Query Match 61.8%; Score 34; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 84 ARGNYGNYA 92
||||| |::

RESULT 11
S26317

Ig heavy chain V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 17-Apr-1998
C;Accession: S26317
R;Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A;Title: Antibodies that are specific for a single amino acid interchange in a protei
A;Reference number: S26309; MUID:91341421
A;Accession: S26317
A;Molecule type: mRNA
A;Residues: 1-110 <STA>
A;Cross-references: EMBL:X59186
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 61.8%; Score 34; DB 2; Length 110;
Best Local Similarity 66.7%; Pred. No. 12;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 86 ARGNYGNYA 94
||||| |::

RESULT 12
B69265

conserved hypothetical protein AF0122 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: B69265
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod-
..; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiaich, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A;Reference number: A69250; MUID:98049343
A;Accession: B69265
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-210 <KLE>

A;Cross-references: GB:AE001098; GB:AE000782; NID:g2689421; PID:g2650532; TIGR:AF0122
C;Superfamily: conserved hypothetical protein AF0119

Query Match 61.8%; Score 34; DB 1; Length 210;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 128 RHAYGSF 134
|||||

RESULT 13

D/1087
probable translation initiation factor eIF-2 alpha chain - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 26-Aug-1999
C:Accession: D/1087
R:Kawabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekinaka, M.; Ohkuku, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Kushida, N.; Oguchi, N. Nucleic Acids Res. 16, 10441-10452, 1988
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic archaeon Pyrococcus horikoshii
A:Reference number: A/1000; MUID:98344137
A:Accession: D/1087
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-275 <KAW>
A:Cross-references: GB:AP000004; NID:g3236131; PIDN:BAA30058.1; PID:d1031001; PID:g32573
A:Experimental source: strain OR3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 61.8%; Score 34; DB 2; Length 275;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8

|||||
Db 23 HNYGAF 28

RESULT 14

G/5130
translation initiation factor aif-2, subunit alpha (aif2a) PAB0568 - Pyrococcus abyssi
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 24-Nov-1999
C:Accession: G/5130
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A:Reference number: A/5001
A:Accession: G/5130
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-275 <KAW>
A:Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49760.1; PID:el51565
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: aif2a; PAB0568
C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 61.8%; Score 34; DB 2; Length 275;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8

|||||
Db 23 HNYGAF 28

RESULT 15

P/5864
inorganic pyrophosphatase (EC 3.6.1.1) - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein YBR011c; protein YBR0202; pyrophosphate phosphohydrolase
C:Species: Saccharomyces cerevisiae
C:Date: 30-Nov-1980 #sequence_revision 09-Sep-1994 #text_change 05-Nov-1999
C:Accession: S45864; S07679; A01014; S29189
R:Entian, K.D.; Koetter, P.; Rose, M.; Li, Z.; Therman, R.; Brendel, M.; Baur, A.; Bole
submitted to the Protein Sequence Database, August 1994
A:Reference number: S45862
A:Accession: S45864

A:Molecule type: DNA
A:Residues: 1-287 <ENT>
A:Cross-references: EMBL:Z35880; NID:g536205; PIDN:CAA84949.1; PID:g536206; GSPDB:GNO
A:Experimental source: strain S288C
R:Kolakowski Jr., L.F.; Schloesser, M.; Cooperman, B.S.
Nucleic Acids Res. 16, 10441-10452, 1988
A:Title: Cloning, molecular characterization and chromosome localization of the inorganic pyrophosphatase gene from *Saccharomyces cerevisiae*
A:Reference number: S07679; MUID:89083474
A:Accession: S07679
A:Molecule type: DNA
A:Residues: 1-266, 'L', 268-287 <KOL>
A:Cross-references: EMBL:X13253; NID:g4198; PIDN:CAA31629.1; PID:g4199
R:Cohen, S.A.; Sterner, R.; Keim, P.S.; Heinrikson, R.L.
J. Biol. Chem. 253, 889-897, 1978
A:Title: Covalent structural analysis of yeast inorganic pyrophosphatase.
A:Reference number: A92241; MUID:78087552
A:Accession: A01014
A:Molecule type: protein
A:Residues: 2-40, 'D', 42-71, 'N', 73, 75-117, 'N', 119-123, 'Q', 125-136, 'E', 138-186, 'D', 188-190
A:Note: this is the final paper in a series
A:Note: no disulfide bonds are present
R:Raznikov, A.V.; Sklyankina, V.A.; Ayaeva, S.M.
FEBS Lett. 308, 62-64, 1992
A:Title: Tyrosine-89 is important for enzymatic activity of *S. cerevisiae* inorganic pyrophosphatase
A:Reference number: S29189; MUID:92354770
A:Accession: S29189
A:Molecule type: protein
A:Residues: 83-105, 'E', 107-112 <RAZ>
R:Bond, M.W.; Chiu, N.Y.; Cooperman, B.S.
Biochemistry 19, 94-102, 1980
A:Title: Identification of an arginine important for enzymatic activity within the covalent structure of yeast inorganic pyrophosphatase
A:Reference number: A90443
A:Accession: A90443
A:Contents: annotation; active site
C:Genetics:
A:Gene: SGD:IPPI; PPA; MIPS:YBR011c
A:Cross-references: SGD:S0000215; MIPS:YBR011c
A:Map position: 2R
C:Function:
A:Description: catalyzes hydrolysis of pyrophosphate to orthophosphate
A:Note: requires divalent metal cation
C:Superfamily: inorganic pyrophosphatase
C:Keywords: homodimer; hydrolase
F:2-287/Product: inorganic pyrophosphate #status experimental <MAT>
F:79/Binding site: pyrophosphate (Arg) #status experimental

Query Match 61.8%; Score 34; DB 1; Length 287;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8

|||||
Db 92 HNYGAF 97

Search completed: May 27, 2000, 19:26:46
Job time: 1769 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 20:07:18 ; Search time 69.28 Seconds
(without alignments)
4.396 Million cell updates/sec

Title: US-09-016-061-76
Perfect score: 55
Sequence: 1 ARHNYGSFAM 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	63.6	473	1 SVE_AQUAE	O6721 aquifex aeo
2	34	61.8	275	1 IF2A_PYRHO	O58655 pyrococcus
3	34	61.8	284	1 IPYR_PICPA	O13505 pichia past
4	34	61.8	286	1 IPYR_KUOLA	P13998 kluyveromyc
5	34	61.8	286	1 IPYR_YEAST	P00817 saccharomyc
6	34	61.8	321	1 CCSA_MAIZE	P46659 zea mays (m
7	34	61.8	321	1 CCSA_ORYSA	P12215 oryza sativ
8	34	61.8	629	1 KSYK_RAT	O64725 rattus norv
9	34	61.8	682	1 VGS0_BPML5	O05262 mycobacteri
10	33	60.0	448	1 NCAP_CVHOC	P33469 human coron
11	33	60.0	470	1 SYE2_RICPR	O92ct8 rickettsia
12	33	60.0	583	1 NIR_BETVE	P38500 betula verr
13	33	60.0	594	1 NIR_SPIOL	P05314 spinacia ol
14	32	58.2	65	1 CCSA_OENBE	P31565 oenothera b
15	32	58.2	65	1 CCSA_PEA	P31172 pisum sativ
16	32	58.2	196	1 WBB1_ECOLI	P37750 escherichia
17	32	58.2	197	1 W61A_METJA	P81310 methanococc
18	32	58.2	198	1 HB2C_HUMAN	P01911 homo sapien
19	32	58.2	266	1 HB2A_HUMAN	P01913 homo sapien
20	32	58.2	266	1 HB2B_HUMAN	P01912 homo sapien
21	32	58.2	266	1 HB2C_HUMAN	P01914 homo sapien
22	32	58.2	266	1 HB2D_CANFA	P18470 canis famil
23	32	58.2	266	1 HB2D_HUMAN	P13759 homo sapien
24	32	58.2	266	1 HB2E_HUMAN	P04229 homo sapien
25	32	58.2	266	1 HB2F_HUMAN	P13758 homo sapien
26	32	58.2	266	1 HB2H_HUMAN	P13760 homo sapien
27	32	58.2	266	1 HB2I_HUMAN	P20039 homo sapien
28	32	58.2	266	1 HB2J_HUMAN	P13761 homo sapien
29	32	58.2	313	1 CCSA_TOBAC	P12216 nicotiana t
30	32	58.2	328	1 CCSA_ARATH	P56770 arabidopsis
31	32	58.2	349	1 YJY9_YEAST	P41903 saccharomyc
32	32	58.2	469	1 YQJ8_CAEEL	P34631 caenorhabdi
33	32	58.2	480	1 SYE_HAEIN	P43818 haemophilus
34	32	58.2	528	1 PRI2_YEAST	P20457 saccharomyc

ALIGNMENTS

RESULT 1

SYE_AQUAE

ID	SYE_AQUAE	STANDARD;	PRT;	473 AA.
AC	O6721;			
DT	15-FEB-2000 (Rel. 39, Created)			
DT	15-FEB-2000 (Rel. 39, Last sequence update)			
DT	15-FEB-2000 (Rel. 39, Last annotation update)			
DE	GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE) (GLURS).			
GN	GLTX OR AQ1221.			
OS	Aquifex aeolicus.			
OC	Bacteria; Aquificales; Aquificaceae; Aquifex.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=VF5;			
RX	MEDLINE; 98196666.			
RA	Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Huber R., Graham D.E., Overbeek R., Sneed M.A., Keller M., Aufay M., Swanson R.V., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;			
RA	"The complete genome of the hyperthermophilic bacterium Aquifex aeolicus";			
RT	Nature 392:353-358(1998).			
RL	-1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) = AMP + PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).			
CC	-1- SUBUNIT: MONOMER (BY SIMILARITY).			
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC.			
CC	-1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC	EMBL; AE000729; AAC07230.1; --			
DR	PRINTS; PR00987; TRNASYNTHGLU			
DR	PROSITE; PS00178; AA-TRNA_LIGASE_I; 1.			
DR	PFAM; PF00749; tRNA-synt_ic; 1.			
KW	Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.			
FT	SIMILAR 10 20 "HIGH" REGION.			
FT	SIMILAR 242 246 "KMSK" REGION.			
FT	BINDING 245 245 ATP (BY SIMILARITY).			
SO	SEQUENCE 473 AA; 55121 MW; 5CB4DL590973E07A CRC64;			

Query Match 63.6%; Score 35; DB 1; Length 473;

Best Local Similarity 60.0%; Pred. No. 12;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 ARHNYGSFAM 10

Db 31 ARHNNGGFVL 40

RESULT 2

```

IP2A_PVRHO
ID IF2A_PVRHO STANDARD; PRT; 275 AA.
AC OS8655;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
GN PH0961.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Pyrococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE; 98344137.
RA Kawabayashi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo H., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
CC (BY SIMILARITY).
CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
CC CHAIN (BY SIMILARITY).
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AJ001000; CAA04453.1;
CC HSSP; P00817; IWGI.
CC PROSITE; PS00387; PPASE; 1.
CC PFAM; PF00719; Pyrophosphatase; 1.
CC KW Hydrolase; Magnesium.
CC FT INIT_MET 0 0 BY SIMILARITY.
CC FT ACT_SITE 56 56 PROBABLE.
CC FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
CC SQ SEQUENCE 284 AA; 31937 MW; 3DAD27970D775D6 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 275;
Best Local Similarity 83.3%; Pred. No. 11;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 23 HNYGAF 28
|||||
IPYR_PICPA
ID IPYR_PICPA STANDARD; PRT; 284 AA.
AC O13505;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
DE HYDROLASE) (PPASE).
GN IP1.
OS Pichia pastoris (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Pichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-11430;
RX MEDLINE; 99034033.
RA Cosano I.C., Alvarez P., Molina M., Nombela C.;
RT "Cloning and sequence analysis of the Pichia pastoris TRP1 and
RT HIS3 genes.";
RL Yeast 14:861-867(1998).

```

```

CC -!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O -> 2 ORTHOPHOSPHATE.
CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AJ001000; CAA04453.1;
CC HSSP; P00817; IWGI.
CC PROSITE; PS00387; PPASE; 1.
CC PFAM; PF00719; Pyrophosphatase; 1.
CC KW Hydrolase; Magnesium.
CC FT INIT_MET 0 0 BY SIMILARITY.
CC FT ACT_SITE 56 56 PROBABLE.
CC FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
CC SQ SEQUENCE 284 AA; 31937 MW; 3DAD27970D775D6 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 284;
Best Local Similarity 83.3%; Pred. No. 11;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 91 HNYGAF 96
|||||
IPYR_KLULA
ID IPYR_KLULA STANDARD; PRT; 286 AA.
AC P13998;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
DE HYDROLASE) (PPASE).
GN IP1 OR IPP.
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Kluyveromyces.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89189093.
RA Stark M.J.R., Milner J.S.;
RT "Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a
RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
RT and histone H3.";
RL Yeast 5:35-50(1989).
RN [2]
RP SIMILARITY TO E.COLI AND YEAST PPASES.
RX MEDLINE; 90254161.
RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
RA Cooperman B.S.;
RT "Conservation of functional residues between yeast and E. coli
RT inorganic pyrophosphatases.";
RL Biochim. Biophys. Acta 1038:338-345(1990).
CC -!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O -> 2 ORTHOPHOSPHATE.
CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC
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 CC -----

DR EMBL; X14230; CAA32446.1; -;
 DR PIR; S07894; PWVKL.
 DR HSP; P00817; PPASE.
 DR PROSITE; PS00387; PPASE; 1.
 DR PRAM; PF00719; Pyrophosphatase; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 286 AA; 32034 MW; 11647F4ABD916A2F CRC64;

Query Match 61.8%; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 12;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8

|||||

Db 91 HNYGAF 96

RESULT 5

IPYR_YEAST
 ID IPYR_YEAST STANDARD; PRT; 286 AA.
 AC P00817;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI OR PPAL OR PPA OR YBR011C OR YBR0202.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-X2180;
 RX MEDLINE; 89083474.
 RA Kolakowski L.F. Jr., Schloesser M., Cooperman B.S.;
 RT "Cloning, molecular characterization and chromosome localization of
 RT the inorganic pyrophosphatase (PPA) gene from *S. cerevisiae*.";
 RL Nucleic Acids Res. 16:10441-10452(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C;
 RA Entian K.-D., Koetter P., Rose M., Li Z., Thermann R., Brendel M.,
 RA Baur A., Boles E., Miosga T., Schaaff-Gerstenschlaeger I.,
 RA Zimmermann F.K.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE.
 RX MEDLINE; 78087552.
 RA Cohen S.A., Sterner R., Keim P.S., Heinrikson R.L.;
 RT "Covalent structural analysis of yeast inorganic pyrophosphatase.";
 RL J. Biol. Chem. 253:889-897(1978).
 RN [4]
 RP SEQUENCE OF 25-35 AND 239-251.
 RC STRAIN-S288C;
 RX MEDLINE; 95203288.
 RA Garrels J.I., Fletcher B., Kobayashi R., Latter G.I., Schwender B.,
 RA Volpe T., Warner J.R., McLaughlin C.S.;
 RT "Protein identifications for a *Saccharomyces cerevisiae* protein
 RT database";
 RL Electrophoresis 15:1466-1486(1994).
 RN [5]
 RP SEQUENCE OF 239-249.
 RC STRAIN-ATCC 38531 / Y41;

RX MEDLINE; 97089742.
 RA Norbeck J., Blomberg A.;
 RT "Protein expression during exponential growth in 0.7 M NaCl medium of
 RT *Saccharomyces cerevisiae*.";
 RL FEMS Microbiol. Lett. 137:1-8(1996).
 RN [6]
 RP ACTIVE SITE.
 RX MEDLINE; 80109718.
 RA Bond M.W., Chiu N.Y., Cooperman B.S.;
 RT "Identification of an arginine important for enzymatic activity
 RT within the covalent structure of yeast inorganic pyrophosphatase.";
 RL Biochemistry 19:94-102(1980).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RA Arutunian E.G., Terzian S.S., Voronova A.A., Kuranova I.P.,
 RA Smirnova E.A., Vainstein B.K., Hohne W.E., Hansen G.;
 RT "X-ray diffraction study of inorganic pyrophosphatase from baker's
 RT yeast at the 3-A resolution.";
 RL Dokl. Akad. Nauk SSSR 258:1481-1492(1981).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE; 97148342.
 RA Heikinheimo P., Lehtonen J., Baykov A., Lahti R., Cooperman B.S.,
 RA Goldman A.;
 RT "The structural basis for pyrophosphatase catalysis.";
 RL Structure 4:1491-1508(1996).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RA Swaminathan K., Cooperman B.S., Lahti R., Voet D.;
 RL Submitted (DEC-1997) to the PDB data bank.
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF MUTANTS LYS-78 AND LYS-117.
 RX MEDLINE; 99096888.
 RA Tuominen V., Heikinheimo P., Kajander T., Torkkel T., Hyytia T.,
 RA Kapyla J., Lahti R., Cooperman B.S., Goldman A.;
 RT "The R78K and D117E active-site variants of *Saccharomyces cerevisiae*
 RT soluble inorganic pyrophosphatase: structural studies and mechanistic
 RT implications";
 RL J. Mol. Biol. 284:1565-1580(1998).
 RN [11]
 RP SIMILARITY TO E.COLI AND K.LACTIS PPASES.
 RX MEDLINE; 90254161.
 RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihtinen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RT "Conservation of functional residues between yeast and *E. coli*
 RT inorganic pyrophosphatases";
 RL Biochim. Biophys. Acta 1038:338-345(1990).
 CC -|- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -|- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY. IT BINDS UP TO 4 DIVALENT
 CC CATIONS PER SUBUNIT, WITH THREE REQUIRED FOR ACTIVITY.
 CC -|- SUBUNIT: HOMODIMER.
 CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -|- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; X13253; CAA31629.1; -;
 DR EMBL; Z35880; CAA84949.1; -;
 DR PIR; S45864; PWBY.
 DR PIR; 1PYP; 15-OCT-91.
 DR PDB; 1YPP; 07-DEC-96.
 DR PDB; 1WGI; 19-NOV-97.
 DR PDB; 1WGJ; 19-NOV-97.
 DR PDB; 1HUJ; 08-APR-98.
 DR PDB; 1HUK; 08-APR-98.
 DR PDB; 117E; 23-DEC-98.

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DR PDB: 8PRK; 23-DEC-98.
DR SWISS-2DPAGE; P00817; YEAST.
DR YEPD; 7305; -.
DR SGD; L0000872; Ipp1.
DR PROSITE; PS00387; PRPASE; 1.
DR PFAM; PF00719; Pyrophosphatase; 1.
KW Hydrolase; Magnesium; 3D-structure.
FT INIT_MPT 0
FT ACT_SITE 56 56 PROBABLE.
FT BINDING 78 78 INORGANIC PYROPHOSPHATE.
FT CONFLICT 40 40 N -> D (IN REF. 3).
FT CONFLICT 71 71 D -> N (IN REF. 3).
FT CONFLICT 74 74 MISSING (IN REF. 3).
FT CONFLICT 123 123 E -> Q (IN REF. 3).
FT CONFLICT 136 136 Q -> E (IN REF. 3).
FT CONFLICT 186 186 N -> D (IN REF. 3).
FT CONFLICT 224 224 D -> N (IN REF. 3).
FT CONFLICT 266 266 L -> P (IN REF. 2).
FT STRAND 4 7
FT STRAND 16 20
FT STRAND 25 25
FT TURN 28 30
FT TURN 38 41
FT STRAND 45 45
FT STRAND 55 55
FT STRAND 79 79
FT TURN 97 98
FT TURN 111 112
FT STRAND 121 123
FT TURN 131 132
FT STRAND 135 135
FT STRAND 138 146
FT STRAND 151 158
FT TURN 160 161
FT TURN 165 167
FT HELIX 172 175
FT TURN 176 177
FT TURN 179 180
FT HELIX 182 197
FT STRAND 203 203
FT HELIX 205 207
FT STRAND 210 210
FT HELIX 212 230
FT TURN 231 231
FT TURN 245 246
FT TURN 248 249
FT TURN 251 252
FT TURN 255 260
FT TURN 274 275
SQ SEQUENCE 286 AA; 32184 MW; F29390260B60C8B2 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 286;
Best Local Similarity 83.3%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 91 HNYGAF 96

RESULT 6
CCSA_MAIZE STANDARD; PRT; 321 AA.
AC P46659;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA.
GN CCSA.
OS Zea mays (Maize).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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PDB: 8PRK; 23-DEC-98.
DR SWISS-2DPAGE; P00817; YEAST.
DR YEPD; 7305; -.
DR SGD; L0000872; Ipp1.
DR PROSITE; PS00387; PRPASE; 1.
DR PFAM; PF00719; Pyrophosphatase; 1.
KW Hydrolase; Magnesium; 3D-structure.
FT INIT_MPT 0
FT ACT_SITE 56 56 PROBABLE.
FT BINDING 78 78 INORGANIC PYROPHOSPHATE.
FT CONFLICT 40 40 N -> D (IN REF. 3).
FT CONFLICT 71 71 D -> N (IN REF. 3).
FT CONFLICT 74 74 MISSING (IN REF. 3).
FT CONFLICT 123 123 E -> Q (IN REF. 3).
FT CONFLICT 136 136 Q -> E (IN REF. 3).
FT CONFLICT 186 186 N -> D (IN REF. 3).
FT CONFLICT 224 224 D -> N (IN REF. 3).
FT CONFLICT 266 266 L -> P (IN REF. 2).
FT STRAND 4 7
FT STRAND 16 20
FT STRAND 25 25
FT TURN 28 30
FT TURN 38 41
FT STRAND 45 45
FT STRAND 55 55
FT STRAND 79 79
FT TURN 97 98
FT TURN 111 112
FT STRAND 121 123
FT TURN 131 132
FT STRAND 135 135
FT STRAND 138 146
FT STRAND 151 158
FT TURN 160 161
FT TURN 165 167
FT HELIX 172 175
FT TURN 176 177
FT TURN 179 180
FT HELIX 182 197
FT STRAND 203 203
FT HELIX 205 207
FT STRAND 210 210
FT HELIX 212 230
FT TURN 231 231
FT TURN 245 246
FT TURN 248 249
FT TURN 251 252
FT TURN 255 260
FT TURN 274 275
SQ SEQUENCE 286 AA; 32184 MW; F29390260B60C8B2 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 321;
Best Local Similarity 62.5%; Pred. No. 13;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAM 10
Db 311 HSYGSFTL 318

RESULT 7
CCSA_ORYSA STANDARD; PRT; 321 AA.
AC P12215;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA.
GN CCSA.
OS Oryza sativa (Rice).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
euphyllophytes; Poaceae; Oryza.
OC [1]
RN SEQUENCE FROM N.A.
RP STRAIN=CV. NIPPONBARE;
RA Suglura M.;
RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
RN [2]
RN COMPLETE GENOME.
RX MEDLINE: 89364698.
RA Hiratsuka J., Shimada H., Whittier R., Ishibashi T., Sakamoto M.,
RA Mori M., Kondo C., Honji Y., Sun C.-R., Meng B.-Y., Li Y.-Q.,
RA Kanno A., Nishizawa Y., Hirai A., Shinozaki K., Suglura M.;
RT "The complete sequence of the rice (Oryza sativa) chloroplast genome:
intermolecular recombination between distinct trna genes accounts for
a major plastid DNA inversion during the evolution of the cereals.";
RL Mol. Gen. Genet. 217:185-194(1989).
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCME/CYCK/CCLI/NRFE/CCSA FAMILY.
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euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Poaceae; Zea.
[1]
RN SEQUENCE FROM N.A.
RX MEDLINE: 95395841.
RA Maier R.M., Neckermann K., Igloi G.L., Koessel H.;
RT "Complete sequence of the maize chloroplast genome: gene content,
hotspots of divergence and fine tuning of genetic information by
transcript editing.";
RL J. Mol. Biol. 251:614-628(1995).
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
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CC -!- SIMILARITY: BELONGS TO THE CCME/CYCK/CCLI/NRFE/CCSA FAMILY.
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CC -----
DR EMBL; X86563; CAA60348.1; -.
DR MAZEDB; I18255; -.
DR PFAM; PF01578; CytC_asm; 1.
KW Cytochrome c-type biogenesis; Chloroplast.
SQ SEQUENCE 321 AA; 36693 MW; AF981BAR461A5D1B CRC64;

Query Match 61.8%; Score 34; DB 1; Length 321;
Best Local Similarity 62.5%; Pred. No. 13;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAM 10
Db 311 HSYGSFTL 318

RESULT 7
CCSA_ORYSA STANDARD; PRT; 321 AA.
AC P12215;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA.
GN CCSA.
OS Oryza sativa (Rice).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euphyllophytes; Spermatophyta; Magnoliophyta; Liliopsida; Poales;
euphyllophytes; Poaceae; Oryza.
OC [1]
RN SEQUENCE FROM N.A.
RP STRAIN=CV. NIPPONBARE;
RA Suglura M.;
RL Submitted (JUL-1989) to the EMBL/GenBank/DBJ databases.
RN [2]
RN COMPLETE GENOME.
RX MEDLINE: 89364698.
RA Hiratsuka J., Shimada H., Whittier R., Ishibashi T., Sakamoto M.,
RA Mori M., Kondo C., Honji Y., Sun C.-R., Meng B.-Y., Li Y.-Q.,
RA Kanno A., Nishizawa Y., Hirai A., Shinozaki K., Suglura M.;
RT "The complete sequence of the rice (Oryza sativa) chloroplast genome:
intermolecular recombination between distinct trna genes accounts for
a major plastid DNA inversion during the evolution of the cereals.";
RL Mol. Gen. Genet. 217:185-194(1989).
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCME/CYCK/CCLI/NRFE/CCSA FAMILY.
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CC -----
 DR EMBL; X15901; CAA33952.1; -;
 DR PIR; J00288; J00288.
 DR PFAM; PF01578; CytC_asm; 1.
 KW Cytochrome c-type biogenesis; Chloroplast.
 SQ SEQUENCE 321 AA; 36702 MW; D959FE24A619B650 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 321;
 Best Local Similarity 62.5%; Pred. No. 13;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSPAM 10
 |:||||:
 Db 312 HSYGSFTL 319

RESULT 8
 KSYK_RAT
 ID KSYK_RAT STANDARD; PRT; 629 AA.
 AC Q64725;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE TYROSINE-PROTEIN KINASE SYK (EC 2.7.1.112) (SPLEEN TYROSINE KINASE).
 SYK.
 OS Rattus norvegicus (Rat).
 GN Syk.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95279402.
 RA Rowley R.B., Bolen J.B., Fargnoli J.;
 RT "Molecular cloning of rodent p72Syk. Evidence of alternative mRNA
 RT splicing.";
 RL J. Biol. Chem. 270:12659-12664(1995).
 CC -|- FUNCTION: MAY PARTICIPATE IN SIGNALING PATHWAYS. PLAYS A ROLE IN
 CC LYMPOCYTE ACTIVITY.
 CC -|- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE - ADP + PROTEIN
 CC TYROSINE PHOSPHATE.
 CC -|- ALTERNATIVE PRODUCTS: TWO ISOFORMS; SYKA AND SYKB (SHOWN HERE);
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -|- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
 CC -|- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
 CC -|- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE SYK/ZAP-70 SUBFAMILY.

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DR EMBL; U21684; AAA75167.1; -;
 DR EMBL; U21683; AAA75166.1; -;
 DR HSP; P43405; ICSY.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 2.
 DR PFAM; PF00017; SH2; 2.
 DR PFAM; PF00069; pkinase; 1.
 KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW SH2 domain; Alternative splicing.
 FT DOMAIN 14 106 SH2.

FT DOMAIN 167 258 SH2.
 FT DOMAIN 365 625 PROTEIN KINASE.
 FT NP_BIND 371 379 ATP (BY SIMILARITY).
 FT BINDING 396 396 ATP (BY SIMILARITY).
 FT ACT_SITE 488 488 BY SIMILARITY.
 FT MOD_RES 519 519 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 FT VARSPPLIC 277 299 MISSING (IN ISOFORM SYK6).
 SQ SEQUENCE 629 AA; 71528 MW; 81169A643EC6A6FE CRC64;

Query Match 61.8%; Score 34; DB 1; Length 629;
 Best Local Similarity 70.0%; Pred. No. 27;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSPAM 10
 |:||||:
 Db 195 ARDNGSPAL 204

RESULT 9
 VG50_BPML5 STANDARD; PRT; 682 AA.
 AC Q05262;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE PUTATIVE ADENOSYLCOBALAMIN-DEPENDENT RIBONUCLEOTIDE REDUCTASE
 DE (EC 1.17.4.2) (GP50).
 GN 50.
 OS Mycobacteriophage L5.
 OC Viruses.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 93211282.
 RA Hatfull G.F., Sarkis G.J.;
 RT "DNA sequence, structure and gene expression of mycobacteriophage L5:
 RT a phage system for mycobacterial genetics.";
 RL Mol. Microbiol. 7:395-405(1993).
 CC -|- CATALYTIC ACTIVITY: 2'-DEOXYRIBONUCLEOSIDE TRIPHOSPHATE +
 CC OXIDIZED THIOREDOXIN + H(2)O - RIBONUCLEOSIDE TRIPHOSPHATE +
 CC REDUCED THIOREDOXIN.
 CC -----
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DR EMBL; Z18946; CAA79426.1; -;
 DR PIR; S30995; S30995.
 KW Oxidoreductase; DNA replication.
 SQ SEQUENCE 682 AA; 76331 MW; 8B2A71B873BC04A8 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 682;
 Best Local Similarity 60.0%; Pred. No. 29;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSPAM 10
 |:||||:
 Db 311 AKEGYGSFAV 320

RESULT 10
 NCAP_CVHOC STANDARD; PRT; 448 AA.
 ID NCAP_CVHOC
 AC P33469;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE NUCLEOCAPSID PROTEIN.

GN N.
 OS Human coronavirus (strain OC43).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 OC Coronaviridae; Coronavirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89243809.
 RA Kanahora T., Soe L.H., Lai M.M.C.;
 RT "Sequence analysis of nucleocapsid gene and leader RNA of human
 RT coronavirus OC43";
 RL Virus Res. 12:1-9(1989).
 DR PIR; A60003; A60003.
 DR PFAM; PF00937; Corona_nucleoca; 1.
 KW Nucleocapsid.
 SQ SEQUENCE 448 AA; 49316 MW; 5193AB1AE0D75626 CRC64;

 Query Match 60.0%; Score 33; DB 1; Length 448;
 Best Local Similarity 85.7%; Pred. No. 29;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 2 RHNYGSF 8
 DB 103 RHNRGSF 109
 ||| |||

 RESULT 11
 SYE2_RICPR STANDARD; PRT; 470 AA.
 AC Q9ZCT8;
 ID 15-FEB-2000 (Rel. 39, Created)
 DT 15-FEB-2000 (Rel. 39, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE GLUTAMYL-TRNA SYNTHETASE 2 (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE 2)
 DE (GLU RS 2).
 GN GLTX2 OR RP623.
 OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsieae; Rickettsia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MADRID E;
 RX MEDLINE; 99039499.
 RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
 RA Sacheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
 RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
 RT "The genome sequence of Rickettsia prowazekii and the origin of
 RT mitochondria";
 RL Nature 396:133-140(1998).
 CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) = AMP +
 CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -----
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 CC -----
 CC EMBL; AJ235272; CAAL15066.1; -.
 CC HSSP; P27000; 1GLN.
 DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE NEG.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
 FT SIMILAR 10 20 "HIGH" REGION.
 FT SIMILAR 239 243 "KMSK" REGION.
 FT BINDING 242 242 ATP (BY SIMILARITY).
 SQ SEQUENCE 470 AA; 53696 MW; DFICE50A20B8A9FD CRC64;

Query Match 60.0%; Score 33; DB 1; Length 470;
 Best Local Similarity 75.0%; Pred. No. 31;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QY 1 ARHNYGSF 8
 DB 31 ARHNRGKF 38
 |||| | |

 RESULT 12
 NIR_BETVE STANDARD; PRT; 583 AA.
 AC P38500;
 ID 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE FERREDOXIN--NITRITE REDUCTASE PRECURSOR (EC 1.7.7.1).
 GN NIRL.
 OS Betula verrucosa (White birch) (Betula pendula).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids I; Fagales; Betulaceae; Betula.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LEAF;
 RX MEDLINE; 92167960.
 RA Friemann A., Brinkmann K., Hachtel W.;
 RT "Sequence of a cDNA encoding nitrite reductase from the tree Betula
 RT pendula and identification of conserved protein regions.";
 RL Mol. Gen. Genet. 231:411-416(1992).
 CC -1- CATALYTIC ACTIVITY: AMMONIA + H(2)O + OH(-) + 3 OXIDIZED
 CC FERREDOXIN = NITRITE + 3 REDUCED FERREDOXIN.
 CC -1- COFACTOR: THIS ENZYME CONTAINS ONE SIROHEME AND ONE 4FE-4S
 CC IRON-SULFUR CENTER AS PROSTHETIC GROUPS.
 CC -1- PATHWAY: SECOND STEP IN NITRATE ASSIMILATION (DENITRIFICATION).
 CC -1- SUBUNIT: MONOMER.
 CC -1- INDUCTION: BY NITRATE.
 CC -1- SIMILARITY: THE C-TERMINAL DOMAIN IS A 4FE-4S/SIROHEME DOMAIN
 CC FOUND IN NITRITE REDUCTASES (EC 1.6.6.4 AND EC 1.7.7.1) AND
 CC SULFITE REDUCTASES (EC 1.8.1.2 AND EC 1.8.7.1).
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 CC -----
 CC EMBL; X60093; CAA42690.1; -.
 DR PIR; S20495; S20495.
 DR PRINTS; PR00397; SIROHAEM.
 DR PROSITE; PS00365; NIR_SIR; 1.
 DR PFAM; PF01077; NIR_SIR; 1.
 KW Oxidoreductase; Chloroplast; Transit peptide; Nitrate assimilation;
 KW Heme; Iron-sulfur; 4Fe-4S.
 FT TRANSIT 1 22 CHLOROPLAST (POTENTIAL).
 FT CHAIN 23 583 FERREDOXIN--NITRITE REDUCTASE.
 FT METAL 461 461 IRON-SULFUR OR HEME IRON (POTENTIAL).
 FT METAL 467 467 IRON-SULFUR OR HEME IRON (POTENTIAL).
 FT METAL 502 502 IRON-SULFUR OR HEME IRON (POTENTIAL).
 FT METAL 506 506 IRON-SULFUR (4FE-4S) AND SIROHEME
 FT (BY SIMILARITY).
 SQ SEQUENCE 583 AA; 65229 MW; 482111EF7E66991F CRC64;

 Query Match 60.0%; Score 33; DB 1; Length 583;
 Best Local Similarity 55.6%; Pred. No. 39;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

 QY 2 RHNYGSFAM 10
 DB 120 KHYGRFMM 128
 :||:| | |

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAM 10
:|||||
Db 132 KHYGFEWM 140

RESULT 14
CCSA_OENBE STANDARD; PRT; 65 AA.

AC P31565;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA (FRAGMENT).
GN CCSA.

OS Oenothera bertiana (Bertero's evening primrose).
OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euryhalophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Mytales; Onagraceae; Oenothera.
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE; 93169690.

RA Nimzyk R., Schoendorf T., Hachtel W.;
RT "In-frame length mutations associated with short tandem repeats are
located in unassigned open reading frames of Oenothera chloroplast
DNA.";
RL Curr. Genet. 23:265-270(1993).

CC -1- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
HEME ATTACHMENT (BY SIMILARITY).

CC -1- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.

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CC -----
CC EMBL; X64617; CAA45900.1; -;
CC EMBL; X64614; CAA45894.1; -;
CC PIR; S19981; S19981.
CC PIR; S19988; S19988.

CC Cytochrome c-type biogenesis; Chloroplast.
KW NON_TER 1
SQ SEQUENCE 65 AA; 7441 MW; 343B66DDA1492COC CRC64;

Query Match 58.2%; Score 32; DB 1; Length 65;
Best Local Similarity 83.3%; Pred. No. 6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
:|||||
Db 57 HSYGSF 62

RESULT 15
CCSA_PEA STANDARD; PRT; 65 AA.

AC P31172;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA (FRAGMENT).
GN CCSA.

OS Pisum sativum (Garden pea).
OG Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euryhalophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
RN [1]

RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RX MEDLINE; 88232431.
RA Back E., Burkhardt W., Moyer M., Privalle L., Rothstein S.;
RT "Isolation of cDNA clones coding for spinach nitrite reductase:
complete sequence and nitrate induction.";
RL Mol. Gen. Genet. 212:20-26(1988).
RN [2]

CC SEQUENCE FROM N.A.
CC STRAIN=CV. DARK GREEN BLOOMSDALE; TISSUE=LEAF;
CC MEDLINE; 91329742.
RA Back E., Dunne W., Schneiderbauer A., de Framond A., Rastogi R.,
RA Rothstein S.J.;
RT "Isolation of the spinach nitrite reductase gene promoter which
confers nitrate inducibility on GUS gene expression in transgenic
tobacco.";
RL Plant Mol. Biol. 17:9-18(1991).

CC -1- CATALYTIC ACTIVITY: AMMONIA + H(2)O + OH(-) + 3 OXIDIZED
FERREDOXIN - NITRITE + 3 REDUCED FERREDOXIN.
CC -1- COFACTOR: THIS ENZYME CONTAINS ONE SIROHEME AND ONE 4FE-4S
IRON-SULFUR CENTER AS PROSTHETIC GROUPS.
CC -1- PATHWAY: SECOND STEP IN NITRATE ASSIMILATION (DENITRIFICATION).
CC -1- SUBUNIT: MONOMER.
CC -1- INDUCTION: BY NITRATE.
CC -1- SIMILARITY: THE C-TERMINAL DOMAIN IS A 4FE-4S/SIROHEME DOMAIN
FOUND IN NITRITE REDUCTASES (EC 1.6.6.4 AND EC 1.7.7.1) AND
SULFITE REDUCTASES (EC 1.8.1.2 AND EC 1.8.7.1).

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CC -----
CC EMBL; X07568; CAA30453.1; -;
CC EMBL; X17031; CAA34893.1; -;
CC PIR; S16603; S16603.
CC PRINTS: PR00397; SIROHAEM.
CC PROSITE: PS00365; NIR_SIR; 1.
CC PFAM: PF01077; NIR_SIR; 1.
CC Oxidoreductase; Chloroplast; Transit peptide; Nitrate assimilation;
KW Heme; Iron-sulfur; 4Fe-4S.
FT TRANSIT 1 32
FT CHAIN 33 594
FT METAL 473 473
FT METAL 479 479
FT METAL 514 514
FT METAL 518 518
FT VARIANT 221 221
FT SEQUENCE 594 AA; 66394 MW; 2B3DCAAC16DE06A3 CRC64;

Query Match 60.0%; Score 33; DB 1; Length 594;
Best Local Similarity 55.6%; Pred. No. 40;

```
CC Pisum.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV, ALASKA:
RX MEDLINE; 91355950.
RA Nagano Y., Ishikawa H., Matsuno R., Sasaki Y.;
RT "Nucleotide sequence and expression of the ribosomal protein L2 gene
RL in pea chloroplasts.";
RL Plant Mol. Biol. 17:541-545(1991).
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; X59015; CAA41754.1; -.
DR PIR; SI7441; SI7441.
KW Cytochrome c-type biogenesis; Chloroplast.
FT NON_TER 1
SQ SEQUENCE 65 AA; 7396 MW; 9E523E0C70B102AA CRC64;

Query Match 58.2%; Score 32; DB 1; Length 65;
Best Local Similarity 83.3%; Pred. NO. 6;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
Db 57 HSYGSF 62
!::|||
```

Search completed: May 27, 2000, 20:07:19
Job time: 991 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:38:42 ; Search time 199.56 Seconds
(without alignments)
3.474 Million cell updates/sec

Title: US-09-016-061-76
Perfect score: 55
Sequence: 1 ARHNGSFAM 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SPTREMBL12:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	39	70.9	446	5	O62086 caenorhabdi
2	38	69.1	89	7	O19495 gallus gall
3	36.5	66.4	89	7	Q30217 O19495
4	36	65.5	39	7	P79474 Q30217
5	36	65.5	39	7	P79477 cervus elap
6	36	65.5	39	7	P79478 cervus elap
7	36	65.5	39	7	P79479 cervus elap
8	36	65.5	78	6	O97835 ovis aries
9	36	65.5	78	6	O97839 ovis aries
10	36	65.5	78	6	O97844 ovis aries
11	36	65.5	78	6	O97968 ovis aries
12	36	65.5	79	7	O19191 prionailuru
13	36	65.5	79	7	O19192 prionailuru
14	36	65.5	79	7	O19380 felis silve
15	36	65.5	79	7	O19381 felis silve
16	36	65.5	79	7	O19382 felis silve
17	36	65.5	79	7	O19396 felis silve
18	36	65.5	79	7	O19397 felis silve
19	36	65.5	79	7	O19405 felis silve
20	36	65.5	79	7	O19406 felis silve

21	36	65.5	79	7	O19407 felis silve
22	36	65.5	79	7	O19408 felis silve
23	36	65.5	79	7	O19435 felis silve
24	36	65.5	81	7	Q30568 macaca fasc
25	36	65.5	81	7	Q30571 macaca fasc
26	36	65.5	81	7	Q30737 macaca neme
27	36	65.5	81	7	Q30739 macaca neme
28	36	65.5	81	7	Q30563 macaca fasc
29	36	65.5	81	7	Q30740 macaca neme
30	36	65.5	82	7	O95598 phasianus c
31	36	65.5	82	7	Q30606 macaca mula
32	36	65.5	82	7	Q30608 macaca mula
33	36	65.5	82	7	Q30637 macaca mula
34	36	65.5	82	7	Q30638 macaca mula
35	36	65.5	82	7	Q30658 macaca mula
36	36	65.5	82	7	Q30659 macaca mula
37	36	65.5	82	7	Q30666 macaca mula
38	36	65.5	82	7	Q30667 macaca mula
39	36	65.5	82	7	Q30668 macaca mula
40	36	65.5	82	7	O19287 macaca mula
41	36	65.5	82	7	O19288 macaca mula
42	36	65.5	83	7	O98002 ovis aries
43	36	65.5	83	7	Q9XS06 odocoileus
44	36	65.5	83	7	Q9XR25 odocoileus
45	36	65.5	83	7	Q9XR24 odocoileus

ALIGNMENTS

RESULT 1
O62086 PRELIMINARY; PRT; 446 AA.
AC O62086;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-JAN-1999 (Tremblrel. 09, Last annotation update)
DE C31H5.6 PROTEIN.
GN C31H5.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP KERSHAW J.;
RA Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP MEDLINE: 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., COULSON A.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans";
RL Nature 368:32-38(1994).
DR EMBL: Z93778; CAB07846.1; -;
SQ SEQUENCE 446 AA; 50763 MW; B347C0C8 CRC32;

Query Match 70.9%; Score 39; DB 5; Length 446;
Best Local Similarity 87.5%; Pred. No. 7.6;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 RHNYGSSA 9
| | | | | | |
Db 51 RHNYGSSA 58

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RESULT 2
ID O19495 PRELIMINARY; PRT; 89 AA.
AC O19495;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DE 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE MHC CLASS II BETA 1 DOMAIN (FRAGMENT).
GN B-LBI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-15.151-5; TISSUE-BURSA;
RA PHARR G.T.; DODGSON J.B.; HUNT H.D.; BACON L.D.;
RL Immunogenetics 47:350-354(1998).
DR EMBL; U91532; AAC15813.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 89 89
SQ SEQUENCE 89 AA; 10724 MW; FDAC6024 CRC32;

Query Match 69.1%; Score 38; DB 7; Length 89;
Best Local Similarity 85.7%; Pred. No. 2.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 75 RHNYGDF 81

RESULT 3
ID Q30217 PRELIMINARY; PRT; 89 AA.
AC Q30217;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE DB9 PROTEIN (FRAGMENT).
GN DB9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95279172.
RA ARVIDSSON A.K.; SVENSSON A.C.; WIDMARK E.; ANDERSSON G.; RASK L.;
RA LARHAMMAR D.;
RT "Characterization of three separated exons in the HLA class II DR
region of the human major histocompatibility complex.";
RL Hum. Immunol. 42:254-264(1995).
DR EMBL; S78510; AAD14284.1; -.
FT NON_TER 1 1
FT NON_TER 89 89
SQ SEQUENCE 89 AA; 10489 MW; 5453AC0A CRC32;

Query Match 66.4%; Score 36.5; DB 7; Length 89;
Best Local Similarity 66.7%; Pred. No. 4.3;
Matches 8; Conservative 1; Mismatches 0; Indels 3; Gaps 1;

Qy 2 RHNYG---SFAM 10
Db 75 RHNYGVFESFM 86

RESULT 4
ID P79474 PRELIMINARY; PRT; 39 AA.

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AC P79474;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DE 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea; Cervidae;
OC Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.
RA SWARBRICK P.A.; CRAWFORD A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBDJ databases.
DR EMBL; U63077; AAB37777.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4767 MW; E01AA287 CRC32;

Query Match 65.5%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 2.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 5
ID P79477 PRELIMINARY; PRT; 39 AA.
AC P79477;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DE 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea; Cervidae;
OC Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.
RA SWARBRICK P.A.; CRAWFORD A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBDJ databases.
DR EMBL; U63080; AAB37780.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match 65.5%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 2.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 6
ID P79478 PRELIMINARY; PRT; 39 AA.
AC P79478;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DE 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea; Cervidae;
OC Cervinae; Cervus.

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RN  [1]
RP  SEQUENCE FROM N.A.
RA  SWARBRICK P.A., CRAWFORD A.M.;
RL  Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR  EMBL; U63081; AAB37781.1; -.
KW  MHC.
FT  NON_TER 1 1
   NON_TER 39 39
SQ  SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match 65.5%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 2.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 7
P79479
ID P79479 PRELIMINARY; PRT; 39 AA.
AC P79479;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE MHC CLASS II DB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae;
OC Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.
RA SWARBRICK P.A., CRAWFORD A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63082; AAB37782.1; -.
KW MHC.
FT NON_TER 1 1
   NON_TER 39 39
SQ SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match 65.5%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 2.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 8
O97835
ID O97835 PRELIMINARY; PRT; 78 AA.
AC O97835;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLA-DRB1*N20.2.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=7407; TISSUE=BLOOD;
RA AIDA Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017207; BAA36764.1; -.
FT NON_TER 1 1
   NON_TER 78 78
SQ SEQUENCE 78 AA; 9645 MW; 0A246905 CRC32;

Query Match 65.5%; Score 36; DB 6; Length 78;
Best Local Similarity 85.7%; Pred. No. 4.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

FT NON_TER 78 78
SQ SEQUENCE 78 AA; 9677 MW; D2252D9D CRC32;

Query Match 65.5%; Score 36; DB 6; Length 78;
Best Local Similarity 85.7%; Pred. No. 4.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 72 RHNYGVF 78

RESULT 9
O97839
ID O97839 PRELIMINARY; PRT; 78 AA.
AC O97839;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLA-DRB1*N2.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SUFFOLK BREED AND CORRIDALE BREED; TISSUE=BLOOD;
RA AIDA Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017212; BAA36769.1; -.
FT NON_TER 1 1
   NON_TER 78 78
SQ SEQUENCE 78 AA; 9430 MW; 2883C99C CRC32;

Query Match 65.5%; Score 36; DB 6; Length 78;
Best Local Similarity 85.7%; Pred. No. 4.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 72 RHNYGVF 78

RESULT 10
O97844
ID O97844 PRELIMINARY; PRT; 78 AA.
AC O97844;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLA-DRB1*N8.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SUFFOLK BREED; TISSUE=BLOOD;
RA AIDA Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017220; BAA36777.1; -.
FT NON_TER 1 1
   NON_TER 78 78
SQ SEQUENCE 78 AA; 9645 MW; 0A246905 CRC32;

Query Match 65.5%; Score 36; DB 6; Length 78;

```

Best Local Similarity 85.7%; Pred. No. 4.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 72 RHNYGVF 78

RESULT 11
O97968 PRELIMINARY; PRT; 78 AA.
AC O97968;
DT 01-JAN-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLADRBI*W21.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
RN Caprinae; Ovis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VARIOUS STRAINS;
RA AIDA Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017231; BAA36788.1; -.
DR EMBL; AB017204; BAA36761.1; -.
FT NON_TER 1 1
FT NON_TER 78 78
SQ SEQUENCE 78 AA; 9436 MW; 72250CEB CRC32;

Query Match 65.5%; Score 36; DB 6; Length 78;
Best Local Similarity 85.7%; Pred. No. 4.7;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 72 RHNYGVF 78

RESULT 12
O19191 PRELIMINARY; PRT; 79 AA.
AC O19191;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
GN MHCMAIR-DRB.
OS Prionailurus bengalensis iriomotensis (Iriomote cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Prionailurus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97211851.
RA YUHKI N., O'BRIEN S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB genes.";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51546; AAB65582.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 9582 MW; 8EEF2C7D CRC32;

Query Match 65.5%; Score 36; DB 7; Length 79;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 72 RHNYGVF 78

RESULT 13
O19192 PRELIMINARY; PRT; 79 AA.
AC O19192;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
GN MHCMAIR-DRB.
OS Prionailurus bengalensis iriomotensis (Iriomote cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Prionailurus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97211851.
RA YUHKI N., O'BRIEN S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB genes.";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51547; AAB65583.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 9582 MW; ED9F80F0 CRC32;

Query Match 65.5%; Score 36; DB 7; Length 79;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 72 RHNYGVF 78

RESULT 14
O19380 PRELIMINARY; PRT; 79 AA.
AC O19380;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
GN MHCFECA-DRB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97211851.
RA YUHKI N., O'BRIEN S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB genes.";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51498; AAB65533.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 9659 MW; F352AD23 CRC32;

Query Match 65.5%; Score 36; DB 7; Length 79;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 72 RHNYGVF 78

RESULT 15
O19381
ID O19381 PRELIMINARY; PRT; 79 AA.
AC O19381;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
GN MHCFCFA-DRB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97211851.
RA YUHKI N., O'BRIEN S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
genes.";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51499; AAB65534.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 79
SQ SEQUENCE 79 AA; 9610 MW; 1F7FB873 CRC32;

Query Match 65.5%; Score 36; DB 7; Length 79;
Best Local Similarity 85.7%; Pred. No. 4.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
| | | | |
Db 72 RHNYGVF 78

Search completed: May 27, 2000, 19:38:42
Job time: 2375 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:21:37 ; Search time 148.45 Seconds
(without alignments)
1.596 Million cell updates/sec

Title: US-09-016-061-76
Perfect score: 55
Sequence: 1 ARHNYGSFAM 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	55	100.0	10	1 W76028	LM609 grafted anti
2	50	90.9	10	1 W76024	LM609 grafted anti
3	50	90.9	10	1 W76025	LM609 grafted anti
4	50	90.9	10	1 W76026	LM609 grafted anti
5	50	90.9	10	1 W76027	LM609 grafted anti
6	50	90.9	10	1 W76029	LM609 grafted anti
7	50	90.9	10	1 W76030	LM609 grafted anti
8	50	90.9	10	1 W76010	LM609 grafted anti
9	50	90.9	117	1 W76001	Vitaxin antibody h
10	50	90.9	117	1 W76003	LM609 antibody hea
11	47	85.5	10	1 W76021	LM609 grafted anti
12	46	83.6	10	1 W76039	LM609 grafted anti
13	46	83.6	10	1 W76040	LM609 grafted anti
14	46	83.6	10	1 W76022	LM609 grafted anti
15	46	83.6	10	1 W76023	LM609 grafted anti
16	45	81.8	10	1 W76037	LM609 grafted anti
17	45	81.8	10	1 W76020	LM609 grafted anti
18	42	76.4	110	1 W84099	Vitronectin alpha-
19	42	76.4	117	1 W84093	Murine vitronectin
20	42	76.4	117	1 W84097	Humanised anti- α p
21	41	74.5	10	1 W76038	LM609 grafted anti
22	41	74.5	119	1 W01578	Lead binding Mab 8
23	36	65.5	117	1 W79157	Human IGE receptor
24	36	65.5	117	1 R79155	Human IGE receptor
25	36	65.5	117	1 W27357	Heavy chain variab
26	36	65.5	117	1 W27526	Heavy chain variab
27	36	65.5	117	1 W27354	Heavy chain variab
28	36	65.5	239	1 W73874	Human antiFc epsil
29	36	65.5	242	1 W73876	Human antiFc epsil
30	34	61.8	123	1 W07438	Anti-DNA antibody
31	33	60.0	80	1 R13396	HLA-DRw12a antigen
32	33	60.0	80	1 R13397	HLA-DRw12b antigen
33	32	58.2	11	1 W22700	Peptide sequence #
34	32	58.2	15	1 W25799	Synthetic human S1

35 32 58.2 18 1 W27062 Chemically syntheses
36 32 58.2 25 1 R49334 DRI beta chain pos
37 32 58.2 25 1 W41656 Immunomodulatory p
38 32 58.2 36 1 W03964 VDJ joint protein,
39 32 58.2 36 1 W41127 VH251 DXP'1 J6 mu
40 32 58.2 78 1 W71230 Major histocompata
41 32 58.2 80 1 R21415 Human leukocyte an
42 32 58.2 84 1 P00034 Peptide of human/m
43 32 58.2 89 1 R24276 DRI. Method and k1
44 32 58.2 89 1 W00380 HLA-DRB1*08 and *1
45 32 58.2 93 1 W10491 Beta1 region of Cl

ALIGNMENTS

RESULT 1

W76028
ID W76028 standard; Protein; 10 AA.
AC W76028;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #10.
KW Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;
KW LM609; inhibitor; Integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49865.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
Integrin - and related grafted antibodies based on murine monoclonal
LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis of blood vessels (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00051;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAM 10

Db 1 ARHNYGSFAM 10

RESULT 2

W76024

ID W76024 standard; Protein; 10 AA.

AC W76024;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #6.

KW Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus SP.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49861.
 DR Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0038;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 Db 1 ARHNYGSFA 9

RESULT 3
 W76025
 ID W76025 standard; Protein; 10 AA.

AC W76025;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #7.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

OS Mus SP.
 PN WO9833919-A2.

PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.

PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.

DR N-PSDB; V49862.

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

PS Claim 62; Page 41; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit-binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0038;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 Db 1 ARHNYGSFA 9

RESULT 4

W76026
 ID W76026 standard; Protein; 10 AA.

AC W76026;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #8.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

OS Mus SP.
 PN WO9833919-A2.

PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.

PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.

DR N-PSDB; V49863.

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

PS Claim 62; Page 41; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 90.9%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0038;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 Db 1 ARHNYGSFA 9

RESULT 5

W76027
 ID W76027 standard; Protein; 10 AA.

AC W76027;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #9.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49864.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT Integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;
 Query Match 90.9%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0038;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFA 9
 Db | | | | | | | | | |
 1 ARHNYGSFA 9
 RESULT 6
 ID W76029 standard; Protein; 10 AA.
 AC W76029;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #11.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49866.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT Integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;
 Query Match 90.9%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0038;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFA 9
 Db | | | | | | | | | |
 1 ARHNYGSFA 9
 RESULT 7
 ID W76030 standard; Protein; 10 AA.
 AC W76030;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #12.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49867.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT Integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;
 Query Match 90.9%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0038;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFA 9
 Db | | | | | | | | | |
 1 ARHNYGSFA 9

Query Match 90.9%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0038;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFA 9
 Db | | | | | | | | | |
 1 ARHNYGSFA 9

```

RESULT 8
W76010
ID W76010 standard; Protein; 10 AA.
AC W76010;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #1.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49847.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Disclosure: Page 40: 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC Vitaxin bind selectively to integrin alphaVbeta3 and can be used to
CC inhibit binding of alphaVbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
CC Sequence 10 AA;
SQ

Query Match 90.9%; Score 50; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0038;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9
|||||||

RESULT 9
W76001
ID W76001 standard; Protein; 117 AA.
AC W76001;
DT 02-NOV-1998 (first entry)
DE Vitaxin antibody heavy chain variable region protein fragment.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49820.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 43; Fig 2a; 129pp; English.
CC This sequence represents the LM609 antibody variable heavy chain region.
CC LM609 and the antibody vitaxin bind selectively to integrin alphaVbeta3
CC and can be used to inhibit binding of alphaVbeta3 to a ligand and thus
CC block integrin-mediated signal transduction. This is useful in the
CC treatment, prevention and diagnosis of alphaVbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
CC Sequence 117 AA;
SQ

Query Match 90.9%; Score 50; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 97 ARHNYGSFA 105
|||||||

PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 1; Fig 1a; 129pp; English.
CC This sequence represents a fragment of the vitaxin antibody variable
CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
CC integrin alphaVbeta3 and can be used to inhibit binding of alphaVbeta3
CC to a ligand and thus block integrin-mediated signal transduction. This is
CC useful in the treatment, prevention and diagnosis of alphaVbeta3-mediated
CC disease, specifically angiogenesis and restenosis (but also e.g.
CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
CC osteoporosis etc.). The antibodies contain non-murine framework regions
CC so are suitable for use in humans. Enhanced types of LM609 have affinity
CC more than 90 times greater than that of parent the parent antibody.
CC Sequence 117 AA;
SQ

Query Match 90.9%; Score 50; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 97 ARHNYGSFA 105
|||||||

ID W76003 standard; Protein; 117 AA.
AC W76003;
DT 02-NOV-1998 (first entry)
DE LM609 antibody heavy chain variable region protein fragment.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49822.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 43; Fig 2a; 129pp; English.
CC This sequence represents the LM609 antibody variable heavy chain region.
CC LM609 and the antibody vitaxin bind selectively to integrin alphaVbeta3
CC and can be used to inhibit binding of alphaVbeta3 to a ligand and thus
CC block integrin-mediated signal transduction. This is useful in the
CC treatment, prevention and diagnosis of alphaVbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
CC Sequence 117 AA;
SQ

Query Match 90.9%; Score 50; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.047;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
Db 97 ARHNYGSFA 105
|||||||

PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 1; Fig 1a; 129pp; English.
CC This sequence represents a fragment of the vitaxin antibody variable
CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
CC integrin alphaVbeta3 and can be used to inhibit binding of alphaVbeta3
CC to a ligand and thus block integrin-mediated signal transduction. This is
CC useful in the treatment, prevention and diagnosis of alphaVbeta3-mediated
CC disease, specifically angiogenesis and restenosis (but also e.g.
CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
CC osteoporosis etc.). The antibodies contain non-murine framework regions
CC so are suitable for use in humans. Enhanced types of LM609 have affinity
CC more than 90 times greater than that of parent the parent antibody.
CC Sequence 117 AA;
SQ

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RESULT 11
W76021
ID W76021 standard; Protein; 10 AA.
AC W76021;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #3.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PI (IXSY-) IXSYS INC.
DR Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB; V49858.
DR Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 83.6%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSF 8
Db 1 ARHNYGSF 8
|||||||

RESULT 13
W76040
ID W76040 standard; Protein; 10 AA.
AC W76040;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #16.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PI (IXSY-) IXSYS INC.
DR Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB; V49877.
DR Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 43; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 85.5%; Score 47; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.013;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSYA 9
|||||||

RESULT 12
W76039
ID W76039 standard; Protein; 10 AA.
AC W76039;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #15.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PI (IXSY-) IXSYS INC.
DR Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB; V49876.
DR Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

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QY 1 ARHNYGSF 8
| | | | | | | |
Db 1 ARHNYGSF 8

RESULT 14

W76022
ID W76022 standard; Protein; 10 AA.

AC W76022;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #4.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
PT N-PSDB; V49859.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 83.6%; Score 46; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.019;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
| | | | | | | |
Db 1 ARHNYGSF 8

RESULT 15

W76023
ID W76023 standard; Protein; 10 AA.

AC W76023;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #5.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49860.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 83.6%; Score 46; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.019;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
| | | | | | | |
Db 1 ARHNYGSF 8

Search completed: May 27, 2000, 19:21:37

Job time: 1591 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2000, 19:26:46 ; Search time 163.56 Seconds
(without alignments)
3.585 Million cell updates/sec

Title: US-09-016-061-78
Perfect score: 56
Sequence: 1 ARHNYGSPAG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues
Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_63:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	69.6	446	2 T19625	hypothetical prote
2	38	67.9	697	3 T41445	hypothetical prote
3	36	64.3	82	2 I51106	Major Histocompati
4	36	64.3	89	2 S38688	MHC class II histo
5	36	64.3	89	2 S38683	MHC class II histo
6	36	64.3	89	2 S38684	MHC class II histo
7	36	64.3	225	2 I47095	MHC class II OVAR-
8	35	62.5	320	2 T09288	late embryonic abu
9	35	62.5	347	2 Q43771	phosphatidylcholin
10	35	62.5	405	1 Q4BE35	BBRF3 protein - hu
11	34	60.7	108	2 S26316	Ig heavy chain V r
12	34	60.7	110	2 S26317	Ig heavy chain V r
13	34	60.7	110	2 T02485	hypothetical prote
14	34	60.7	210	1 B69265	conserved hypothet
15	34	60.7	275	2 D71087	probable translati
16	34	60.7	275	2 G75130	translation initia
17	34	60.7	287	1 PWBY	inorganic pyrophos
18	34	60.7	287	1 PWVKL	inorganic pyrophos
19	34	60.7	384	1 SYECSM	methionine adenosy
20	34	60.7	384	2 H64187	methionine adenosy
21	34	60.7	386	2 S51436	probable membrane
22	34	60.7	400	2 D96657	methionine adenosy
23	34	60.7	403	2 T70899	probable metk prot
24	34	60.7	502	2 T08776	hypothetical prote
25	34	60.7	609	2 S45930	probable amino aci
26	34	60.7	856	2 T13159	E1B-55kDa-associat
27	34	60.7	939	2 S28394	probable serine/th
28	33	58.9	80	2 I54469	MHC HLA-DR-beta-1
29	33	58.9	80	2 I68777	MHC HLA-DR beta-1
30	33	58.9	81	2 I54550	HLA DRB1*1202 - hu

31	33	58.9	85	2 I59634	MHC class II DR-be
32	33	58.9	89	2 S38676	MHC class II histo
33	33	58.9	89	2 S38680	MHC class II histo
34	33	58.9	89	2 S57512	MHC class II histo
35	33	58.9	123	2 C25239	MHC class II histo
36	33	58.9	167	2 T16454	hypothetical prote
37	33	58.9	200	2 D32526	class II histocomp
38	33	58.9	228	2 T35418	probable transcrip
39	33	58.9	237	2 C27060	class II histocomp
40	33	58.9	257	2 A32283	MHC class II histo
41	33	58.9	266	2 I54287	gene HLA-DRB1 prot
42	33	58.9	266	2 A27618	class II histocomp
43	33	58.9	266	2 I54295	lymphocyte antigen
44	33	58.9	279	2 T05421	hypothetical prote
45	33	58.9	347	2 T31120	mreb - Vibrio chol

ALIGNMENTS

RESULT 1
T19625
hypothetical protein C31H5.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19625
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19625
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-446 <WIL>
A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6
A:Experimental source: clone C31H5
C:Genetics:
A:Gene: CESP:C31H5.6
A:Map position: 1
A:Introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3

Query Match 69.6%; Score 39; DB 2; Length 446;
Best Local Similarity 87.5%; Pred. No. 9;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSFA 9
Db 51 RHNYGSHA 58
|||||

RESULT 2
T41445
hypothetical protein SPCC594.01 - fission yeast (Schizosaccharomyces pombe) (fragment
C:Species: Schizosaccharomyces pombe
C>Date: 27-Nov-1999 #sequence_revision 27-Nov-1999 #text_change 27-Nov-1999
C:Accession: T41445
R:Rieger, M.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, September 1998
A:Reference number: Z21994
A:Accession: T41445
A:Status: preliminary
A:Residues: 1-697 <RIE>
A:Cross-references: EMBL:AL031523; PIDN:CAA20660.1; GSPDB:GN00068; SPDB:SPCC594.01

Query Match 67.9%; Score 38; DB 3; Length 697;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 RHNYGSFAG 10
Db 155 RHRYWSFAG 163
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RESULT 3
I51106
Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)
C:Species: Phasianus colchicus (ring-necked pheasant)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
C:Accession: I51106
R:Witzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.
Immunogenetics 39, 395-403, 1994
A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-necked pheasant
A:Reference number: I51103; MUID:94245280
A:Accession: I51106
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-82 <FIG>
A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.3%; Score 36; DB 2; Length 82;
Best Local Similarity 85.7%; Pred. No. 6.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 75 RHNYGVF 81

RESULT 4
S38688
MHC class II histocompatibility antigen HLA-DR-08 beta chain - Galago senegalensis (fragment)
C:Species: Galago senegalensis
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997
C:Accession: S38688
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from the EMBL Data Library, November 1993
A:Reference number: S38676
A:Accession: S38688
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27158
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.3%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 6.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 75 RHNYGVF 81

RESULT 5
S38683
MHC class II histocompatibility antigen HLA-DR-03 beta chain - Galago senegalensis (fragment)
C:Species: Galago senegalensis
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997
C:Accession: S38683
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from the EMBL Data Library, November 1993
A:Reference number: S38676
A:Accession: S38683
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27153
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.3%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 6.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 75 RHNYGVF 81

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Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 75 RHNYGVF 81

RESULT 6
S38684
MHC class II histocompatibility antigen HLA-DR-04 beta chain - Galago senegalensis (fragment)
C:Species: Galago senegalensis
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997
C:Accession: S38684
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from the EMBL Data Library, November 1993
A:Reference number: S38676
A:Accession: S38684
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27154
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.3%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 6.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 75 RHNYGVF 81

RESULT 7
I47095
MHC class II OVAR-DR-beta-3 - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 23-Jul-1999
C:Accession: I47095
R:Fabb, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.
Anim. Genet. 24, 249-255, 1993
A:Title: Isolation, characterization and evolution of ovine major histocompatibility antigen (MHC) class II OVAR-DR-beta-3
A:Reference number: I47075; MUID:94057592
A:Accession: I47095
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-225 <FAB>
A:Cross-references: GB:L04790; NID:g458880; PIDN:AAA16562.1; PID:g458881
C:Genetics:
A:Gene: OVAR-DRB3
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 64.3%; Score 36; DB 2; Length 225;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 68 RHNYGVF 74

RESULT 8
T09288
late embryonic abundant protein EMB7 - white spruce
C:Species: Picea glauca (white spruce)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
C:Accession: T09288
R:Dong, J.Z.; Dunstan, D.I.
submitted to the EMBL Data Library, June 1996
A:Description: Cloning and characterization of 6 novel plant embryogenesis-associated genes
A:Reference number: Z16629
A:Accession: T09288

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A;Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-320 <DON>

A:Cross-references: EMBL:L47117; NID:g1350542; PID:g1350543

C:Genetics:

A:Gene: EMB7

Query Match 62.5%; Score 35; DB 2; Length 320;
Best Local Similarity 75.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFAG 10

|||||

Db 217 HNYGIAG 224

RESULT 9

S43771

phosphatidylcholine desaturase (EC 1.3.1.35) - *Synechococcus* sp. (strain PCC 7002)
N;Alternate names: Delta-12 desaturase; fatty acid desaturase (EC 1.14.99.-) (misidentified)

C:Species: *Synechococcus* sp.

A:Variety: PCC 7002

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 28-May-1999

C:Accession: S43771

R:Sakamoto, T.; Wada, H.; Nishida, I.; Ohmori, M.; Murata, N.

Plant Mol. Biol. 24, 643-650, 1994

A:Title: Identification of conserved domains in the Delta-12 desaturases of cyanobacteria

A:Reference number: S43771

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-347 <SAK>

A:Cross-references: GB:D13779; NID:g488510; PIDN:BAA02922.1; PID:d1003428; PID:g488511

C:Superfamily: omega-3 fatty acid desaturase

C:Keywords: oxidoreductase

Query Match 62.5%; Score 35; DB 2; Length 347;

Best Local Similarity 77.8%; Pred. No. 40;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

|||||

Db 334 AEHNYISFA 342

RESULT 10

Q0BE35

BBRF3 protein - human herpesvirus 4 (strain B95-8)

C:Species: human herpesvirus 4, Epstein-Barr virus

C:Date: 23-Feb-1985 #sequence_revision 25-Feb-1985 #text_change 16-Jul-1999

C:Accession: G43043; A03777; S33030

R:Bankier, A.T.; Deininger, P.L.; Farrell, P.J.; Barrell, B.G.

Mol. Biol. Med. 1, 21-45, 1983

A:Title: Sequence analysis of the 17,166 bp EcoRI fragment C of B95-8 Epstein-Barr virus

A:Reference number: A93065; MUID:85035713

A:Accession: G43043

A:Molecule type: DNA

A:Residues: 1-405 <BAN>

A:Cross-references: EMBL:V01555; NID:g59074; PIDN:CAA24825.1; PID:g1334889

R:Baer, R.; Bankier, A.T.; Biggin, M.D.; Deininger, P.J.; Farrell, P.J.; Gibson, T.J.; H

Nature 310, 207-211, 1984

A:Title: DNA sequence and expression of the B95-8 Epstein-Barr virus genome.

A:Reference number: A03794; MUID:84270667

A:Contents: annotation; protein coding region

C:Superfamily: cytomegalovirus UL100 protein

Query Match 62.5%; Score 35; DB 1; Length 405;

Best Local Similarity 55.6%; Pred. No. 46;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAG 10

|||||

Db 267 RHNFGFYCG 275

RESULT 11

S26316

Ig heavy chain V region - mouse

C:Species: *Mus musculus* (house mouse)

C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

C:Accession: S26316

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protein

A:Reference number: S26309; MUID:91341421

A:Accession: S26316

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-108 <STA>

A:Cross-references: EMBL:X59190; NID:g52066; PIDN:CAA41900.1; PID:e36170; PID:g133403

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:2-85/Domain: immunoglobulin homology <IMM>

Query Match 60.7%; Score 34; DB 2; Length 108;

Best Local Similarity 66.7%; Pred. No. 20;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

|||||

Db 84 ARGNYGNYA 92

RESULT 12

S26317

Ig heavy chain V region - mouse (fragment)

C:Species: *Mus musculus* (house mouse)

C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 17-Apr-1998

C:Accession: S26317

R:Stark, S.E.; Caton, A.J.

J. Exp. Med. 174, 613-624, 1991

A:Title: Antibodies that are specific for a single amino acid interchange in a protein

A:Reference number: S26309; MUID:91341421

A:Accession: S26317

A:Molecule type: mRNA

A:Residues: 1-110 <STA>

A:Cross-references: EMBL:X59186

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

Query Match 60.7%; Score 34; DB 2; Length 110;

Best Local Similarity 66.7%; Pred. No. 20;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9

|||||

Db 86 ARGNYGNYA 94

RESULT 13

T02485

hypothetical protein F23F1.8 - *Arabidopsis thaliana*

C:Species: *Arabidopsis thaliana* (mouse-ear cress)

C:Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 14-May-1999

C:Accession: T02485

R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; K

submitted to the EMBL Data Library, August 1998

A:Description: *Arabidopsis thaliana* chromosome II BAC F23F1 genomic sequence.

A:Reference number: Z14675

A:Accession: T02485

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA
 A:Residues: 1-110 <R00>
 A:Cross-references: EMBL:AC004680; NID:g3420043; PID:g3420051
 A:Experimental source: cultivar Columbia
 C:Genetics:
 A:Map position: 2
 A:Note: F23F1.8

Query Match 60.7%; Score 34; DB 2; Length 110;
 Best Local Similarity 85.7%; Pred. No. 20;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NYGSFAG 10
 |||||
 Db 50 NYGSFQG 56

RESULT 14

B69265
 conserved hypothetical protein AF0122 - Archaeoglobus fulgidus
 C:Species: Archaeoglobus fulgidus
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: B69265
 R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 .; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archae
 A:Reference number: A69250; MUID:98049343
 A:Accession: B69265
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-210 <KLE>
 A:Cross-references: GB:AE001098; GB:AE000782; NID:g2689421; PID:g2650532; TIGR:AF0122
 C:Superfamily: conserved hypothetical protein AF0119

Query Match 60.7%; Score 34; DB 1; Length 210;
 Best Local Similarity 85.7%; Pred. No. 38;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RNYGSF 8
 |||||
 Db 128 RHAYGSF 134

RESULT 15

D71087
 probable translation initiation factor eIF-2 alpha chain - Pyrococcus horikoshii
 C:Species: Pyrococcus horikoshii
 C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 26-Aug-1999
 C:Accession: D71087
 R:Kawarabayasi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
 DNA Res. 5, 55-76, 1998
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
 A:Reference number: A71000; MUID:98344137
 A:Accession: D71087
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-275 <KAW>
 A:Cross-references: GB:AP000004; NID:g3236131; PIDN:BAA30058.1; PID:dl031001; PID:g32573
 A:Experimental source: strain OT3
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C:Genetics:
 A:Gene: PH0961
 C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 60.7%; Score 34; DB 2; Length 275;

Best Local Similarity 83.3%; Pred. No. 49;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
 |||||
 Db 23 HNYGAF 28

Search completed: May 27, 2000, 19:26:46
 Job time: 1769 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 20:07:19 ; Search time 69.28 Seconds
(without alignments)
4.396 Million cell updates/sec

Title: US-09-016-061-78
Perfect score: 56
Sequence: 1 ARHNYGSFAG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	64.3	218	1 Y4VH_RHISN	Q53216 rhizobium s
2	35	62.5	405	1 VGLM_EBV	P03215 epstein-bar
3	34	60.7	275	1 IF2A_PVRHO	O58655 pyrococcus
4	34	60.7	284	1 IPYR_PICPA	O13505 pichia past
5	34	60.7	286	1 IPYR_KLULA	P13998 kluyveromyc
6	34	60.7	286	1 IPYR_YEAST	P00817 saccharomyc
7	34	60.7	384	1 METK_ECOLI	P04384 escherichia
8	34	60.7	384	1 METK_HAEIN	P43762 haemophilus
9	34	60.7	386	1 PEXD_YEAST	P80667 saccharomyc
10	34	60.7	400	1 METK_BACSU	P54419 bacillus su
11	34	60.7	403	1 METK_MYCTU	P77899 mycobacteri
12	34	60.7	609	1 BAP2_YEAST	P38084 saccharomyc
13	34	60.7	939	1 ST20_YEAST	Q03497 saccharomyc
14	33	58.9	257	1 HB2P_RABIT	P20756 oryctolagus
15	33	58.9	347	1 MREB_ECOLI	P13519 escherichia
16	33	58.9	396	1 METK_TREPA	O83772 treponema p
17	33	58.9	448	1 NCAP_CVHOC	P33469 human coron
18	33	58.9	470	1 SYE2_RICPR	Q9zct8 rickettsia
19	33	58.9	473	1 SYE_AQUAE	O67271 aquifex aeo
20	33	58.9	682	1 VG50_BPMLS	Q05262 mycobacteri
21	33	58.9	722	1 PBPI_YEAST	P53297 saccharomyc
22	33	58.9	1859	1 RPBI_CAEEL	P16356 caenorhabdi
23	32	57.1	65	1 CCSA_OENBE	P31565 oenothera b
24	32	57.1	65	1 CCSA_PEA	P31172 pisum sativ
25	32	57.1	196	1 WBBJ_ECOLI	P37750 escherichia
26	32	57.1	198	1 HB2G_HUMAN	P01911 homo sapien
27	32	57.1	266	1 HB2A_HUMAN	P01913 homo sapien
28	32	57.1	266	1 HB2B_HUMAN	P01912 homo sapien
29	32	57.1	266	1 HB2C_HUMAN	P01914 homo sapien
30	32	57.1	266	1 HB2D_CANFA	P18470 canis famil
31	32	57.1	266	1 HB2D_HUMAN	P13759 homo sapien
32	32	57.1	266	1 HB2E_HUMAN	P04229 homo sapien
33	32	57.1	266	1 HB2F_HUMAN	P13758 homo sapien
34	32	57.1	266	1 HB2H_HUMAN	P13760 homo sapien

ALIGNMENTS

RESULT 1

ID	Y4VH_RHISN	STANDARD;	PRT;	218 AA.
AC	Q53216;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	HYPOTHETICAL 24.6 KD PROTEIN Y4VH.			
GN	Y4VH.			
OS	Rhizobium sp. (strain NGR234).			
OG	Plasmid sym pNGR234a.			
OC	Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;			
OC	Rhizobiaceae; Rhizobium.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 97305956.			
RA	Freiberg C.A., Fellay R., Broughton W.J., Rosenthal A.,			
RA	Perret X.;			
RT	"Molecular basis of symbiosis between Rhizobium and legumes.";			
RL	Nature 387:394-401(1997).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 96389014.			
RA	Freiberg C., Perret X., Broughton W.J., Rosenthal A.;			
RT	"Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.			
RT	NGR234 using dye terminators and a thermostable 'sequenase': a			
RT	beginning.";			
RL	Genome Res. 6:590-600(1996).			
CC	-1- SIMILARITY: NONE OBVIOUS.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	-----			
DR	EMBL; Z68203; CAA92423.1; ..			
DR	EMBL; AE000101; AAB91896.1; ..			
KW	Hypothetical protein; Plasmid.			
SQ	SEQUENCE 218 AA; 24594 MW; 501C6CB38A09A2E5 CRC64;			

Query Match 64.3%; Score 36; DB 1; Length 218;
Best Local Similarity 60.0%; Pred. No. 7.4;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFAG 10

|||:|:|:|

Db 68 ARDNHGSYSY 77

RESULT 2

VGLM_EBV	STANDARD;	PRT;	405 AA.
ID			
AC	P03215;		

DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE GLYCOPROTEIN M.
 GN BBRF3.
 OS Epstein-barr virus (strain B95-8) (Human herpesvirus 4).
 CC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 CC Gammaherpesvirinae; Lymphocryptovirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 84270667.
 RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
 RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Sequin C.,
 RA Tufnell P.S., Barrell B.G.;
 RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
 RL Nature 310:207-211(1984).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: TO OTHER HERPESVIRUSES GLYCOPROTEIN M.
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 CC -----
 DR EMBL; V01555; CAA24825.1; -.
 DR PIR; A03777; QQBE35.
 DR PIR; S33030; S33030.
 DR PFAM; PF01528; Herpes-glycop: 1.
 DR PRINTS; PR00333; HSVINTEGRLMP.
 KW Transmembrane; Glycoprotein; Late protein.
 FT TRANSMEM 18 38
 FT TRANSMEM 77 97 POTENTIAL.
 FT TRANSMEM 122 142 POTENTIAL.
 FT TRANSMEM 150 170 POTENTIAL.
 FT TRANSMEM 208 228 POTENTIAL.
 FT TRANSMEM 246 266 POTENTIAL.
 FT TRANSMEM 268 288 POTENTIAL.
 FT TRANSMEM 300 320 POTENTIAL.
 FT CARBOHYD 56 56
 FT CARBOHYD 367 377 SER/THR-RICH.
 FT DOMAIN 405 AA; 45792 MW; 25A8A46BCDC0AE1 CRC64;
 SQ SEQUENCE 405 AA; 45792 MW; 25A8A46BCDC0AE1 CRC64;

 Query Match 62.5%; Score 35; DB 1; Length 405;
 Best Local Similarity 55.6%; Pred. No. 22;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

 Qy 2 RHNYGSFAG 10
 Db 267 RHNFGFCYG 275
 ||||| : |

 RESULT 3
 ID IF2A_PVRHO STANDARD; PRT; 275 AA.
 AC O58655;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
 GN PH0961.
 OS Pyrococcus horikoshii.
 CC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-OT3;
 RX MEDLINE; 98344137.
 RA Kawarabayashi Y., Sawada M., Horikawa H., Hino Y.,
 RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,

RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kishida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
 RL DNA Res. 5:55-76(1998).
 CC -1- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
 CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
 CC (BY SIMILARITY).
 CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
 CC CHAIN (BY SIMILARITY).
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 CC -----
 DR EMBL; AF000004; BAA30058.1; -.
 DR PFAM; PF00575; SI; 1.
 KW Initiation factor; Protein biosynthesis.
 SQ SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;

 Query Match 60.7%; Score 34; DB 1; Length 275;
 Best Local Similarity 83.3%; Pred. No. 22;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

 Qy 3 HNYGSF 8
 Db 23 HNYGAF 28
 ||||| : |

 RESULT 4
 ID IPYR_PICPA STANDARD; PRT; 284 AA.
 AC O13505;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPP1.
 OS Pichia pastoris (Yeast).
 CC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 CC Saccharomycetaceae; Pichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NRRL Y-11430;
 RX MEDLINE; 99034033.
 RA Cosano I.C., Alvarez P., Molina M., Nombela C.;
 RT "Cloning and sequence analysis of the Pichia pastoris TRP1, IPP1 and
 RT HIS3 genes.";
 RL Yeast 14:861-867(1998).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; AJ001000; CAA04453.1; -.

DR HSSP; P00817; 1WGI.
 DR PROSITE; PS00387; PPASE; 1.
 DR PFAM; PF00719; Pyrophosphatase; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 284 AA; 31937 MW; 3DAD27970D7775D6 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 284;
 Best Local Similarity 83.3%; Pred. No. 23;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
 DB 91 HNYGAF 96
 |||||

RESULT 5
 ID IPYR_KLULA STANDARD; PRT; 286 AA.
 AC P13998;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI OR IPP.
 OS Kluuyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Kluuyveromyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89189093.
 RA Stark M.J.R., Milner J.S.;
 RT "Cloning and analysis of the Kluuyveromyces lactis TRP1 gene: a
 RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
 RT and histone H3";
 RL Yeast 5:35-50(1989).
 RN [2]
 RP SIMILARITY TO E.COLI AND YEAST PPASES.
 RX MEDLINE; 90254161.
 RA Lahiri R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RT "Conservation of functional residues between yeast and E. coli
 RT inorganic pyrophosphatases";
 RL Biochim. Biophys. Acta 1038:338-345(1990).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O -> 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC -1- MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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DR EMBL; X14230; CAA32446.1; -.
 DR PIR; S07894; PWVL.
 DR HSSP; P00817; 1WGI.
 DR PROSITE; PS00387; PPASE; 1.
 DR PFAM; PF00719; Pyrophosphatase; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 286 AA; 32034 MW; 11647FA4B9D916A2F CRC64;

Query Match 60.7%; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 23;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
 DB 91 HNYGAF 96
 |||||

RESULT 6
 ID IPYR_YEAST STANDARD; PRT; 286 AA.
 AC P00817;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI OR PPAL OR PPA OR YBR011C OR YBR0202.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-X2180;
 RX MEDLINE; 89083474.
 RA Kolakowski L.F. Jr., Schloesser M., Cooperman B.S.;
 RT "Cloning, molecular characterization and chromosome localization of
 RT the inorganic pyrophosphatase (PPA) gene from S. cerevisiae";
 RL Nucleic Acids Res. 16:10441-10452(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C;
 RA Entian K.-D., Koetter P., Rose M., Li Z., Thermann R., Brendel M.,
 RA Baur A., Boles E., Miosga T., Schaaff-Gerstenschlaeger I.,
 RA Zimmermann F.K.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE.
 RX MEDLINE; 78087552.
 RA Cohen S.A., Sterner R., Keim P.S., Heinrichson R.L.;
 RT "Covalent structural analysis of yeast inorganic pyrophosphatase";
 RL J. Biol. Chem. 253:889-897(1978).
 RN [4]
 RP SEQUENCE OF 25-35 AND 239-251.
 RC STRAIN-S288C;
 RX MEDLINE; 95203288.
 RA Garrels J.I., Fitcher B., Kobayashi R., Latter G.I., Schwender B.,
 RA Volpe T., Warner J.R., McLaughlin C.S.;
 RT "Protein identifications for a Saccharomyces cerevisiae protein
 RT database";
 RL Electrophoresis 15:1466-1486(1994).
 RN [5]
 RP SEQUENCE OF 239-249.
 RC STRAIN-ATCC 38531 / Y41;
 RX MEDLINE; 97089742.
 RA Norbeck J., Blomberg A.;
 RT "Protein expression during exponential growth in 0.7 M NaCl medium of
 RT Saccharomyces cerevisiae";
 RL FEMS Microbiol. Lett. 137:1-8(1996).
 RN [6]
 RP ACTIVE SITE.
 RX MEDLINE; 80109718.
 RA Bond M.W., Chiu N.Y., Cooperman B.S.;
 RT "Identification of an arginine important for enzymatic activity
 RT within the covalent structure of yeast inorganic pyrophosphatase";
 RL Biochemistry 19:94-102(1980).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RA Arutunian E.G., Terzian S.S., Voronova A.A., Kuranova I.P.,
 RA Smirnova E.A., Vainstein B.K., Hohne W.E., Hansen G.;

RT "X-ray diffraction study of inorganic pyrophosphatase from baker's
 RL yeast at the 3-A resolution.";
 RL Dokl. Akad. Nauk SSSR 258:1481-1492(1981).
 [8]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE; 97148342.
 RA Heikinheimo P., Lehtonen J., Baykov A., Lahti R., Cooperman B.S.,
 RA Goldman A.;
 RA "The structural basis for pyrophosphatase catalysis.";
 RT Structure 4:1491-1508(1996).
 RL
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RA Swaminathan K., Cooperman B.S., Lahti R., Voet D.;
 RL Submitted (DEC-1997) to the PDB data bank.
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF MUTANTS LYS-78 AND LYS-117.
 RX MEDLINE; 99096888.
 RA Tuominen V., Heikinheimo P., Kajander T., Torkkel T., Hyytia T.,
 RA Kapyla J., Lahti R., Cooperman B.S., Goldman A.;
 RA "The R78K and D117E active-site variants of Saccharomyces cerevisiae
 soluble inorganic pyrophosphatase: structural studies and mechanistic
 RT implications.";
 RL J. Mol. Biol. 284:1565-1580(1998).
 RN [11]
 RP SIMILARITY TO E.COLI AND K.LACTIS PPASES.
 RX MEDLINE; 90254161.
 RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RA "Conservation of functional residues between yeast and E. coli
 RT inorganic pyrophosphatases.";
 RL Biochim. Biophys. Acta 1038:338-345(1990).
 CC -|- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -|- COPACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY. IT BINDS UP TO 4 DIVALENT
 CC CATIONS PER SUBUNIT, WITH THREE REQUIRED FOR ACTIVITY.
 CC -|- SUBUNIT: HOMODIMER.
 CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -|- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X13253; CAA31629.1; -;
 DR EMBL; Z35880; CAA84949.1; -;
 DR PIR; SA5864; PWBY.
 DR PDB; 1PYP; 15-OCT-91.
 DR PDB; 1YPP; 07-DEC-96.
 DR PDB; 1WGI; 19-NOV-97.
 DR PDB; 1WJG; 19-NOV-97.
 DR PDB; 1HUJ; 08-APR-98.
 DR PDB; 1HUK; 08-APR-98.
 DR PDB; 117E; 23-DEC-98.
 DR PDB; 8PRK; 23-DEC-98.
 DR SWISS-2DPAGE; P00817; YEAST.
 DR YEPD; 7305; -;
 DR SGD; L0000872; IPPI.
 DR PROSITE; PS00387; PPASE; 1.
 DR PFAM; PF00719; Pyrophosphatase; 1.
 KW Hydroxylase; Magnesium; 3D-structure.
 FT INIT_MET 0
 FT ACT_SITE 56 56 PROBABLE
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE.
 FT CONFLICT 40 40 N -> D (IN REF. 3).
 FT CONFLICT 71 71 D -> N (IN REF. 3).
 FT CONFLICT 74 74 MISSING (IN REF. 3).
 FT CONFLICT 123 123 E -> Q (IN REF. 3).
 FT CONFLICT 136 136 Q -> E (IN REF. 3).
 FT CONFLICT 186 186 N -> D (IN REF. 3).

FT CONFLICT 224 224 D -> N (IN REF. 3).
 FT CONFLICT 266 266 L -> P (IN REF. 2).
 FT STRAND 4 7
 FT STRAND 16 20
 FT STRAND 25 25
 FT TURN 28 30
 FT TURN 38 41
 FT STRAND 45 45
 FT STRAND 55 55
 FT STRAND 79 79
 FT TURN 97 98
 FT TURN 111 112
 FT STRAND 121 123
 FT TURN 131 132
 FT STRAND 135 135
 FT STRAND 138 146
 FT STRAND 151 158
 FT TURN 160 161
 FT TURN 165 167
 FT HELIX 172 175
 FT TURN 176 177
 FT TURN 179 180
 FT HELIX 182 197
 FT STRAND 203 203
 FT HELIX 205 207
 FT STRAND 210 210
 FT HELIX 212 230
 FT TURN 231 231
 FT TURN 245 246
 FT TURN 248 249
 FT TURN 251 252
 FT TURN 255 260
 FT TURN 274 275
 SQ SEQUENCE 286 AA; 32184 MW; F29390260B60C8B2 CRC64;
 Query Match 60.7%; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 23;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HNYGSF 8
 DB 91 HNYGAF 96
 RESULT 7
 METK_ECOLI
 ID METK_ECOLI STANDARD; PRT; 384 AA.
 AC P04384; P30869;
 DT 20-MAR-1987 (Rel. 04, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE
 DE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).
 GN METK OR METX.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 85054924.
 RA Markham G.D., Deparasis J., Gatmaitan J.;
 RT "The sequence of metk, the structural gene for S-adenosylmethionine
 RT synthetase in Escherichia coli.";
 RL J. Biol. Chem. 259:14505-14507(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN-K12 / MG1655;
 RX MEDLINE; 97426617.
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;

RT "The complete genome sequence of Escherichia coli K-12.;"
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE; 94049123.
RA Satishchandran C., Taylor J.C., Markham G.D.;
RT "Isotypes of S-adenosylmethionine synthetase are encoded by tandemly
RT duplicated genes in Escherichia coli.;"
RL Mol. Microbiol. 9:835-846(1993).
RN [4]
RP SEQUENCE OF 1-63 FROM N.A.
RX MEDLINE; 90330576.
RA Moore R.C., Boyle S.M.;
RT "Nucleotide sequence and analysis of the speA gene encoding
RT biosynthetic arginine decarboxylase in Escherichia coli.;"
RL J. Bacteriol. 172:4631-4640(1990).
RN [5]
RP X-RAY CRYSTALLOGRAPHY.
RX MEDLINE; 96132894.
RA Takusagawa F., Kamitori S., Misaki S., Markham G.D.;
RT "Crystal structure of S-adenosylmethionine synthetase.;"
RL J. Biol. Chem. 271:136-147(1995).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).
RX MEDLINE; 96180683.
RA Takusagawa F., Kamitori S., Markham G.D.;
RT "Structure and function of S-adenosylmethionine synthetase: crystal
RT structures of S-adenosylmethionine synthetase with ADP, BrADP, and
RT PPI at 2.8-A resolution.;"
RL Biochemistry 35:2586-2596(1996).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS).
RX MEDLINE; 96304769.
RA Fu Z., Hu Y., Markham G.D., Takusagawa F.;
RT "Flexible loop in the structure of S-adenosylmethionine synthetase
RT crystallized in the tetragonal modification.;"
RL J. Biomol. Struct. Dyn. 13:727-739(1996).
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE +
CC PYROPHOSPHATE + S-ADENOSYLMETHIONINE.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SUBUNIT: HOMOTETRAMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -1- CAUTION: WAS ORIGINALLY (REF.3) THOUGHT TO DIFFER FROM METX THAT
CC WAS ASSIGNED TO BE A SECOND ADOMET SYNTHETASE BEFORE BEING SHOWN
CC TO BE IDENTICAL TO METK.
CC -----
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CC -----
DR EMBL; K02129; AAA24164.1; -
DR EMBL; U28377; AAA69109.1; -
DR EMBL; AF000377; AAC75979.1; -
DR EMBL; M98266; AAB05197.1; -
DR EMBL; M31770; AAA24645.1; -
DR FIC; A00590; SYECSM.
DR PDB; 1MXA; 11-JUL-96.
DR PDB; 1MXB; 11-JUL-96.
DR PDB; 1MXC; 11-JUL-96.
DR PDB; 1FUG; 01-AUG-96.
DR PDB; 1XRA; 08-MAR-96.
DR PDB; 1XRB; 08-MAR-96.
DR PDB; 1XRC; 08-MAR-96.
DR SWISS-2DPAGE; P04384; COLI.
DR ECO2DBASE; C044.6; 6TH EDITION.

DR ECGENE; EG10589; METK.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
DR PFAM; PF00438; S-AdoMet_synt; 1.
KW Transferase; One-carbon metabolism; ATP-binding; 3D-structure.
FT NP_BIND 116 121 ATP (POTENTIAL).
FT BINDING 144 144 ATP (POTENTIAL).
FT CONFLICT 50 61 MVLVGGEITTSA -> IGFSWRRNHQRP (IN REF.
FT 1 AND 4).
FT CONFLICT 123 133 MFGVATNETDV -> DVSATOLMKPTC (IN REF. 1).
FT CONFLICT 159 161 PWL -> RV (IN REF. 1 AND 3).
FT CONFLICT 172 172 Q -> S (IN REF. 1).
FT CONFLICT 252 252 Y -> T (IN REF. 1).
FT CONFLICT 305 305 V -> L (IN REF. 1).
FT CONFLICT 337 337 MISSING (IN REF. 1).
FT CONFLICT 339 339 Y -> I (IN REF. 1).
FT CONFLICT 375 376 QL -> HV (IN REF. 3).
FT CONFLICT 378 378 R -> P (IN REF. 3).
SQ SEQUENCE 384 AA; 41951 MW; 97FA8CF17B542941 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 384;
Best Local Similarity 60.0%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAG 10
Db 256 ARHGGGAFSG 265
||| |:
METK_HAEIN STANDARD; PRT; 384 AA.
ID METK_HAEIN
AC P43762;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE
DE ADENOSYLTTRANSFERASE) (ADOMET SYNTHETASE).
GN METK OR HILL172.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20;
RX MEDLINE; 95350630.
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus
RT influenzae Rd.;"
RL Science 269:496-512(1995).
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE +
CC PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; U32797; AAC22825.1; -
DR HSSP; P04384; 1FUG.
DR TIGR; H1172; -
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
DR PFAM; PF00438; S-Carbon synt; 1.
KW Transferase; One-carbon metabolism; ATP-binding.
NP_BIND 116 121 ATP (POTENTIAL).
FT BINDING 144 144 ATP (POTENTIAL).
SQ SEQUENCE 384 AA; 41973 MW; 354F873092C331B7 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 384;
Best Local Similarity 60.0%; Pred. No. 31;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSPAG 10
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DB 256 ARHGGAFSG 265

RESULT 9
PEXD_YEAST
ID PEXD_YEAST STANDARD; PRT; 386 AA.
AC P80667;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PEROXISOMAL MEMBRANE PROTEIN PAS20 (PEROXIN-13).
GN PEX13 OR PAS20 OR YLR191W OR L9470.1.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97011156.
RA Elgerema Y., Kwast L., Klein A., Voorn-Brouwer T., van den Berg M.,
RA Tabak H.F., Distel B.;
RT "The SH3 domain of the Saccharomyces cerevisiae peroxisomal membrane
RT protein Pex13p functions as a docking site for pex5p, a mobile
RT receptor for the import pex1-containing proteins.";
RL J. Cell Biol. 135:97-109(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C / AB972;
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
RA Favell A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
RA Miller N., Nhan M., Pauley A., Peluso D., Rifkin L., Riles L.,
RA Taich A., Trevasakis E., Vignati D., Wilcox L., Wohlman P., Vaudin M.,
RA Wilson R., Waterston R.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PARTIAL SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=S288C;
RX MEDLINE; 97011157.
RA Erdmann R., Blobel G.;
RT "Identification of Pex13p a peroxisomal membrane receptor for the
RT PPS1 recognition factor.";
RL J. Cell Biol. 135:111-121(1996).
CC -1- FUNCTION: COMPONENT OF THE PEROXISOMAL TRANSLLOCATION MACHINERY
CC WITH PEX14 AND PEX17. INTERACTS WITH THE PPS1 RECEPTOR
CC (PAS10/PEX5)
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PEROXISOMAL.
CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
CC -----
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CC -----
DR EMBL; S82971; AAB46885.1; -
DR EMBL; U37420; AAB79308.1; -
DR EMBL; U17246; AAB67453.1; -
DR EMBL; U14913; AAB67448.1; -
DR HSSP; Q06187; 1AWK.
DR SGD; L0003024; PAS20.
DR PRINTS; PR00452; SH3DOMAIN.
DR PROSITE; PS50002; SH3; 1.
DR PFAM; PF00018; SH3; 1.
KW Peroxisome; Transport; Protein transport; Transmembrane; SH3 domain.
FT DOMAIN 1 263 LUMENAL (POTENTIAL).
FT TRANSMEM 264 280 POTENTIAL.
FT DOMAIN 281 386 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 306 372 SH3.
SQ SEQUENCE 386 AA; 42706 MW; DBEA9A2372185860 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 386;
Best Local Similarity 75.0%; Pred. No. 32;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSPAG 10
   :|||||
DB 117 NNYGSPYG 124

RESULT 10
METK_BACSU
ID METK_BACSU STANDARD; PRT; 400 AA.
AC P54419; O34566;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE
DE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).
GN METK OR METE.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Bacillus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168 / PY79;
RX MEDLINE; 96345628.
RA Vocum R., Perkins J.B., Howitt C.L., Pero J.;
RT "Cloning and characterization of the metE gene encoding S-
RT adenosylmethionine synthetase from Bacillus subtilis.";
RL J. Bacteriol. 178:4604-4610(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98048467.
RA Lapidus A., Galleron N., Sorokin A., Ehrlich S.D.;
RT "Sequencing and functional annotation of the Bacillus subtilis genes
RT in the 200 kb rnb-dnaB region.";
RL Microbiology 143:3431-3441(1997).
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP.
CC -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE +
CC PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC -----
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CC EMBL; U52812; AAB17066.1; -.
CC EMBL; AF008220; AAC0242.1; -.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR EMBL; Z99119; CAB15033.1; -.
DR HSSP; P04384; IXRC.
DR SUBTILIST; BG11840; METK.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
DR PFAM; PF00438; S-AdoMet_synt; 1.
KW Transferase; One-carbon metabolism; ATP-binding.
FT NP_BIND 129 134 ATP (POTENTIAL).
FT BINDING 157 157 ATP (POTENTIAL).
FT CONFLICT 26 26 S -> Y (IN REF. 1).
FT CONFLICT 111 111 Q -> P (IN REF. 1).
FT CONFLICT 140 140 A -> V (IN REF. 1).
SQ SEQUENCE 400 AA; 44042 MW; EF3D97DCD375714A CRC64;

Query Match 60.7%; Score 34; DB 1; Length 400;
Best Local Similarity 60.0%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFAG 10
Db 270 ARHGGGAFSG 279

RESULT 11
METK_MYCTU
ID METK_MYCTU STANDARD; PRT; 403 AA.
AC P77899;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE S-ADENOSYLMETHIONINE SYNTHETASE (EC 2.5.1.6) (METHIONINE
DE ADENOSYLTRANSFERASE) (ADOMET SYNTHETASE).
GN METK OR RV1392 OR MTCY21B4.09.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
[1]
RN SEQUENCE FROM N.A.
RC STRAIN-H37RV;
RX MEDLINE; 98295987.
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jorgels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E.,
RA Taylor K., Whitehead S., Barrell B.G.;
RT Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544 (1998).
CC -1- FUNCTION: CATALYZES THE FORMATION OF S-ADENOSYLMETHIONINE FROM
CC METHIONINE AND ATP (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + L-METHIONINE + H(2)O = ORTHOPHOSPHATE +
CC PYROPHOSPHATE + S-ADENOSYL-L-METHIONINE.
CC -1- PATHWAY: ACTIVATED METHYL CYCLE.
CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ADOMET SYNTHETASE FAMILY.
CC
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CC EMBL; Z80108; CAB02194.1; -.
DR HSSP; P04384; IXRC.
DR PROSITE; PS00376; ADOMET_SYNTHETASE_1; 1.
DR PROSITE; PS00377; ADOMET_SYNTHETASE_2; 1.
DR PFAM; PF00438; S-AdoMet_synt; 1.
DR TUBERCULIST; RV1392; -.
KW Transferase; One-carbon metabolism; ATP-binding.
FT NP_BIND 131 136 ATP (BY SIMILARITY).
SQ SEQUENCE 403 AA; 43046 MW; 2E18BF05D8267972 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 403;
Best Local Similarity 60.0%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFAG 10
Db 276 ARHGGGAFSG 285

RESULT 12
BAP2_YEAST
ID BAP2_YEAST STANDARD; PRT; 609 AA.
AC P38084;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE LEU/VAL/ILE AMINO-ACID PERMEASE (BRANCHED-CHAIN AMINO-ACID PERMEASE
DE 2).
GN BAP2 OR YBR068C OR YBR0629.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN SEQUENCE FROM N.A.
RC STRAIN-S288C;
RL Domdey H., Gassenhuber H., Obermaier B., Piravandi E.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN SEQUENCE OF 604-609 FROM N.A.
RC STRAIN-S288C;
RA Feldmann H., Mannhaupt G., Schwarzlose C., Vetter I.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RX MEDLINE; 96096693.
RA Grauslund M., Didion T., Klelland-Brandt M.C., Andersen H.A.;
RT "BAP2, a gene encoding a permease for branched-chain amino acids in
RT Saccharomyces cerevisiae."
RL Biochim. Biophys. Acta 1269:275-280 (1995).
CC -1- FUNCTION: AMINO ACID PERMEASE FOR LEUCINE, VALINE AND ISOLEUCINE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.
CC
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CC EMBL; Z35937; CAA85012.1; -.
DR PIR; S45930; S45930.
DR SGD; L0003157; BAP2.
DR PROSITE; PS00218; AMINO_ACID_PERMEASE; 1.
DR PFAM; PF00324; aa_permeases; 1.
KW Transport; Amino-acid transport; Transmembrane.
FT TRANSMEM 100 120 POTENTIAL.
FT TRANSMEM 124 144 POTENTIAL.
FT TRANSMEM 174 194 POTENTIAL.
FT TRANSMEM 211 231 POTENTIAL.

Query Match 60.7%; Score 34; DB 1; Length 403;
Best Local Similarity 60.0%; Pred. No. 33;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFAG 10
Db 276 ARHGGGAFSG 285

RESULT 12
BAP2_YEAST
ID BAP2_YEAST STANDARD; PRT; 609 AA.
AC P38084;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE LEU/VAL/ILE AMINO-ACID PERMEASE (BRANCHED-CHAIN AMINO-ACID PERMEASE
DE 2).
GN BAP2 OR YBR068C OR YBR0629.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN SEQUENCE FROM N.A.
RC STRAIN-S288C;
RL Domdey H., Gassenhuber H., Obermaier B., Piravandi E.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN SEQUENCE OF 604-609 FROM N.A.
RC STRAIN-S288C;
RA Feldmann H., Mannhaupt G., Schwarzlose C., Vetter I.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RX MEDLINE; 96096693.
RA Grauslund M., Didion T., Klelland-Brandt M.C., Andersen H.A.;
RT "BAP2, a gene encoding a permease for branched-chain amino acids in
RT Saccharomyces cerevisiae."
RL Biochim. Biophys. Acta 1269:275-280 (1995).
CC -1- FUNCTION: AMINO ACID PERMEASE FOR LEUCINE, VALINE AND ISOLEUCINE.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
CC -1- SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.
CC
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FT TRANSMEM 236 256 POTENTIAL.
FT TRANSMEM 290 310 POTENTIAL.
FT TRANSMEM 329 349 POTENTIAL.
FT TRANSMEM 375 395 POTENTIAL.
FT TRANSMEM 428 448 POTENTIAL.
FT TRANSMEM 452 472 POTENTIAL.
FT TRANSMEM 501 521 POTENTIAL.
FT TRANSMEM 537 557 POTENTIAL.
SQ SEQUENCE 609 AA; 67670 MW; 02249C5F744E16E5 CRC64;

Query Match 60.7%; Score 34; DB 1; Length 609;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFAG 10
|||:||||
Db 273 HNPAGFAG 280

RESULT 13
ST20_YEAST STANDARD; PRT; 939 AA.
AC Q03497;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE SERINE/THREONINE-PROTEIN KINASE STE20 (EC 2.7.1.-).
GN STE20 OR YHL007C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93099855.
RA Leberer E., Dignard D., Harscus D., Thomas D.Y., Whiteway M.;
RT "The protein kinase homologue Ste20p is required to link the yeast
RT pheromone response G-protein beta gamma subunits to downstream
RT signalling components."
RL EMO J. 11:4815-4824(1992).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93133807.
RA Ramer S.W., Davis R.W.;
RT "A dominant truncation allele identifies a gene, STE20, that encodes
RT a putative protein kinase necessary for mating in Saccharomyces
RT cerevisiae."
RL Proc. Natl. Acad. Sci. U.S.A. 90:452-456(1993).
[3]
RP SEQUENCE FROM N.A.
RX STRAIN-S288C / AB972;
RX MEDLINE; 94378003.
RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J.,
RA Du Z., Favell A., Fulton L., Gattung S., Geisel C., Kirsten J.,
RA Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
RA Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
RA Nham M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K.,
RA Vignati D., Wilcox L., Wohlman P., Waterston R., Willson R.,
RA Vaudin M.;
RT "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
RT VIII."
RL Science 265:2077-2082(1994).
CC -1- FUNCTION: REQUIRED TO LINK THE PHEROMONE RESPONSE G-PROTEIN BETA
CC GAMMA SUBUNITS TO DOWNSTREAM SIGNALING COMPONENTS. IT IS THOUGHT
CC THAT IT CAN PHOSPHORYLATE STE5. NEEDED FOR MATING IN HAPLOID
CC CELLS. INDUCTION OF A MATING-SPECIFIC GENE FUS1, INDUCTION OF
CC MATING-SPECIFIC MORPHOLOGIES, AND PHEROMONE-INDUCED PROLIFERATION
CC ARREST. PHOSPHORYLATES STE11.
CC -1- PATHWAY: RESPONSE TO PHEROMONE-INDUCED SIGNAL.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- PTM: AUTOPHOSPHORYLATED ON SERINE RESIDUES.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC STE20 SUBFAMILY.
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EMBL; M94719; AAA35111.1; -
EMBL; L04655; AAA35038.1; -
EMBL; L04655; AAA35039.1; -
EMBL; U11581; AAB69747.1; -
PIR; S28394; S28394.
PIR; S46821; S46821.
HSP; Q63450; 1A06.
SGD; L0002123; STE20.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
DR PFAM; PF00069; kinase; 1.
DR PFAM; PF00786; PBD; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphomonoesterase; Phosphorylation.
KW DOMAIN 95 REGULATORY.
FT DOMAIN 620 871 PROTEIN KINASE.
FT NP_BIND 626 634 ATP (BY SIMILARITY).
FT BINDING 649 649 ATP (BY SIMILARITY).
FT ACT_SITE 739 739 BY SIMILARITY.
FT CONFLICT 19 19 N -> S (IN REF. 2).
FT CONFLICT 134 134 I -> M (IN REF. 2).
FT CONFLICT 271 271 P -> S (IN REF. 2).
SQ SEQUENCE 939 AA; 102362 MW; 69C1C12F5B87733C CRC64;

Query Match 60.7%; Score 34; DB 1; Length 939;
Best Local Similarity 75.0%; Pred. No. 78;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFAG 10
|||||
Db 440 HNYGSRTG 447

RESULT 14
HB2P_RABIT STANDARD; PRT; 257 AA.
ID HB2P_RABIT
AC P20756;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE RLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DP BETA CHAIN PRECURSOR (D10
DE HAPLOTYPE).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 88199085.
RA Sittisombut N., Mordacq J., Knight K.L.;
RT "Rabbit MHC. II. Sequence analysis of the R-DP alpha- and
RT beta-genes."
RL J. Immunol. 140:3237-3243(1988).
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EMBL; M21468; AAA31393.1; -

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RP SEQUENCE OF 1-12.
RC STRAIN-K12 / EMG2.
RX MEDLINE; 9743975.
RA Link A.J., Robison K., Church G.M.:
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of Escherichia coli K-12.";
RL Electrophoresis 18:1259-1313(1997).
CC -1- FUNCTION: INVOLVED IN FORMATION OF THE ROD SHAPE OF THE CELL. MAY
CC ACT AS A NEGATIVE REGULATOR OF FTSI.
CC -1- SIMILARITY: BELONGS TO THE FTSA/MREB FAMILY.
CC -----
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CC -----
CC EMBL; M22055; AAA83891.1; -.
CC EMBL; U18997; AAA58054.1; ALT_INIT.
CC EMBL; AE000404; AAC76283.1; ALT_INIT.
CC EMBL; M31792; AAA24154.1; -.
CC PIR; A31843; BVCECB.
CC ECGENE; EG10608; MREB.
CC Cell shape.
KW CONFLICT 60 61 KQ -> NE (IN REF. 1).
FT CONFLICT 265 265 T -> I (IN REF. 1).
FT CONFLICT 277 278 QC -> HT (IN REF. 1).
SQ SEQUENCE 347 AA; 36952 MW; 1393696D8CDAEF93 CRC64;

Query Match 58.9%; Score 33; DB 1; Length 347;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 RHNYSFAG 10
DB 203 RNYGSLIG 211
{|||||I

Search completed: May 27, 2000, 20:07:19
Job time: 991 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:38:42 ; Search time 199.56 Seconds
(without alignments)
3.474 Million cell updates/sec

Title: US-09-016-061-78
Perfect score: 56
Sequence: 1 ARHNGSFAG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SPTREMBL12.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_prodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	69.6	446	5	O62086 caenorhabdi
2	38	67.9	89	7	O19495 gallus gall
3	38	67.9	697	3	O74504 schizosacch
4	36	64.3	39	7	P79474 cervus elap
5	36	64.3	39	7	P79477 cervus elap
6	36	64.3	39	7	P79478 cervus elap
7	36	64.3	39	7	P79479 cervus elap
8	36	64.3	78	6	O97835 ovis aries
9	36	64.3	78	6	O97839 ovis aries
10	36	64.3	78	6	O97844 ovis aries
11	36	64.3	78	6	O97968 ovis aries
12	36	64.3	79	7	O19191 prionailuru
13	36	64.3	79	7	O19192 prionailuru
14	36	64.3	79	7	O19380 felis silve
15	36	64.3	79	7	O19381 felis silve
16	36	64.3	79	7	O19382 felis silve
17	36	64.3	79	7	O19396 felis silve
18	36	64.3	79	7	O19397 felis silve
19	36	64.3	79	7	O19405 felis silve
20	36	64.3	79	7	O19406 felis silve

21	36	64.3	79	7	O19407 felis silve
22	36	64.3	79	7	O19408 felis silve
23	36	64.3	79	7	O19435 felis silve
24	36	64.3	81	7	O30568 macaca fasc
25	36	64.3	81	7	O30571 macaca fasc
26	36	64.3	81	7	O30737 macaca neme
27	36	64.3	81	7	O30739 macaca neme
28	36	64.3	81	7	O30563 macaca fasc
29	36	64.3	81	7	O30740 macaca neme
30	36	64.3	82	7	O95598 phasianus c
31	36	64.3	82	7	O30606 macaca mula
32	36	64.3	82	7	O30608 macaca mula
33	36	64.3	82	7	O30637 macaca mula
34	36	64.3	82	7	O30638 macaca mula
35	36	64.3	82	7	O30658 macaca mula
36	36	64.3	82	7	O30659 macaca mula
37	36	64.3	82	7	O30666 macaca mula
38	36	64.3	82	7	O30667 macaca mula
39	36	64.3	82	7	O30668 macaca mula
40	36	64.3	82	7	O19287 macaca mula
41	36	64.3	82	7	O19288 macaca mula
42	36	64.3	83	7	O98002 ovis aries
43	36	64.3	83	7	O9XS06 odocolleus
44	36	64.3	83	7	O9XR25 odocolleus
45	36	64.3	83	7	O9XR24 odocolleus

ALIGNMENTS

RESULT 1
O62086 PRELIMINARY; PRT; 446 AA.
ID O62086
AC O62086;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JAN-1999 (TREMBLrel. 09, Last annotation update)
DE C3IH5.6 PROTEIN.
GN C3IH5.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RA KERSHAW J.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HARKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LATSTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans.";
RL Nature 368:32-38(1994).
DR EMBL; 293778; CAB07846.1; -.
SQ SEQUENCE 446 AA; 50763 MW; B347C0C8 CRC32;

Query Match 69.6%; Score 39; DB 5; Length 446;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYSFA 9
| | | | |

Db 51 RHNYSFA 58

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RESULT 2
O19495 PRELIMINARY; PRT; 89 AA.
AC O19495;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JAN-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS II BETA 1 DOMAIN (FRAGMENT).
GN B-LBI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-15.151-5; TISSUE-BURSA;
RA PHARR G.T., DODGSON J.B., HUNT H.D., BACON L.D.;
RL Immunogenetics 47:350-354(1998).
DR EMBL; U91532; AAC15813.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 89
SQ SEQUENCE 89 AA; 10724 MW; FDAG6024 CRC32;

Query Match 67.9%; Score 38; DB 7; Length 89;
Best Local Similarity 85.7%; Pred. No. 3.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 75 RHNYGDF 81

RESULT 3
O74504 PRELIMINARY; PRT; 697 AA.
AC O74504;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE HYPOTHETICAL 77.8 KD PROTEIN (FRAGMENT).
GN SPC594.01.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Archiascomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-972H-;
RA RIEGER M., LYNE M., RAJANDREAM M.A., BARRELL B.G.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL031523; CAA20660.1; -.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 697 AA; 77841 MW; 9BC8CB3F CRC32;

Query Match 67.9%; Score 38; DB 3; Length 697;
Best Local Similarity 77.8%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAG 10
Db 155 RHNYGSFAG 163

RESULT 4
P79474 PRELIMINARY; PRT; 39 AA.
AC P79474;

DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
OC Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.
RA SWARBRICK P.A., CRAWFORD A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63077; AAB37777.1; -.
KW MHC.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4767 MW; E01AA287 CRC32;

Query Match 64.3%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 3.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 5
P79477 PRELIMINARY; PRT; 39 AA.
AC P79477;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
OC Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.
RA SWARBRICK P.A., CRAWFORD A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63080; AAB37780.1; -.
KW MHC.
FT NON_TER 1
FT NON_TER 39
SQ SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match 64.3%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 3.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 6
P79478 PRELIMINARY; PRT; 39 AA.
AC P79478;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
OC Cervinae; Cervus.
RN [1]

```


RP SEQUENCE FROM N.A.
 RA SWARBRICK P.A., CRAWFORD A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63081; AAB37781.1; -.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4806 MW; 4984754A CRC32;

Query Match 64.3%; Score 36; DB 7; Length 39;
 Best Local Similarity 85.7%; Pred. No. 3.5;
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

OY 2 RHNYGSF 8
 Db 25 RHNYGVF 31

RESULT 7
 ID P79479 PRELIMINARY; PRT; 39 AA.
 AC P79479;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
 OC Cervinae; Cervus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SWARBRICK P.A., CRAWFORD A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63082; AAB37782.1; -.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4806 MW; 4984754A CRC32;

Query Match 64.3%; Score 36; DB 7; Length 39;
 Best Local Similarity 85.7%; Pred. No. 3.5;
 Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

OY 2 RHNYGSF 8
 Db 25 RHNYGVF 31

RESULT 8
 ID O97835 PRELIMINARY; PRT; 78 AA.
 AC O97835;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
 GN OLA-DRB1*N20.2
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae; Bovidae;
 OC Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=7407; TISSUE=BLOOD;
 RA AIDA Y.;
 RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017207; BAA36764.1; -.
 FT NON_TER 1 1
 FT NON_TER 78 78

SQ SEQUENCE 78 AA; 9677 MW; D2252D9D CRC32;
 Query Match 64.3%; Score 36; DB 6; Length 78;
 Best Local Similarity 85.7%; Pred. No. 7.2;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 RHNYGSF 8
 Db 72 RHNYGVF 78

RESULT 9
 ID O97839 PRELIMINARY; PRT; 78 AA.
 AC O97839;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
 GN OLA-DRB1*N2.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae; Bovidae;
 OC Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SUFFOLK BREED AND CORRIDALE BREED; TISSUE=BLOOD;
 RA AIDA Y.;
 RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017212; BAA36769.1; -.
 FT NON_TER 1 1
 FT NON_TER 78 78
 SQ SEQUENCE 78 AA; 9430 MW; 2883C99C CRC32;

Query Match 64.3%; Score 36; DB 6; Length 78;
 Best Local Similarity 85.7%; Pred. No. 7.2;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 RHNYGSF 8
 Db 72 RHNYGVF 78

RESULT 10
 ID O97844 PRELIMINARY; PRT; 78 AA.
 AC O97844;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
 GN OLA-DRB1*N8.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae; Bovidae;
 OC Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SUFFOLK BREED; TISSUE=BLOOD;
 RA AIDA Y.;
 RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017220; BAA36777.1; -.
 FT NON_TER 1 1
 FT NON_TER 78 78
 SQ SEQUENCE 78 AA; 9645 MW; 0A246905 CRC32;

Query Match 64.3%; Score 36; DB 6; Length 78;
 Best Local Similarity 85.7%; Pred. No. 7.2;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

|||||

Db 72 RHNYGVF 78

RESULT 11

O97968

ID O97968 PRELIMINARY; PRT; 78 AA.

AC O97968;

DT 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)

DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).

GN OLA-DRB1*W21.

OS Ovis aries (Sheep).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Caprinae; Ovis.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-VARIOUS STRAINS;

RA AIDA Y.;

RT "Ovis aries DNA for MHC class II DRB1 exon 2.";

RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB017231; BAA36788.1; -.

DR EMBL; AB017204; BAA36761.1; -.

FT NON_TER 1

FT NON_TER 78

SQ SEQUENCE 78 AA; 9436 MW; 72250CEB CRC32;

Query Match

Best Local Similarity 64.3%; Score 36; DB 6; Length 78;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

|||||

Db 72 RHNYGVF 78

RESULT 12

O19191

ID O19191 PRELIMINARY; PRT; 79 AA.

AC O19191;

DT 01-JAN-1998 (TREMBlrel. 05, Created)

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)

DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).

GN MHCMAIR-DRB.

OS Prionailurus bengalensis iriomotensis (Iriomote cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Carnivora; Fissipedia; Felidae; Prionailurus.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 97211851.

RA YUHKI N., O'BRIEN S.J.;

RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB

genes.";

RL J. Immunol. 158:2822-2833(1997).

DR EMBL; U51546; AAB65582.1; -.

DR PFAM; PF00969; MHC_II_beta; 1.

KW MHC.

FT NON_TER 1

FT NON_TER 79

SQ SEQUENCE 79 AA; 9582 MW; 8EEF2C7D CRC32;

Query Match

Best Local Similarity 64.3%; Score 36; DB 7; Length 79;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

|||||

Db 72 RHNYGVF 78

RESULT 13

O19192

ID O19192 PRELIMINARY; PRT; 79 AA.

AC O19192;

DT 01-JAN-1998 (TREMBlrel. 05, Created)

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)

DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).

GN MHCMAIR-DRB.

OS Prionailurus bengalensis iriomotensis (Iriomote cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Carnivora; Fissipedia; Felidae; Prionailurus.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 97211851.

RA YUHKI N., O'BRIEN S.J.;

RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB

genes.";

RL J. Immunol. 158:2822-2833(1997).

DR EMBL; U51547; AAB65583.1; -.

DR PFAM; PF00969; MHC_II_beta; 1.

KW MHC.

FT NON_TER 1

FT NON_TER 79

SQ SEQUENCE 79 AA; 9582 MW; ED9F80F0 CRC32;

Query Match

Best Local Similarity 64.3%; Score 36; DB 7; Length 79;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

|||||

Db 72 RHNYGVF 78

RESULT 14

O19380

ID O19380 PRELIMINARY; PRT; 79 AA.

AC O19380;

DT 01-JAN-1998 (TREMBlrel. 05, Created)

DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)

DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)

DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).

GN MHCPECA-DRB.

OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 97211851.

RA YUHKI N., O'BRIEN S.J.;

RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB

genes.";

RL J. Immunol. 158:2822-2833(1997).

DR EMBL; U51498; AAB65533.1; -.

DR PFAM; PF00969; MHC_II_beta; 1.

KW MHC.

FT NON_TER 1

FT NON_TER 79

SQ SEQUENCE 79 AA; 9659 MW; F352AD23 CRC32;

Query Match

Best Local Similarity 64.3%; Score 36; DB 7; Length 79;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

Db 72 RHNYGVF 78

RESULT 15
O19381
ID O19381 PRELIMINARY; PRT; 79 AA.
AC O19381;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
GN MHCPECA-DRB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97211851.
RA YUHKI N., O'BRIEN S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
genes";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51499; AAB65334.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 9610 MW; 1F7FB873 CRC32;

Query Match 64.3%; Score 36; DB 7; Length 79;
Best Local Similarity 85.7%; Pred. No. 7.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 RHNYGSF 8
Db 72 RHNYGVF 78

Search completed: May 27, 2000, 19:38:42
Job time: 2375 sec

GenCore version 4.5
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_ OM protein - protein search, using sw model

Run on: May 27, 2000, 19:21:37 ; Search time 148.45 Seconds
(without alignments)
1.596 Million cell updates/sec

Title: US-09-016-061-78
Perfect score: 56
Sequence: 1 ARHNYGSFAG 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	10	1 W76029	LM609 grafted anti
2	50	89.3	10	1 W76024	LM609 grafted anti
3	50	89.3	10	1 W76025	LM609 grafted anti
4	50	89.3	10	1 W76026	LM609 grafted anti
5	50	89.3	10	1 W76027	LM609 grafted anti
6	50	89.3	10	1 W76028	LM609 grafted anti
7	50	89.3	10	1 W76030	LM609 grafted anti
8	50	89.3	10	1 W76010	LM609 grafted anti
9	50	89.3	117	1 W76001	Vitaxin antibody h
10	50	89.3	117	1 W76003	LM609 antibody hea
11	47	83.9	10	1 W76021	LM609 grafted anti
12	46	82.1	10	1 W76039	LM609 grafted anti
13	46	82.1	10	1 W76040	LM609 grafted anti
14	46	82.1	10	1 W76022	LM609 grafted anti
15	46	82.1	10	1 W76023	LM609 grafted anti
16	45	80.4	10	1 W76037	LM609 grafted anti
17	45	80.4	10	1 W76020	LM609 grafted anti
18	42	75.0	110	1 W84099	Vitronectin alpha-
19	42	75.0	117	1 W84093	Murine vitronectin
20	42	75.0	117	1 W84097	Humanised anti- α p
21	41	73.2	10	1 W76038	LM609 grafted anti
22	36	64.3	117	1 R79157	Human IgE receptor
23	36	64.3	117	1 R79155	Human IgE receptor
24	36	64.3	117	1 W27357	Heavy chain variab
25	36	64.3	117	1 W27526	Heavy chain variab
26	36	64.3	117	1 W27354	Heavy chain variab
27	36	64.3	119	1 W01578	Lead binding Mab 8
28	36	64.3	239	1 W73874	Human antiFc epsil
29	36	64.3	242	1 W73876	Human antiFc epsil
30	34	60.7	402	1 R54204	snaC gene product
31	34	60.7	412	1 R80060	S-adenosylmethioni
32	33	58.9	80	1 R13396	HLA-DR β 12a antigen
33	33	58.9	80	1 R13397	HUA-DR β 12b antigen
34	33	58.9	304	1 W46807	Endo-beta-1,4-gluc

ALIGNMENTS

RESULT 1

W76029
ID W76029 standard; Protein; 10 AA.
AC W76029;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #11.
KW Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;
KW LM609; inhibitor; Integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49866.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62: Page 41: 129pp: English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation, rheumatoid
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 100.0%; Score 56; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00058;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAG 10

Db 1 ARHNYGSFAG 10

RESULT 2

W76024
ID W76024 standard; Protein; 10 AA.

AC W76024;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #6.

KW Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;

Cellulase polypept
Aspergillus niger
Endo beta-1,4-gluc
Streptomyces sp. t
H. pylori GHP0 146
Peptide sequence #
Synthetic human S1
Chemically synthes
DRI beta chain pos
Immunomodulatory p
VDJ joint protein,

35 33 58.9 331 1 W15563
36 33 58.9 331 1 W14596
37 33 58.9 332 1 W46814
38 33 58.9 407 1 W82683
39 33 58.9 409 1 W98824
40 32 57.1 11 1 W22700
41 32 57.1 15 1 W25799
42 32 57.1 18 1 W27062
43 32 57.1 25 1 R49334
44 32 57.1 25 1 W41656
45 32 57.1 36 1 W03964

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PR 30-JAN-1998; U01826.
 PF 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49861.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region, LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 89.3%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 | | | | | | | |
 Db 1 ARHNYGSFA 9

RESULT 3
 W76025
 ID W76025 standard; Protein; 10 AA.
 AC W76025;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #7.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PR 30-JAN-1998; U01826.
 PF 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49862.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region, LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 89.3%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 | | | | | | | |
 Db 1 ARHNYGSFA 9

RESULT 4
 W76026
 ID W76026 standard; Protein; 10 AA.
 AC W76026;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #8.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PR 30-JAN-1998; U01826.
 PF 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49863.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region, LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 89.3%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 | | | | | | | |
 Db 1 ARHNYGSFA 9

RESULT 5
 W76027
 ID W76027 standard; Protein; 10 AA.

AC W76027;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #9.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49864.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 89.3%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 DB 1 ARHNYGSFA 9

RESULT 6
 W76028
 ID W76028 standard; Protein; 10 AA.
 AC W76028; 129pp; English.
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #10.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49865.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 89.3%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 DB 1 ARHNYGSFA 9

RESULT 7
 W76030
 ID W76030 standard; Protein; 10 AA.
 AC W76030;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #12.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49867.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.

Query Match 89.3%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0061;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 DB 1 ARHNYGSFA 9

```

RESULT 8
W76010
ID W76010 standard; Protein; 10 AA.
AC W76010;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #1.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49847.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Disclosure: Page 40; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 89.3%; Score 50; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0061; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9
|||||

RESULT 9
W76001
ID W76001 standard; Protein; 117 AA.
AC W76001;
DT 02-NOV-1998 (first entry)
DE Vitaxin antibody heavy chain variable region protein fragment.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49820.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 43; Fig 2a; 129pp; English.
CC This sequence represents the LM609 antibody variable heavy chain region.
CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC block integrin-mediated signal transduction. This is useful in the
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
SQ Sequence 117 AA;

Query Match 89.3%; Score 50; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.074; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 ARHNYGSFA 9
Db 97 ARHNYGSFA 105
|||||

RESULT 10
W76003
ID W76003 standard; Protein; 117 AA.
AC W76003;
DT 02-NOV-1998 (first entry)
DE LM609 antibody heavy chain variable region protein fragment.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49822.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 43; Fig 2a; 129pp; English.
CC This sequence represents the LM609 antibody variable heavy chain region.
CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC block integrin-mediated signal transduction. This is useful in the
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
SQ Sequence 117 AA;

Query Match 89.3%; Score 50; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.074; Mismatches 0; Indels 0; Gaps 0;
Matches 9; Conservative 0;

Qy 1 ARHNYGSFA 9
Db 97 ARHNYGSFA 105
|||||

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QY 1 ARHNYGSF 8
Db 1 ARHNYGSF 8

RESULT 14
W76022
ID W76022 standard; Protein; 10 AA.
AC W76022;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #4.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR N-PSDB; V49859.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related nucleic acid, used to treat, prevent or diagnose
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
CC inhibit binding of alphaVbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 82.1%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
Db 1 ARHNYGSF 8

Search completed: May 27, 2000, 19:21:37
Job time: 1591 sec

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Query Match 82.1%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
Db 1 ARHNYGSF 8

RESULT 15
W76023
ID W76023 standard; Protein; 10 AA.
AC W76023;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #5.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:26:46 ; Search time 163.56 Seconds
(without alignments)
3.585 Million cell updates/sec

Title: US-09-016-061-80
Perfect score: 54
Sequence: 1 ARHNYGSFAA 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_63:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	79.6	446	2 T19625	hypothetical prote
2	36	66.7	82	2 I51106	Major Histocompat
3	36	66.7	89	2 S38688	MHC class II histo
4	36	66.7	89	2 S38683	MHC class II histo
5	36	66.7	89	2 S38684	MHC class II histo
6	36	66.7	225	2 I47095	MHC class II OVAR-
7	35	64.8	347	2 S43771	phosphatidylcholin
8	34	63.0	108	2 S26316	Ig heavy chain v r
9	34	63.0	110	2 S26317	Ig heavy chain v r
10	34	63.0	113	2 S26468	Ig heavy chain v r
11	34	63.0	210	1 B69265	conserved hypothet
12	34	63.0	275	2 D71087	probable translati
13	34	63.0	275	2 G75130	translation initia
14	34	63.0	287	1 PBWY	inorganic pyrophos
15	34	63.0	287	1 PWVKL	inorganic pyrophos
16	33	61.1	65	2 S17441	hypothetical prote
17	33	61.1	80	2 I54469	MHC HLA-DR-beta-1
18	33	61.1	80	2 I68777	MHC HLA-DR beta-1
19	33	61.1	81	2 I54550	HLA DRB1*1202 - hu
20	33	61.1	85	2 I59634	MHC class II DR-be
21	33	61.1	89	2 S38676	MHC class II histo
22	33	61.1	89	2 S38680	MHC class II histo
23	33	61.1	89	2 S57512	MHC class II histo
24	33	61.1	123	2 C25239	MHC class II histo
25	33	61.1	167	2 T16454	hypothetical prote
26	33	61.1	200	2 D32526	class II histocomp
27	33	61.1	237	2 C27060	class II histocomp
28	33	61.1	266	2 I54287	gene HLA-DRE1 prot
29	33	61.1	266	2 A27618	class II histocomp
30	33	61.1	266	2 I54295	lymphocyte antigen

ALIGNMENTS

RESULT 1

T19625

hypothetical protein C31H5.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T19625

R:Kershaw, J. submitted to the EMBL Data Library, April 1997

A:Reference number: Z19153

A:Accession: T19625

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-446 <WIL>

A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6

A:Experimental source: Clone C31H5

C:Genetics:

A:Gene: CESP:C31H5.6

A:Map position: 1

A:Introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3

Query Match

Best Local Similarity 79.6%; Score 43; DB 2; Length 446;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSFAA 10

Db 51 RHNYGSFAA 59

RESULT 2

I51106

Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)

C:Species: Phasianus colchicus (ring-necked pheasant)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999

C:Accession: I51106

R:Wittzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.

Immunogenetics 39, 395-403, 1994

A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-ne

A:Reference number: I51103; MUID:94245280

A:Accession: I51106

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: DNA

A:Residues: 1-82 <WIT>

A:Cross-references: EMBL:X75406; NID:q496926; PIDN:CAA53160.1; PID:q496927

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match

Best Local Similarity 66.7%; Score 36; DB 2; Length 82;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

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Db      75 RHNYGVF 81
||||| |
RESULT  3
S38688
MHC class II histocompatibility antigen HLA-DR-08 beta chain - Galago senegalensis (frag
C:Species: Galago senegalensis
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997
C:Accession: S38688
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced f
A:Reference number: S38676
A:Accession: S38688
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27158
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match      66.7%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 4.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 RHNYGSF 8
||||| |
Db      75 RHNYGVF 81

RESULT  6
I47095
MHC class II OVAR-DR-beta-3 - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 23-Jul-1999
C:Accession: I47095
R:Pabb, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.
Anim. Genet. 24, 249-255, 1993
A:Title: Isolation, characterization and evolution of ovine major histocompatibility
A:Reference number: I47075; MUID:94057592
A:Accession: I47095
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-225 <FAB>
A:Cross-references: GB:L04790; NID:9458880; PIDN:AAA16562.1; PID:9458881
C:Genetics:
A:Gene: OVAR-DRB3
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match      66.7%; Score 36; DB 2; Length 225;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 RHNYGSF 8
||||| |
Db      68 RHNYGVF 74

RESULT  7
S43771
phosphatidylcholine desaturase (EC 1.3.1.35) - Synecococcus sp. (strain PCC 7002)
N:Alternate names: Delta-12 desaturase; fatty acid desaturase (EC 1.14.99.-) (misiden
C:Species: Synecococcus sp.
A:Variety: PCC 7002
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 28-May-1999
C:Accession: S43771
R:Sakamoto, T.; Wada, H.; Nishida, I.; Ohmori, M.; Murata, N.
Plant Mol. Biol. 24, 643-650, 1994
A:Title: Identification of conserved domains in the Delta-12 desaturases of cyanobact
A:Reference number: S43770; MUID:94207189
A:Accession: S43771
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-347 <SAK>
A:Cross-references: GB:D13779; NID:9488510; PIDN:BAA02922.1; PID:dl003428; PID:9468851
C:Superfamily: omega-3 fatty acid desaturase
C:Keywords: oxidoreductase

Query Match      64.8%; Score 35; DB 2; Length 347;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 ARHNYGSFA 9
||||| |
Db      334 AEHNYISFA 342

RESULT  8
S26316
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999

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C:Accession: S26316
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
A:Reference number: S26309; MUID:91341421
A:Accession: S26316
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <STA>
A:Cross-references: EMBL:X59190; NID:g52066; PIDN:CAA41900.1; PID:s36170; PID:g1334035
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:2-85/Domain: immunoglobulin homology <IMM>

Query Match 63.0%; Score 34; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
||| |||:
Db 84 ARGNYGNYA 92

RESULT 9
S26317
Ig heavy chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1998 #sequence_revision 19-Mar-1998 #text_change 17-Apr-1998
C:Accession: S26317
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
A:Reference number: S26309; MUID:91341421
A:Accession: S26317
A:Molecule type: mRNA
A:Residues: 1-110 <STA>
A:Cross-references: EMBL:X59186
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 63.0%; Score 34; DB 2; Length 110;
Best Local Similarity 66.7%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
||| |||:
Db 86 ARGNYGNYA 94

RESULT 10
S26468
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26468
R:Kavaler, J.
submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S26468
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <KAV>
A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 63.0%; Score 34; DB 2; Length 113;
Best Local Similarity 60.0%; Pred. No. 13;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFAA 10
||| |||:
Db 93 ARHPVGNYYA 102

RESULT 11
B69265
conserved hypothetical protein AF0122 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: B69265
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Klrkness, E
.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artlach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A:Reference number: A69250; MUID:98049343
A:Accession: B69265
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-210 <KLE>
A:Cross-references: GB:AE001098; GB:AE000782; NID:g2689421; PID:g2650532; TIGR:AF0122
C:Superfamily: conserved hypothetical protein AF0119

Query Match 63.0%; Score 34; DB 1; Length 210;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
||| |||:
Db 128 RHAYGSF 134

RESULT 12
D71087
probable translation initiation factor eIF-2 alpha chain - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 26-Aug-1999
C:Accession: D71087
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Se
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophili
A:Reference number: A71000; MUID:98344137
A:Accession: D71087
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-275 <KAW>
A:Cross-references: GB:AP000004; NID:g2326131; PIDN:BAA30058.1; PID:g1031001; PID:g32
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBa
C:Genetics:
A:Gene: PH0961
C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 63.0%; Score 34; DB 2; Length 275;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
||| |||:
Db 23 HNYGAF 28

RESULT 13
G75130
translation initiation factor alf-2, subun it alpha (alf2a) PAB0568 - Pyrococcus abys
C:Species: Pyrococcus abyssi

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 24-Nov-1999

C:Accession: G75130
R:anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure
A:Reference number: A75001
A:Accession: G75130
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-275 <KAW>
A:Cross-references: GB:A248285; GB:AL096836; NID:g5458067; PIDN:CAB49760.1; PID:el51565
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: aif2A; PAB0568
C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 63.0%; Score 34; DB 2; Length 275;
Best Local Similarity 83.3%; Pred. No. 31;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
||||:|
DB 23 HNYGAF 28

RESULT 14

PWBY

Inorganic pyrophosphatase (EC 3.6.1.1) - yeast (*Saccharomyces cerevisiae*)
N:Alternate names: protein YBR011c; protein YBR0202; pyrophosphate phosphohydrolase
C:Species: *Saccharomyces cerevisiae*
C:Date: 30-Nov-1980 #sequence_revision 09-Sep-1994 #text_change 05-Nov-1999
C:Accession: S45864; S07679; A01014; S29189
R:Entian, K.D.; Koetter, P.; Rose, M.; Li, Z.; Thermann, R.; Brendel, M.; Baur, A.; Bole submitted to the Protein Sequence Database, August 1994
A:Reference number: S45862
A:Accession: S45864
A:Molecule type: DNA
A:Residues: 1-287 <ENT>
A:Cross-references: EMBL:Z35880; NID:g536205; PIDN:CAA84949.1; PID:g536206; GSPDB:GN0000
A:Experimental source: strain S288C
R:Kolakowski Jr., L.F.; Schloesser, M.; Cooperman, B.S.
Nucleic Acids Res. 16, 10441-10452, 1988
A:Title: Cloning, molecular characterization and chromosome localization of the inorganic
A:Reference number: S07679; MUID:89083474
A:Accession: S07679
A:Molecule type: DNA
A:Residues: 1-266, 'L', 268-287 <KOL>
A:Cross-references: EMBL:X13253; NID:g4198; PIDN:CAA31629.1; PID:g4199
R:Cohen, S.A.; Sterner, R.; Kelm, P.S.; Heinrikson, R.L.
J. Biol. Chem. 253, 889-897, 1978
A:Title: Covalent structural analysis of yeast inorganic pyrophosphatase.
A:Reference number: A92241; MUID:78087552
A:Accession: A01014

A:Molecule type: protein
A:Residues: 2-40, 'D', 42-71, 'N', 73, 75-117, 'N', 119-123, 'Q', 125-136, 'E', 138-186, 'D', 188-224
A:Note: This is the final paper in a series
A:Note: no disulfide bonds are present
R:Raznikov, A.V.; Sklyankina, V.A.; Avaeva, S.M.
FEBS Lett. 308, 62-64, 1992
A:Title: Tyrosine-89 is important for enzymatic activity of *S. cerevisiae* inorganic pyrophosphatase
A:Reference number: S29189; MUID:92354770
A:Accession: S29189

A:Molecule type: protein
A:Residues: 83-105, 'E', 107-112 <RAZ>
R:Bond, M.W.; Chiu, N.Y.; Cooperman, B.S.
Biochemistry 19, 94-102, 1980
A:Title: Identification of an arginine important for enzymatic activity within the covalent
A:Reference number: A90443
A:Contents: annotation; active site
C:Genetics:
A:Gene: SGO; IPPI; PPA; MIPS:YBR011c
A:Cross-references: SGD:S0000215; MIPS:YBR011c

A:Map position: 2R

C:Function:
A:Description: catalyzes hydrolysis of pyrophosphate to orthophosphate
A:Note: requires divalent metal cation
C:Superfamily: inorganic pyrophosphatase
C:Keywords: homodimer; hydrolase
F:2-287/Product: inorganic pyrophosphate #status experimental <MAT>
F:79/Binding site: pyrophosphate (Arg) #status experimental

Query Match 63.0%; Score 34; DB 1; Length 287;
Best Local Similarity 83.3%; Pred. No. 33;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
||||:|
DB 92 HNYGAF 97

RESULT 15

PWKL

Inorganic pyrophosphatase (EC 3.6.1.1) - yeast (*Kluyveromyces marxianus* var. *lactis*)
C:Species: *Kluyveromyces marxianus* var. *lactis*, *Candida spharica*
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Jun-1999
C:Accession: S07894
R:Stark, M.J.R.; Milner, J.S.
Yeast 5, 35-50, 1989

A:Title: Cloning and analysis of the *Kluyveromyces lactis* TRP1 gene: a chromosomal locus
A:Reference number: S07892; MUID:89189093
A:Accession: S07894
A:Molecule type: DNA
A:Residues: 1-287 <STA>
A:Cross-references: EMBL:X14230; NID:g2900; PIDN:CAA32446.1; PID:g2903

C:Genetics:
A:Gene: IPP
C:Superfamily: inorganic pyrophosphatase
C:Keywords: hydrolase
F:79,151/Active site: Arg, Glu #status predicted

Query Match 63.0%; Score 34; DB 1; Length 287;
Best Local Similarity 83.3%; Pred. No. 33;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
||||:|
DB 92 HNYGAF 97

Search completed: May 27, 2000, 19:26:46
Job time: 1769 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 20:07:19 ; Search time 69.28 seconds
(without alignments)
4.396 Million cell updates/sec

Title: US-09-016-061-80
Perfect score: 54
Sequence: 1 ARHNYGSFAA 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	63.0	275	1 IF2A_PYRHO	O58655 pyrococcus
2	34	63.0	284	1 IPYR_PICPA	O13505 pichia past
3	34	63.0	286	1 IPYR_KIULA	P13998 kluyveromyc
4	34	63.0	286	1 IPYR_YEAST	P00817 saccharomyc
5	33	61.1	65	1 CCSA_PEA	P31172 pisum sativ
6	33	61.1	328	1 CCSA_ARATH	P56770 arabidopsis
7	33	61.1	448	1 NCAP_CVHOC	P33469 human coron
8	33	61.1	470	1 SYE2_RICPR	Q9zct8 rickettsia
9	33	61.1	473	1 SYE_AQUAE	O62721 aquifex aeo
10	33	61.1	682	1 VG5Q_BPML5	O05262 mycobacteri
11	33	61.1	789	1 ACOX_YEAST	P39533 saccharomyc
12	33	61.1	1386	1 RPOD_MARPO	P06274 marchantia
13	32	59.3	65	1 CCSA_ORNBE	P31565 oenothera b
14	32	59.3	98	1 VG7_BPPH2	P13848 bacterioph
15	32	59.3	98	1 VG7_BPP2A	P07533 bacterioph
16	32	59.3	196	1 WBBI_ECOLI	P37750 escherichia
17	32	59.3	198	1 HB2G_HUMAN	P01911 homo sapien
18	32	59.3	266	1 HB2A_HUMAN	P01913 homo sapien
19	32	59.3	266	1 HB2F_HUMAN	P01912 homo sapien
20	32	59.3	266	1 HB2C_HUMAN	P01914 homo sapien
21	32	59.3	266	1 HB2D_CANFA	P18470 canis famil
22	32	59.3	266	1 HB2D_HUMAN	P13759 homo sapien
23	32	59.3	266	1 HB2E_HUMAN	P04259 homo sapien
24	32	59.3	266	1 HB2F_HUMAN	P13758 homo sapien
25	32	59.3	266	1 HB2H_HUMAN	P13760 homo sapien
26	32	59.3	266	1 HB2I_HUMAN	P20039 homo sapien
27	32	59.3	266	1 HB2J_HUMAN	P13761 homo sapien
28	32	59.3	313	1 CCSA_TOBAC	P12216 nicotiana t
29	32	59.3	321	1 CCSA_MAIZE	P46659 zea mays (m
30	32	59.3	321	1 CCSA_ORISA	P12215 oryza sativ
31	32	59.3	349	1 YJY9_YEAST	P41903 saccharomyc
32	32	59.3	528	1 PR12_YEAST	P20457 saccharomyc
33	32	59.3	560	1 THSI_HALVO	O30561 halobacteri
34	32	59.3	629	1 KSYK_YEAST	O64725 rattus norv

35 32 59.3 649 1 GPDM_SCHPO 014400 schizosacch
36 32 59.3 809 1 UBPI_YEAST P25037 saccharomyc
37 32 59.3 1074 1 PLD1_HUMAN Q13393 homo sapien
38 32 59.3 1267 1 VL3_REOVD P17378 reovirus (t
39 32 59.3 1267 1 VL3_REOVL P17376 reovirus (t
40 31 57.4 201 1 PRCG_HUMAN P49721 homo sapien
41 31 57.4 201 1 PRCG_RAT P40307 rattus norv
42 31 57.4 330 1 PROX_ECOLI P14177 escherichia
43 31 57.4 480 1 VP5_BRD P21230 broadhaven
44 31 57.4 737 1 YNC2_CAEEL P34535 caenorhabdi
45 31 57.4 853 1 PHSI_DICDI Q00766 dictyostell

ALIGNMENTS

RESULT 1
IF2A_PYRHO
ID IF2A_PYRHO STANDARD; PRT; 275 AA.
AC O58655;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
GN PH0961.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-OT3;
RX MEDLINE; 98344137.
RA Kwarabayasi Y., Savada M., Horikawa H., Haikawa Y., Hino Y.,
Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
CC -1- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
(BY SIMILARITY).
CC -1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
CHAIN (BY SIMILARITY).

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CC EMBL; AP000004; BAA30058.1; -;
DR PFAM; PF00575; SI; 1.
KW Initiation factor; Protein biosynthesis.
SQ SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 275;
Best Local Similarity 83.3%; Pred. No. 11;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
Db 23 HNYGAF 28

RESULT 2
IPYR_PICPA STANDARD; PRT; 284 AA.
ID IPYR_PICPA
AC O13505;

DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPP1.
 OS Pichia pastoris (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Pichia.
 RN [1]
 RC STRAIN-NRRL Y-11430;
 RX MEDLINE; 99034033.
 RA Cosano I.C., Alvarez P., Molina M., Nombela C.;
 RT "Cloning and sequence analysis of the Pichia pastoris TRP1, IPP1 and
 RT HIS3 genes.";
 RL Yeast 14:861-867(1998).
 CC -!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O -> 2 ORTHOPHOSPHATE.
 CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AJ001000; CAA04453.1; -
 DR HSSP; P00817; IWGI.
 DR PROSITE; PS00387; PPASE; 1.
 DR PFAM; PF00719; Pyrophosphatase; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 284 AA; 31937 MW; 30AD27970D7775D6 CRC64;

 Query Match 63.0%; Score 34; DB 1; Length 284;
 Best Local Similarity 83.3%; Pred. No. 11;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HNYGSF 8
 DB 91 HNYGAF 96
 ||||:|
 RESULT 3
 IPYR_KLULA IPYR_KLULA STANDARD; PRT; 286 AA.
 AC P13998:
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPP1 OR IPP.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Kluyveromyces.
 RN [1]
 RC SEQUENCE FROM N.A.
 RX MEDLINE; 89189093.
 RA Stark M.J.R., Milner J.S.;
 RT "Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a
 RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
 RT and histone H3.";
 RL Yeast 5:35-50(1989).

[2]
 RN SIMILARITY TO E. COLI AND YEAST PPASES.
 RX MEDLINE; 90254161.
 RA Lahti R., Kolakowski L.F. Jr., Heino J., Vihinen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RT "Conservation of functional residues between yeast and E. coli
 RT inorganic pyrophosphatases.";
 RL Biochim. Biophys. Acta 1038:338-345(1990).
 CC -!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O -> 2 ORTHOPHOSPHATE.
 CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; X14230; CAA32446.1; -
 DR PIR; S07894; PWVKL.
 DR HSSP; P00817; IWGI.
 DR PROSITE; PS00387; PPASE; 1.
 DR PFAM; PF00719; Pyrophosphatase; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 286 AA; 32034 MW; 11647FABD516A2F CRC64;

 Query Match 63.0%; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 11;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HNYGSF 8
 DB 91 HNYGAF 96
 ||||:|
 RESULT 4
 IPYR_YEAST IPYR_YEAST STANDARD; PRT; 286 AA.
 AC P00817;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPP1 OR PPA1 OR PPA OR YBR011C OR YBR0202.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomyces.
 RN [1]
 RC SEQUENCE FROM N.A.
 RX STRAIN-X2180;
 RX MEDLINE; 89083474.
 RA Kolakowski L.F. Jr., Schloesser M., Cooperman B.S.;
 RT "Cloning, molecular characterization and chromosome localization of
 RT the inorganic pyrophosphatase (PPA) gene from S. cerevisiae.";
 RL Nucleic Acids Res. 16:10441-10452(1988).
 RN [2]
 RC SEQUENCE FROM N.A.
 RX STRAIN-S288C;
 RA Entian K.-D., Koetter P., Rose M., Li Z., Thermann R., Brendel M.,
 RA Baur A., Boles E., Miosga T., Schaaff-Gerstenschlaeger I.,
 RA Zimmermann F.K.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]

RP SEQUENCE. 78087552.
RX MEDLINE; 78087552.
RA Cohen S.A., Sterner R., Keim P.S., Heinrikson R.L.;
RT "Covalent structural analysis of yeast inorganic pyrophosphatase.";
RL J. Biol. Chem. 253:889-897(1978).
RN [4]
RP SEQUENCE OF 25-35 AND 239-251.
RC STRAIN=S288C;
RX MEDLINE; 95203288.
RA Garrels J.I., Fletcher B., Kobayashi R., Latter G.I., Schwender B.,
RV Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a Saccharomyces cerevisiae protein
database.";
RL Electrophoresis 15:1466-1486(1994).
RN [5]
RP SEQUENCE OF 239-249.
RC STRAIN=ATCC 38531 / Y41;
RX MEDLINE; 97089742.
RA Norbeck J., Blomberg A.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
Saccharomyces cerevisiae.";
RL FEMS Microbiol. Lett. 137:1-8(1996).
RN [6]
RP ACTIVE SITE.
RX MEDLINE; 80109718.
RA Bond M.W., Chiu N.Y., Cooperman B.S.;
RT "Identification of an arginine important for enzymatic activity
within the covalent structure of yeast inorganic pyrophosphatase.";
RL Biochemistry 19:94-102(1980).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RA Arutunian E.G., Terzian S.S., Voronova A.A., Kuranova I.P.,
RV Smirnova E.A., Vainstein B.K., Hohne W.E., Hansen G.;
RT "X-ray diffraction study of inorganic pyrophosphatase from baker's
yeast at the 3-A resolution.";
RL Dokl. Akad. Nauk SSSR 258:1481-1492(1981).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE; 97148342.
RA Heikinheimo P., Lehtonen J., Baykov A., Lahti R., Cooperman B.S.,
RV Goldman A.;
RT "The structural basis for pyrophosphatase catalysis.";
RL Structure 4:1491-1508(1996).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RA Swaminathan K., Cooperman B.S., Lahti R., Voet D.;
RT Submitted (DEC-1997) to the PDB data bank.
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF MUTANTS LYS-78 AND LYS-117.
RX MEDLINE; 99096888.
RA Tuominen V., Heikinheimo P., Kajander T., Torkkel T., Hyytiä T.,
RV Kapiya J., Lahti R., Cooperman B.S., Goldman A.;
RT "The R78K and D117E active-site variants of Saccharomyces cerevisiae
soluble inorganic pyrophosphatase: structural studies and mechanistic
implications.";
RL J. Mol. Biol. 284:1565-1580(1998).
RN [11]
RP SIMILARITY TO E.COLI AND K.LACTIS PPASES.
RX MEDLINE; 90254161.
RA Lahti R., Kolakowski L.F. Jr., Heino J., Vihinen M., Pohjanoksa K.,
RV Cooperman B.S.;
RT "Conservation of functional residues between yeast and E. coli
inorganic pyrophosphatases.";
RL Biochim. Biophys. Acta 1038:338-345(1990).
CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY. IT BINDS UP TO 4 DIVALENT
CATIONS PER SUBUNIT, WITH THREE REQUIRED FOR ACTIVITY.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC -----
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CC EMBL; X13253; CAA31629.1; -;
CC EMBL; Z35880; CAA84949.1; -;
CC PIR; S45864; PMBY.
CC PDB; 1PYP; 15-OCT-91.
CC PDB; 1YPP; 07-DEC-96.
CC PDB; 1WGI; 19-NOV-97.
CC PDB; 1WUJ; 19-NOV-97.
CC PDB; 1HUK; 08-APR-98.
CC PDB; 1HUK; 08-APR-98.
CC PDB; 117E; 23-DEC-98.
CC PDB; 117E; 23-DEC-98.
CC SWISS-2DPAGE; P00817; YEAST.
CC YEPD; 7305; -;
CC SGD; L0000872; IPP1.
CC PROSITE; PS00387; PPASE; 1.
CC PFAM; PF00719; Pyrophosphatase; 1.
CC KW Hydrolase; Magnesium; 3D-structure.
CC INIT_MET 0
CC ACT_SITE 56 56 PROBABLE.
CC BINDING 78 78 INORGANIC PYROPHOSPHATE.
CC CONFLICT 40 40 N -> D (IN REF. 3).
CC CONFLICT 71 71 D -> N (IN REF. 3).
CC CONFLICT 74 74 MISSING (IN REF. 3).
CC CONFLICT 123 123 E -> Q (IN REF. 3).
CC CONFLICT 136 136 Q -> E (IN REF. 3).
CC CONFLICT 186 186 N -> D (IN REF. 3).
CC CONFLICT 224 224 D -> N (IN REF. 3).
CC CONFLICT 266 266 L -> P (IN REF. 2).
CC STRAND 4 7
CC STRAND 16 20
CC STRAND 25 25
CC TURN 28 30
CC TURN 38 41
CC STRAND 45 45
CC STRAND 55 55
CC STRAND 79 79
CC TURN 97 98
CC TURN 111 112
CC STRAND 121 123
CC TURN 131 132
CC TURN 135 135
CC STRAND 138 146
CC STRAND 151 158
CC TURN 160 161
CC TURN 165 167
CC TURN 172 175
CC TURN 176 177
CC TURN 179 180
CC TURN 182 197
CC TURN 203 203
CC TURN 205 207
CC STRAND 210 210
CC STRAND 212 230
CC TURN 231 231
CC TURN 245 246
CC TURN 248 249
CC TURN 251 252
CC TURN 255 260
CC TURN 274 275
CC SEQUENCE 286 AA; 32184 MW; F29390260B60C8B2 CRC64;
Query Match 63.0%; Score 34; DB 1; Length 286;
Best Local Similarity 83.3%; Pred. No. 11;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
Qy 3 HNYGSF 8
Db 91 HNYGAF 96

RESULT 5
CCSA_PEA ID CCSA_PEA STANDARD; PRT; 65 AA.
AC P31172;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA (FRAGMENT).
GN CCSA.
OS Pisum sativum (Garden pea).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
OC Pisum.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ALASKA;
RX MEDLINE; 91355950.
RA Nagano Y., Ishikawa H., Matsuno R., Sasaki Y.;
RT "Nucleotide sequence and expression of the ribosomal protein L2 gene
in pea chloroplasts.";
RL Plant Mol. Biol. 17:541-545(1991).
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCLL/NRFE/CCSA FAMILY.
-----
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-----
DR EMBL; X59015; CAA41754.1; -.
DR PIR; S17441; S17441.
KW Cytochrome c-type biogenesis; Chloroplast.
FT NON_TER 1
SQ SEQUENCE 65 AA; 7396 MW; 9E523E0C70B102AA CRC64;

Query Match 61.1%; Score 33; DB 1; Length 65;
Best Local Similarity 62.5%; Pred. No. 3.7;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNYGSFAA 10
Db 57 HSYGSFTS 64

RESULT 6
CCSA_ARATH ID CCSA_ARATH STANDARD; PRT; 328 AA.
AC P56770;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA.
GN CCSA.
OS Arabidopsis thaliana (Mouse-ear cress).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.

Qy 3 HNYGSF 8
Db 91 HNYGAF 96

RESULT 7
NCAP_CVHOC ID NCAP_CVHOC STANDARD; PRT; 448 AA.
AC P33469;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE NUCLEOCAPSID PROTEIN.
GN N.
OS Human coronavirus (strain OC43).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89243809.
RA Kamahora T., Soe L.H., Lai M.M.C.;
RT "Sequence analysis of nucleocapsid gene and leader RNA of human
coronavirus OC43.";
RL Virus Res. 12:1-9(1989).
DR PIR; A60003; A60003.
DR PFAM; PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 448 AA; 49316 MW; 5193AB1AE0D75626 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 448;
Best Local Similarity 85.7%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHYGSF 8
Db 103 RHYGSF 109

RESULT 8
SYE2_RICPR ID SYE2_RICPR STANDARD; PRT; 470 AA.
AC Q9ZCT8;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL--TRNA SYNTHETASE 2 (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE 2)
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DE (GLURS 2).
GN GLTX2 OR RP623.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E;
RA MEDLINE; 99039499.
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sacheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) -> AMP +
CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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CC -----
DR EMBL; AJ235272; CAA15066.1; -.
DR HSSP; P27000; IGLN.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW Aminoacyl-trna synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
FT SIMILAR 239 243 "KMSKS" REGION.
FT BINDING 242 242 ATP (BY SIMILARITY).
SQ SEQUENCE 470 AA; 53696 MW; DF1CE50A208A9FD CRC64;

Query Match 61.1%; Score 33; DB 1; Length 470;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSF 8
Db ||||| 31 ARHNGKF 38

RESULT 9
SYE_AQUAE STANDARD; PRT; 473 AA.
AC O67271;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE)
DE (GLURS).
GN GLTX OR AQ_1221.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE; 98196666.
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) -> AMP +
CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).

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CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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CC -----
DR EMBL; AE000729; AAC07230.1; -.
DR PRINTS; PR00987; TRNASYNTHGLU.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
DR PFAM; PF00749; TRNA-synt_1c; 1.
KW Aminoacyl-trna synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
FT SIMILAR 242 246 "KMSKS" REGION.
FT BINDING 245 245 ATP (BY SIMILARITY).
SQ SEQUENCE 473 AA; 55121 MW; 5CB4D1590973E07A CRC64;

Query Match 61.1%; Score 33; DB 1; Length 473;
Best Local Similarity 75.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSF 8
Db ||||| 31 ARHNGKF 38

RESULT 10
VG50_BPML5 STANDARD; PRT; 682 AA.
AC Q05262;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PUTATIVE ADENOSYLCOBALAMIN-DEPENDENT RIBONUCLEOTIDE REDUCTASE
DE (EC 1.17.4.2) (GP50).
GN 50.
OS Mycobacteriophage L5.
OC Viruses.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93211282.
RA Hatfull G.F., Sarkis G.J.;
RT "DNA sequence, structure and gene expression of mycobacteriophage L5:
RT a phage system for mycobacterial genetics.";
RL Mol. Microbiol. 7:395-405(1993).
CC -1- CATALYTIC ACTIVITY: 2'-DEOXYRIBONUCLEOSIDE TRIPHOSPHATE +
CC OXIDIZED THIOREDOXIN + H(2)O -> RIBONUCLEOSIDE TRIPHOSPHATE +
CC REDUCED THIOREDOXIN.
CC -----
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CC -----
DR EMBL; Z18946; CAA79426.1; -.
DR PIR; S30995; S30995.
KW Oxidoreductase; DNA replication.
SQ SEQUENCE 682 AA; 76331 MW; 8D2A71B873BC04A8 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 682;
Best Local Similarity 66.7%; Pred. No. 46;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9

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Db 311 AKEGSGFA 319
      | : |||||
RESULT 11
ACOX_YEAST
ID ACOX_YEAST STANDARD; PRT; 789 AA.
AC P39533;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE 01-NOV-1997 (Rel. 35, Last annotation update)
DE PUTATIVE ACONITASE IN PRP21-UBP12 INTERGENIC REGION (EC 4.2.1.3).
GN YJ200C OR J0327.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
CC [1]
CC SEQUENCE FROM N.A.
CC STRAIN-S288C;
CC MEDLINE; 95274326.
RA Purnelle B., Coster F., Goffeau A.;
RT "The sequence of a 36 kb segment on the left arm of yeast chromosome
RT X identifies 24 open reading frames including NUC1, PRP21 (SPP91),
RT CDC6, CRY2, the gene for S24, a homologue to the aconitase gene ACO1
RT and two homologues to chromosome III genes.";
RL yeast 10:1235-1249(1994).
CC -|- CATALYTIC ACTIVITY: CITRATE - CIS-ACONITATE + H(2)O.
CC -|- SIMILARITY: BELONGS TO THE ACONITASE/IPM ISOMERASE FAMILY.
CC -----
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CC -----
DR EMBL; X77688; CAA54757.1; -.
DR EMBL; Z49475; CAA89495.1; -.
DR PIR; S46631; S46631.
DR HSSP; P16276; 6ACN.
DR PRINTS; PR00415; ACONITASE.
DR PROSITE; PS00450; ACONITASE_1; 1.
DR PROSITE; PS01244; ACONITASE_2; 1.
DR PFAM; PF00330; aconitase; 1.
DR PFAM; PF00694; Aconitase_C; 1.
DR Hypothetical protein; Lyase; Tricarboxylic acid cycle; Iron-sulfur;
KW 4Fe-4S.
FT METAL 385 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 448 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 451 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 789 AA; 86583 MW; FABA4FE482D3F993 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 789;
Best Local Similarity 60.0%; Pred. No. 53;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ARHNYGSFAA 10
      | : ||||| : |
Db 663 AEHNYGEGA 672

RESULT 12
RPOD_MARPO
ID RPOD_MARPO STANDARD; PRT; 1386 AA.
AC P06274;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DE 01-OCT-1989 (Rel. 12, Last annotation update)
DE DNA-DIRECTED RNA POLYMERASE BETA" CHAIN (EC 2.7.7.6).
*GN RPOC2.
OS Marchantia polymorpha (Liverwort).

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OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Marchantiopsida;
OC Marchantiales; Marchantiaceae; Marchantia.
RN [1]
RP SEQUENCE FROM N.A.
RA Ohyama K.;
RL Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
RN [2]
RP COMPLETE GENOME.
RA Ohyama K., Fukuzawa H., Kohchi T., Shirai H., Sano T., Sano S.,
RA Umesono K., Shiki Y., Takeuchi M., Chang Z., Aota S., Inokuchi H.,
RA Ozeki H.;
RT "Chloroplast gene organization deduced from complete sequence of
RT liverwort Marchantia polymorpha chloroplast DNA.";
RL Nature 322:572-574(1986).
CC -|- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -|- CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE = N PYROPHOSPHATE +
CC RNA(N).
CC -|- SUBUNIT: IN CHLOROPLAST THE RNA POLYMERASE IS COMPOSED OF FOUR
CC SUBUNITS: ALPHA, BETA, BETA', AND BETA".
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CC -----
DR EMBL; X04465; CAA28063.1; -.
DR PIR; A00698; RNLVC2.
DR PIR; S01575; S01575.
DR MENDEL; 4115; MARPO; rPOC2; 1.
DR PFAM; PF00623; RNA_pol_A; 1.
KW Transferase; Transcription; DNA-directed RNA polymerase; Chloroplast.
SQ SEQUENCE 1386 AA; 160155 MW; 18BE458FC1A5C3F9 CRC64;

Query Match 61.1%; Score 33; DB 1; Length 1386;
Best Local Similarity 75.0%; Pred. No. 97;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 HNYGSFAA 10
      | : ||||| |
Db 86 HNYGSLHA 93

RESULT 13
CCSA_OENBE
ID CCSA_OENBE STANDARD; PRT; 65 AA.
AC P31565;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA (FRAGMENT).
GN CCSA.
OS Oenothera lutea (Bertero's evening primrose).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eudicotyledons; Magnoliophyta; Magnoliopsida; eudicotyledons;
OC core eudicot; Rosidae; eurosids II; Myrtales; Onagraceae; Oenothera.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93169690.
RA Nimzyk R., Schoendorf T., Hachtel W.;
RT "In-frame length mutations associated with short tandem repeats are
RT located in unassigned open reading frames of Oenothera chloroplast
RT DNA.";
RL Curr. Genet. 23:265-270(1993).
CC -|- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).

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CC -1- SIMILARITY: BELONGS TO THE CMF/CYCK/CCL1/NRFE/CCSA FAMILY.
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 CC -----
 DR EMBL; X64617; CAA45900.1; -;
 DR EMBL; X64614; CAA45894.1; -;
 DR PIR; S19981; S19981.
 DR PIR; S19988; S19988.
 KW Cytochrome c-type biogenesis; Chloroplast.
 FT NON_TER 1
 SQ SEQUENCE 65 AA; 7441 MW; 343E66DDA1492C0C CRC64;
 Query Match 59.3%; Score 32; DB 1; Length 65;
 Best Local Similarity 83.3%; Pred. No. 5.9;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HNYGSF 8
 Db 57 HSYGSF 62
 RESULT 14
 VGT_BPPH2 STANDARD; PRT; 98 AA.
 AC PL3848;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE HEAD MORPHOGENESIS PROTEIN (LATE PROTEIN GP7).
 GN 7.
 OS Bacteriophage phi-29.
 OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Podoviridae.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 87106857.
 RA Vlcek C., Paces V.;
 RT "Nucleotide sequence of the late region of Bacillus phage phi 29
 RT completes the 19,285-bp sequence of phi 29 genome. Comparison with
 RT the homologous sequence of phage PZA.";
 RL Gene 46:215-225(1986).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 87016351.
 RA Innis C.A., Garvey K.J., Ito J.;
 RT "Nucleotide sequence of phage phi 29 gene 7: structure of intergenic
 RT spacer between the major early and late genes.";
 RL Nucleic Acids Res. 14:7129-7129(1986).
 CC -----
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 CC -----
 DR EMBL; M14782; AAA32279.1; -;
 DR EMBL; X04386; CAA27974.1; -;
 DR PIR; A28923; WMBPF9.
 KW Late protein.
 SQ SEQUENCE 98 AA; 11366 MW; FF2E7985D2266E14 CRC64;

Query Match 59.3%; Score 32; DB 1; Length 98;
 Best Local Similarity 66.7%; Pred. No. 9.2;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAA 10
 Db 33 RVNYGSFVS 41
 RESULT 15
 VGT_BPPZA STANDARD; PRT; 98 AA.
 AC P07533;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE HEAD MORPHOGENESIS PROTEIN (LATE PROTEIN GP7).
 GN 7.
 OS Bacteriophage PZA.
 OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Podoviridae.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 87031573.
 RA Paces V., Vlcek C., Urbanek P.;
 RT "Nucleotide sequence of the late region of Bacillus subtilis phage
 RT PZA, a close relative of phi 29.";
 RL Gene 44:107-114(1986).
 CC -----
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 CC -----
 DR EMBL; M1813; AAA88483.1; -;
 DR PIR; A24831; WMBP72.
 KW Late protein.
 SQ SEQUENCE 98 AA; 11281 MW; 444408C39B606A25 CRC64;

Query Match 59.3%; Score 32; DB 1; Length 98;
 Best Local Similarity 66.7%; Pred. No. 9.2;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFAA 10
 Db 33 RVNYGSFVS 41

Search completed: May 27, 2000, 20:07:19
 Job time: 991 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:38:42 ; Search time 199.56 Seconds
(without alignments)
3.474 Million cell updates/sec

Title: US-09-016-061-80
Perfect score: 54
Sequence: 1 ARHNGSFAA 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SPTREMBL12.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	79.6	446	5	O62086
2	38	70.4	89	7	O19495
3	36	66.7	39	7	P79474
4	36	66.7	39	7	P79477
5	36	66.7	39	7	P79478
6	36	66.7	39	7	P79479
7	36	66.7	78	6	O97835
8	36	66.7	78	6	O97839
9	36	66.7	78	6	O97844
10	36	66.7	78	6	O97968
11	36	66.7	79	7	O19191
12	36	66.7	79	7	O19192
13	36	66.7	79	7	O19380
14	36	66.7	79	7	O19381
15	36	66.7	79	7	O19382
16	36	66.7	79	7	O19396
17	36	66.7	79	7	O19397
18	36	66.7	79	7	O19405
19	36	66.7	79	7	O19406
20	36	66.7	79	7	O19407

21	36	66.7	79	7	O19408	O19408 felis silve
22	36	66.7	79	7	O19435	O19435 felis silve
23	36	66.7	81	7	O30568	O30568 macaca fasc
24	36	66.7	81	7	O30571	O30571 macaca fasc
25	36	66.7	81	7	O30737	O30737 macaca neme
26	36	66.7	81	7	O30739	O30739 macaca neme
27	36	66.7	81	7	O30563	O30563 macaca fasc
28	36	66.7	81	7	O30740	O30740 macaca neme
29	36	66.7	82	7	O95598	O95598 phasianus c
30	36	66.7	82	7	O30606	O30606 macaca mulla
31	36	66.7	82	7	O30608	O30608 macaca mulla
32	36	66.7	82	7	O30637	O30637 macaca mulla
33	36	66.7	82	7	O30638	O30638 macaca mulla
34	36	66.7	82	7	O30658	O30658 macaca mulla
35	36	66.7	82	7	O30659	O30659 macaca mulla
36	36	66.7	82	7	O30666	O30666 macaca mulla
37	36	66.7	82	7	O30667	O30667 macaca mulla
38	36	66.7	82	7	O30668	O30668 macaca mulla
39	36	66.7	82	7	O19287	O19287 macaca mulla
40	36	66.7	82	7	O19288	O19288 macaca mulla
41	36	66.7	83	7	O98002	O98002 ovis aries
42	36	66.7	83	7	O9XS06	O9XS06 odocolleus
43	36	66.7	83	7	O9XR25	O9XR25 odocolleus
44	36	66.7	83	7	O9XR24	O9XR24 odocolleus
45	36	66.7	85	7	O30796	O30796 ovis aries

ALIGNMENTS

RESULT 1

O62086 PRELIMINARY; PRT: 446 AA.
ID O62086
AC O62086;
DT 01-AUG-1998 (Tremblrel. 07, Created)
DT 01-AUG-1998 (Tremblrel. 07, Last sequence update)
DT 01-JAN-1999 (Tremblrel. 09, Last annotation update)
DE C3IH5.6 PROTEIN.
GN C3IH5.6.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RA KERSHAW J.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.";
RL Nature 368:32-38(1994).
DR EMBL; 293778; CAB07846.1; -.
SQ SEQUENCE 446 AA; 50763 MW; B347C0C8 CRC32;

Query Match 79.6%; Score 43; DB 5; Length 446;

Best Local Similarity 88.9%; Pred. No. 1.3;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 RHNGSFAA 10

|||||

Db 51 RHNGSHAA 59


```

RESULT 2
ID O19495 PRELIMINARY; PRT; 89 AA.
AC O19495;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE MHC CLASS II BETA 1 DOMAIN (FRAGMENT).
GN B-LBI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-15.151-5; TISSUE-BURSA;
RA PHARR G.T., DODGSON J.B., HUNT H.D., BACON L.D.;
RL Immunogenetics 47:350-354(1998).
DR EMBL; U91532; AAC15813.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 89 89
SQ SEQUENCE 89 AA; 10724 MW; FDAC6024 CRC32;

Query Match 70.4%; Score 38; DB 7; Length 89;
Best Local Similarity 85.7%; Pred. No. 2.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
DB 75 RHNYGDF 81

RESULT 3
ID P79474 PRELIMINARY; PRT; 39 AA.
AC P79474;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
OC Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.
RA SWABRICK P.A., CRAWFORD A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63077; AAB37777.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4767 MW; E01AA287 CRC32;

Query Match 66.7%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
DB 25 RHNYGVF 31

RESULT 4
ID P79477 PRELIMINARY; PRT; 39 AA.
AC P79477;
DT 01-MAY-1997 (TREMBlrel. 03, Created)

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DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
OC Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.
RA SWABRICK P.A., CRAWFORD A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63080; AAB37780.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match 66.7%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
DB 25 RHNYGVF 31

RESULT 5
ID P79478 PRELIMINARY; PRT; 39 AA.
AC P79478;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
OC Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.
RA SWABRICK P.A., CRAWFORD A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63081; AAB37781.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match 66.7%; Score 36; DB 7; Length 39;
Best Local Similarity 85.7%; Pred. No. 2.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
DB 25 RHNYGVF 31

RESULT 6
ID P79479 PRELIMINARY; PRT; 39 AA.
AC P79479;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
OC Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.

```

RA SWARBRICK P.A., CRAWFORD A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63082; AAB37782.1; -.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4806 MW; 4984754A CRC32;

Query Match 66.7%; Score 36; DB 7; Length 39;
 Best Local Similarity 85.7%; Pred. No. 2.4;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 RHNYGSF 8
 Db 25 RHNYGVF 31
 |||||

RESULT 7
 O97835 PRELIMINARY; PRT; 78 AA.
 AC O97835;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
 GN OLA-DRB1*N20.2.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=7407; TISSUE=BLOOD;
 RA AIDA Y.;
 RT "Ovis aries DNA for MHC class II DRB1 exon 2."
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017207; BAA36764.1; -.
 FT NON_TER 1 1
 FT NON_TER 78 78
 SQ SEQUENCE 78 AA; 9677 MW; D2252D9D CRC32;

Query Match 66.7%; Score 36; DB 6; Length 78;
 Best Local Similarity 85.7%; Pred. No. 4.8;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 RHNYGSF 8
 Db 72 RHNYGVF 78
 |||||

RESULT 8
 O97839 PRELIMINARY; PRT; 78 AA.
 AC O97839;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
 GN OLA-DRB1*N2.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SUFFOLK BREED AND CORRIDAILE BREED; TISSUE=BLOOD;
 RA AIDA Y.;
 RT "Ovis aries DNA for MHC class II DRB1 exon 2."
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017212; BAA36769.1; -.
 FT NON_TER 1 1

FT NON_TER 78 78
 SQ SEQUENCE 78 AA; 9430 MW; 2883C99C CRC32;

Query Match 66.7%; Score 36; DB 6; Length 78;
 Best Local Similarity 85.7%; Pred. No. 4.8;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 RHNYGSF 8
 Db 72 RHNYGVF 78
 |||||

RESULT 9
 O97844 PRELIMINARY; PRT; 78 AA.
 AC O97844;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
 GN OLA-DRB1*N8.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SUFFOLK BREED; TISSUE=BLOOD;
 RA AIDA Y.;
 RT "Ovis aries DNA for MHC class II DRB1 exon 2."
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017220; BAA36777.1; -.
 FT NON_TER 1 1
 FT NON_TER 78 78
 SQ SEQUENCE 78 AA; 9645 MW; 0A246905 CRC32;

Query Match 66.7%; Score 36; DB 6; Length 78;
 Best Local Similarity 85.7%; Pred. No. 4.8;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 RHNYGSF 8
 Db 72 RHNYGVF 78
 |||||

RESULT 10
 O97968 PRELIMINARY; PRT; 78 AA.
 AC O97968;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
 GN OLA-DRB1*N21.
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Caprinae; Ovis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VARIOUS STRAINS;
 RA AIDA Y.;
 RT "Ovis aries DNA for MHC class II DRB1 exon 2."
 RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB017231; BAA36788.1; -.
 DR EMBL; AB017204; BAA36761.1; -.
 FT NON_TER 1 1
 FT NON_TER 78 78
 SQ SEQUENCE 78 AA; 9436 MW; 72250CEB CRC32;

Query Match 66.7%; Score 36; DB 6; Length 78;
 Best Local Similarity 85.7%; Pred. No. 4.8;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
 Db 72 RHNYGVF 78

RESULT 11
 O19191 PRELIMINARY; PRT; 79 AA.
 AC O19191;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
 GN MHCMAIR-DRB.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Carnivora; Fissipedia; Felidae; Prionailurus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97211851.
 RA YUHKI N., O'BRIEN S.J.;
 RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB genes.";
 RL J. Immunol. 158:2822-2833(1997).
 DR EMBL; U51546; AAB65582.1; "-."
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 9582 MW; 8EEF2C7D CRC32;

Query Match 66.7%; Score 36; DB 7; Length 79;
 Best Local Similarity 85.7%; Pred. No. 4.9;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
 Db 72 RHNYGVF 78

RESULT 12
 O19192 PRELIMINARY; PRT; 79 AA.
 AC O19192;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
 GN MHCMAIR-DRB.
 OS Prionailurus bengalensis iriomotensis (Iriomote cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Carnivora; Fissipedia; Felidae; Prionailurus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97211851.
 RA YUHKI N., O'BRIEN S.J.;
 RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB genes.";
 RL J. Immunol. 158:2822-2833(1997).
 DR EMBL; U51547; AAB65583.1; "-."
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 9582 MW; ED9F80F0 CRC32;

Query Match 66.7%; Score 36; DB 7; Length 79;

Best Local Similarity 85.7%; Pred. No. 4.9;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
 Db 72 RHNYGVF 78

RESULT 13
 O19380 PRELIMINARY; PRT; 79 AA.
 AC O19380;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
 GN MHCFCFA-DRB.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97211851.
 RA YUHKI N., O'BRIEN S.J.;
 RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB genes.";
 RL J. Immunol. 158:2822-2833(1997).
 DR EMBL; U51498; AAB65533.1; "-."
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 9659 MW; F352AD23 CRC32;

Query Match 66.7%; Score 36; DB 7; Length 79;
 Best Local Similarity 85.7%; Pred. No. 4.9;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
 |||||
 Db 72 RHNYGVF 78

RESULT 14
 O19381 PRELIMINARY; PRT; 79 AA.
 AC O19381;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
 GN MHCFCFA-DRB.
 OS Felis silvestris catus (Cat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97211851.
 RA YUHKI N., O'BRIEN S.J.;
 RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB genes.";
 RL J. Immunol. 158:2822-2833(1997).
 DR EMBL; U51499; AAB65534.1; "-."
 DR PFAM; PF00969; MHC_II_beta; 1.
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 79 79
 SQ SEQUENCE 79 AA; 9610 MW; 1F7FB873 CRC32;

Query Match 66.7%; Score 36; DB 7; Length 79;
 Best Local Similarity 85.7%; Pred. No. 4.9;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
DB 72 RHNYGVF 78

RESULT 15

O19382 PRELIMINARY; PRT; 79 AA.
AC O19382;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS II DRB FIRST EXTRACELLULAR DOMAIN (FRAGMENT).
GN MHCPECA-DRB.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97211851.
RA YUHKI N., O'BRIEN S.J.;
RT "Nature and origin of polymorphism in feline MHC class II DRA and DRB
genes.";
RL J. Immunol. 158:2822-2833(1997).
DR EMBL; U51500; AAB65535.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1
FT NON_TER 79 79
SQ SEQUENCE 79 AA; 9421 MW; CB203F17 CRC32;

Query Match 66.7%; Score 36; DB 7; Length 79;
Best Local Similarity 85.7%; Pred. NO. 4.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
DB 72 RHNYGVF 78

Search completed: May 27, 2000, 19:38:42
Job time: 2375 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:21:37 ; Search time 148.45 Seconds
(without alignments)
1.596 Million cell updates/sec

Title: US-09-016-061-80
Perfect score: 54
Sequence: 1 ARHNYGSFAA 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	10	1 W76030	LM609 grafted anti
2	51	94.4	10	1 W76024	LM609 grafted anti
3	50	92.6	10	1 W76025	LM609 grafted anti
4	50	92.6	10	1 W76026	LM609 grafted anti
5	50	92.6	10	1 W76027	LM609 grafted anti
6	50	92.6	10	1 W76028	LM609 grafted anti
7	50	92.6	10	1 W76029	LM609 grafted anti
8	50	92.6	10	1 W76010	LM609 grafted anti
9	50	92.6	117	1 W76001	Vitaxin antibody h
10	50	92.6	117	1 W76003	LM609 antibody hea
11	47	87.0	10	1 W76021	LM609 grafted anti
12	46	85.2	10	1 W76037	LM609 grafted anti
13	46	85.2	10	1 W76039	LM609 grafted anti
14	46	85.2	10	1 W76040	LM609 grafted anti
15	46	85.2	10	1 W76022	LM609 grafted anti
16	46	85.2	10	1 W76023	LM609 grafted anti
17	45	83.3	10	1 W76020	LM609 grafted anti
18	42	77.8	110	1 W84099	Vitronectin alpha
19	42	77.8	117	1 W84093	Murine vitronectin
20	42	77.8	117	1 W84097	Humanised anti-alp
21	41	75.9	10	1 W76038	LM609 grafted anti
22	36	66.7	117	1 R79157	Human IGE receptor
23	36	66.7	117	1 R79155	Human IGE receptor
24	36	66.7	117	1 W27357	Heavy chain variab
25	36	66.7	117	1 W27526	Heavy chain variab
26	36	66.7	117	1 W27354	Heavy chain variab
27	36	66.7	119	1 W01578	Lead binding Mab 8
28	36	66.7	239	1 W73874	Human antic epsil
29	36	66.7	242	1 W73876	Human antic epsil
30	33	61.1	80	1 R13396	HLA-DRW12a antigen
31	33	61.1	80	1 R13397	HLA-DRW12b antigen
32	32	59.3	11	1 W22700	Peptide sequence #
33	32	59.3	15	1 W25799	Synthetic human S1
34	32	59.3	18	1 W27062	Chemically synthes

35 32 59.3 25 1 R49334 DRI beta chain pos
36 32 59.3 25 1 W41656 Immunomodulatory p
37 32 59.3 36 1 W03964 VDJ joint protein,
38 32 59.3 36 1 W41127 VH251 DXP'1 J6 mu
39 32 59.3 78 1 W71230 Major histocompata
40 32 59.3 80 1 R21415 Human leukocyte an
41 32 59.3 84 1 P90034 Peptide of human/m
42 32 59.3 89 1 R24276 DRI. Method and k1
43 32 59.3 89 1 W00380 HLA-DRB1*08 and *1
44 32 59.3 93 1 W10491 Beta1 region of Cl
45 32 59.3 94 1 R13398 HLA-DRJX6 antigen.

ALIGNMENTS

RESULT 1

W76030
ID W76030 standard; Protein; 10 AA.
AC W76030;
DE 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #12.
KW Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB: V49867.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62: Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 100.0%; Score 54; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.00081;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAA 10

Db 1 ARHNYGSFAA 10

RESULT 2

ID W76024 standard; Protein; 10 AA.

AC W76024;

DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-H region CDR3 protein fragment #6.

KW Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49861.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 CC Sequence 10 AA;

Query Match 94.4%; Score 51; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0027;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAA 10
 | | | | | | | | | |
 DB 1 ARHNYGSFAS 10

RESULT 3
 W76025
 ID W76025 standard; Protein; 10 AA.
 AC W76025;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #7.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49862.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 CC Sequence 10 AA;

Query Match 92.6%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.004;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 | | | | | | | | | |
 DB 1 ARHNYGSFA 9

RESULT 4
 W76026
 ID W76026 standard; Protein; 10 AA.
 AC W76026;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #8.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49863.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 CC Sequence 10 AA;

Query Match 92.6%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.004;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 | | | | | | | | | |
 DB 1 ARHNYGSFA 9

RESULT 5
 W76027
 ID W76027 standard; Protein; 10 AA.

AC W76027;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #9.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49864.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT Integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 92.6%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.004;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 Db 1 ARHNYGSFA 9

RESULT 6
 W76028
 ID W76028 standard; Protein; 10 AA.
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #10.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49866.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT Integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 92.6%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.004;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 Db 1 ARHNYGSFA 9

RESULT 7
 W76029
 ID W76029 standard; Protein; 10 AA.
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #11.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49866.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT Integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 92.6%; Score 50; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.004;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
 |||||
 Db 1 ARHNYGSFA 9

```

RESULT 8
W76010
ID W76010 standard; Protein; 10 AA.
AC W76010;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #1.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis; primer; V-H region; CDR;
complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49847.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
integrin - and related grafted antibodies based on murine monoclonal
LM609, also related nucleic acid, used to treat, prevent or diagnose
angiogenesis or restenosis
PT
PS Disclosure; Page 40; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
LM609 heavy and light chain variable region. LM609 and the antibody
inhibit binding of alphavbeta3 to a ligand and thus block
integrin-mediated signal transduction. This is useful in the treatment,
prevention and diagnosis of alphavbeta3-mediated disease, specifically
angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
arthritis, macular degeneration, osteoporosis etc.). The antibodies
contain non-murine framework regions so are suitable for use in humans.
Enhanced types of LM609 have affinity more than 90 times greater than
that of parent the parent antibody.
CC Sequence 10 AA;
SQ

Query Match 92.6%; Score 50; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 1 ARHNYGSFA 9
|||||||

RESULT 9
W76001
ID W76001 standard; Protein; 117 AA.
AC W76001;
DT 02-NOV-1998 (first entry)
DE Vitaxin antibody heavy chain variable region protein fragment.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49820.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
integrin - and related grafted antibodies based on murine monoclonal
LM609, also related nucleic acid, used to treat, prevent or diagnose
angiogenesis or restenosis
PT
PS Claim 43; Fig 2a; 129pp; English.
CC This sequence represents the LM609 antibody variable heavy chain region.
LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
and can be used to inhibit binding of alphavbeta3 to a ligand and thus
block integrin-mediated signal transduction. This is useful in the
treatment, prevention and diagnosis of alphavbeta3-mediated disease,
specifically angiogenesis and restenosis (but also e.g. (non-)immune
inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
etc.). The antibodies contain non-murine framework regions so are
suitable for use in humans. Enhanced types of LM609 have affinity more
than 90 times greater than that of parent the parent antibody.
CC Sequence 117 AA;
SQ

Query Match 92.6%; Score 50; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 97 ARHNYGSFA 105
|||||||

RESULT 10
W76003
ID W76003 standard; Protein; 117 AA.
AC W76003;
DT 02-NOV-1998 (first entry)
DE LM609 antibody heavy chain variable region protein fragment.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49822.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
integrin - and related grafted antibodies based on murine monoclonal
LM609, also related nucleic acid, used to treat, prevent or diagnose
angiogenesis or restenosis
PT
PS Claim 43; Fig 2a; 129pp; English.
CC This sequence represents the LM609 antibody variable heavy chain region.
LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
and can be used to inhibit binding of alphavbeta3 to a ligand and thus
block integrin-mediated signal transduction. This is useful in the
treatment, prevention and diagnosis of alphavbeta3-mediated disease,
specifically angiogenesis and restenosis (but also e.g. (non-)immune
inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
etc.). The antibodies contain non-murine framework regions so are
suitable for use in humans. Enhanced types of LM609 have affinity more
than 90 times greater than that of parent the parent antibody.
CC Sequence 117 AA;
SQ

Query Match 92.6%; Score 50; DB 1; Length 117;
Best Local Similarity 100.0%; Pred. No. 0.051;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSFA 9
Db 97 ARHNYGSFA 105
|||||||

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RESULT 11
W76021
ID W76021 standard; Protein; 10 AA.
AC W76021;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #3.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB; V49858.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 87.0%; Score 47; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.013;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFA 9
   |||||:|
Db 1 ARHNYGSYA 9

RESULT 12
W76037
ID W76037 standard; Protein; 10 AA.
AC W76037;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #13.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB; V49874.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

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PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 43; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 85.2%; Score 46; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.02;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFAA 10
   ||||:||||
Db 1 ARHNHGSPAS 10

RESULT 13
W76039
ID W76039 standard; Protein; 10 AA.
AC W76039;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #15.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB; V49876.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 43; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 85.2%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ARHNYGSF 8
Db 1 ARHNYGSF 8

RESULT 14
W76040
ID W76040 standard; Protein; 10 AA.
AC W76040;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #16.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC..
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49877.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related nucleic acid, used to treat, prevent or diagnose
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 85.2%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
Db 1 ARHNYGSF 8

Search completed: May 27, 2000, 19:21:37
Job time: 1591 sec

QY 1 ARHNYGSF 8
Db 1 ARHNYGSF 8

RESULT 15
W76022
ID W76022 standard; Protein; 10 AA.
AC W76022;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #4.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC..
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49877.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related nucleic acid, used to treat, prevent or diagnose
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 43; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 85.2%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
Db 1 ARHNYGSF 8

RESULT 15
W76022
ID W76022 standard; Protein; 10 AA.
AC W76022;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #4.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC..
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49877.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related nucleic acid, used to treat, prevent or diagnose
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 85.2%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
Db 1 ARHNYGSF 8

Search completed: May 27, 2000, 19:21:37
Job time: 1591 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 27, 2000, 19:26:46 ; Search time 163.56 Seconds
(without alignments)
4.660 Million cell updates/sec

Title: US-09-016-061-82

Perfect score: 72

Sequence: 1 QASQISNPLHWY 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

PIR_63:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	65	90.3	106	2	PL0267
2	65	90.3	123	2	S35479
3	62	86.1	122	2	S40370
4	61	84.7	107	2	S32188
5	60	83.3	96	2	S37330
6	60	83.3	103	2	S19875
7	59	81.9	95	2	PH0867
8	59	81.9	102	2	S26346
9	59	81.9	104	2	B43413
10	59	81.9	107	2	B45722
11	59	81.9	107	2	A45722
12	59	81.9	138	2	A26471
13	58	80.6	62	2	S42265
14	58	80.6	87	2	I52592
15	58	80.6	88	2	S34088
16	58	80.6	88	2	S34087
17	58	80.6	95	2	PH0862
18	58	80.6	107	2	C45722
19	58	80.6	108	2	S19674
20	58	80.6	110	2	S44118
21	58	80.6	117	2	S43528
22	58	80.6	117	2	S42263
23	58	80.6	127	2	S40367
24	58	80.6	129	1	K1H0WK
25	58	80.6	129	2	S52789
26	55	76.4	122	2	S40314
27	54	75.0	92	1	KVR838
28	54	75.0	93	2	S38564
29	54	75.0	106	2	PC4282
30	54	75.0	107	2	B28044

ALIGNMENTS

RESULT 1

PL0267

Ig kappa chain V region (anti-DNA, DPL2VK) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

C:Accession: PL0267

R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somat

A:Reference number: PL0231; MUID:90111618

A:Accession: PL0267

A:Molecule type: mRNA

A:Residues: 1-106 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-23/Region: framework 1

F:24-34/Region: complementarity-determining 1

F:35-49/Region: framework 2

F:50-56/Region: complementarity-determining 2

F:57-88/Region: framework 3

F:89-97/Region: complementarity-determining 3

F:98-106/Region: framework 4

Query Match 90.3%; Score 65; DB 2; Length 106;

Best Local Similarity 84.6%; Pred. No. 0.00017;

Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNPLHWY 13

DB 24 RASQISNPLHWY 36

RESULT 2

S35479

Ig kappa chain precursor V region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 23-Jul-1999

C:Accession: S35479

R:Takeda, Y.; Wise, K.S.; Hoffman, R.W.

Nucleic Acids Res. 20, 4099, 1992

A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from

A:Reference number: S35479; MUID:92375706

A:Accession: S35479

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-123 <TA>

A:Cross-references: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148

C:Genetics:

A:Map position: 6

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-12/Domain: signal sequence (fragment) #status predicted <SIG>

F:13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>

Query Match 90.3%; Score 65; DB 2; Length 123;
Best Local Similarity 84.6%; Pred. No. 0.0002; 0; Indels 0; Gaps 0;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
:|||||:|||||
DB 36 RASQISNLFHWY 48

RESULT 3

Ig kappa chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 23-Jul-1999
C:Accession: S40370
R:Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A:Title: Expressed human immunoglobulin chi genes and their hypermutation.
A:Reference number: S40312; MUID:94080891
A:Accession: S40370

A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-122 <KLE>
A:Cross-references: EMBL:X72480; NID:g441428; PIDN:CAA51148.1; PID:g441429
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 86.1%; Score 62; DB 2; Length 122;
Best Local Similarity 84.6%; Pred. No. 0.00067; 1; Indels 0; Gaps 0;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
:|||||:|||||
DB 38 RASQISNLFHWY 50

RESULT 4

Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 23-Jul-1999
C:Accession: S32188
R:Izui, S.
submitted to the EMBL Data Library, February 1993
A:Reference number: S32185

A:Accession: S32188
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-107 <IZU>
A:Cross-references: EMBL:X70090; NID:g288253; PIDN:CAA49695.1; PID:g288254
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 84.7%; Score 61; DB 2; Length 107;
Best Local Similarity 76.9%; Pred. No. 0.00087; 2; Mismatches 1; Indels 0; Gaps 0;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
:|||||:|||||
DB 24 RASQDISNLFHWY 36

RESULT 5

Ig kappa chain V region (23.32) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-May-1997
C:Accession: G33730

R:Lawler, A.M.; Kearney, J.F.; Kuehl, M.; Gearhart, P.J.
Proc. Natl. Acad. Sci. U.S.A. 86, 6744-6747, 1989
A:Title: Early rearrangements of genes encoding murine immunoglobulin kappa-chains, u
A:Reference number: A33730; MUID:89367325
A:Accession: G33730

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-96 <LAW>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 83.3%; Score 60; DB 2; Length 96;
Best Local Similarity 76.9%; Pred. No. 0.0012; 3; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
:|||||:|||||
DB 24 RASQISNLFHWY 36

RESULT 6

Ig kappa chain V region (M-T408) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 23-Jul-1999
C:Accession: S19975
R:Weissenborn, W.; Riethmüller, G.; Weiss, E.M.; Rieber, E.P.
submitted to the EMBL Data Library, March 1992
A:Description: Structural characterization of CD4 mAb.
A:Reference number: S19963
A:Accession: S19975

A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-103 <WEI>
A:Cross-references: EMBL:X65097; NID:g52296; PIDN:CAA46225.1; PID:g52297
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 83.3%; Score 60; DB 2; Length 103;
Best Local Similarity 76.9%; Pred. No. 0.0012; 3; Mismatches 0; Indels 0; Gaps 0;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
:|||||:|||||
DB 19 RASQISNLFHWY 31

RESULT 7

Ig kappa chain V region (anti-DNA, R3.5H5G) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 09-May-1997
C:Accession: PH0867
R:Manheimer-Lory, A.; Katz, J.B.; Pillinger, M.; Ghousein, C.; Smith, A.; Diamond, B.
J. Exp. Med. 174, 1639-1652, 1991
A:Title: Molecular characteristics of antibodies bearing an anti-DNA-associated idiot
A:Reference number: PH0862; MUID:92078875
A:Accession: PH0867
A:Molecule type: DNA
A:Residues: 1-95 <MAN>

C:Comment: This antibody is produced by Epstein-Barr virus-transformed B cell that be
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-95/Region: complementarity-determining 3

Query Match 81.9%; Score 59; DB 2; Length 95;
 Best Local Similarity 76.9%; Pred. No. 0.0017;
 Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNFWLHWY 13
 :|||||:|||||
 Db 24 RASQSISNFWLHWY 36

RESULT 8

B43413
 Ig kappa chain V region - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S26346
 R:Stark, S.E.; Caton, A.J.
 J. Exp. Med. 174, 613-624, 1991
 A:Title: Antibodies that are specific for a single amino acid interchange in a protein e
 A:Reference number: S26309; MUID:91341421
 A:Accession: S26346
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-102 <STA>
 A:Cross-references: EMBL:X59211; NID:g52338; PIDN:CAA41921.1; PID:e36191; PID:g1334075
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 81.9%; Score 59; DB 2; Length 102;
 Best Local Similarity 84.6%; Pred. No. 0.0018;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNFWLHWY 13
 :|||||:|||||
 Db 22 RASQSISNFWLHWY 34

RESULT 9

B43413
 Ig kappa chain V region - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-May-1997
 C:Accession: B43413
 R:Tomiyama, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.; Kum
 J. Biol. Chem. 267, 18085-18092, 1992
 A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct specific
 A:Reference number: A43413; MUID:92388177
 A:Accession: B43413
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-104 <TOM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:112818)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 81.9%; Score 59; DB 2; Length 104;
 Best Local Similarity 84.6%; Pred. No. 0.0019;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNFWLHWY 13
 :|||||:|||||
 Db 21 RASQSISNFWLHWY 33

RESULT 10

B45722
 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse (fr
 C:Species: Mus musculus (house mouse)
 C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
 C:Accession: B45722
 R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
 J. Virol. 67, 489-496, 1993

A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
 A:Reference number: A45722; MUID:93100833
 A:Accession: B45722
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1-107 <SIM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:120590)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein

Query Match 81.9%; Score 59; DB 2; Length 107;
 Best Local Similarity 84.6%; Pred. No. 0.0019;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNFWLHWY 13
 :|||||:|||||
 Db 24 RASQSISNFWLHWY 36

RESULT 11

A45722
 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (c
 C:Species: Mus musculus (house mouse)
 C:Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
 C:Accession: A45722
 R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va
 J. Virol. 67, 489-496, 1993
 A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on
 A:Reference number: A45722; MUID:93100833
 A:Accession: A45722
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-107 <SIM>
 A:Note: sequence extracted from NCBI backbone (NCBIP:120589)
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: glycoprotein

Query Match 81.9%; Score 59; DB 2; Length 107;
 Best Local Similarity 84.6%; Pred. No. 0.0019;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNFWLHWY 13
 :|||||:|||||
 Db 24 RASQSISNFWLHWY 36

RESULT 12

A26471
 Ig kappa chain precursor V region (MAK33) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
 C:Accession: A26471
 R:Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
 Gene 51, 13-19, 1987
 A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creat
 A:Reference number: A91572; MUID:87248058
 A:Accession: A26471
 A:Molecule type: mRNA
 A:Residues: 1-138 <BOC>
 A:Cross-references: GB:M16162; NID:g196893; PIDN:AAA38823.1; PID:g196894
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-138/Product: Ig kappa chain V region #status predicted <MAT>

Query Match 81.9%; Score 59; DB 2; Length 138;
 Best Local Similarity 84.6%; Pred. No. 0.0025;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNFWLHWY 13

Reference Number: 334076; MOID:33170387

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 20:07:19 ; Search time 69.28 Seconds
(without alignments)
5.715 Million cell updates/sec

Title: US-09-016-061-82

Perfect score: 72

Sequence: 1 QASQISINFLHWY 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	80.6	129	1 KVIW_HUMAN	P04431 homo sapien
2	54	75.0	92	1 KV09_RABIT	P01690 oryctolagus
3	54	75.0	108	1 KV5K_MOUSE	P01644 mus musculus
4	54	75.0	108	1 KV5L_MOUSE	P01645 mus musculus
5	54	75.0	108	1 KV5M_MOUSE	P01646 mus musculus
6	54	75.0	117	1 KV10_RABIT	P01691 oryctolagus
7	53	73.6	108	1 KVIH_HUMAN	P01594 homo sapien
8	53	73.6	108	1 KV5U_MOUSE	P04946 mus musculus
9	52	72.2	108	1 KV1P_HUMAN	P01608 homo sapien
10	52	72.2	108	1 KV5J_MOUSE	P01643 mus musculus
11	51	70.8	108	1 KVIH_HUMAN	P01600 homo sapien
12	51	70.8	108	1 KV5N_MOUSE	P01647 mus musculus
13	51	70.8	108	1 KV5O_MOUSE	P01648 mus musculus
14	50	69.4	108	1 KVIH_HUMAN	P01593 homo sapien
15	49	68.1	115	1 KV3I_HUMAN	P04433 homo sapien
16	48	66.7	115	1 KV5I_MOUSE	P01642 mus musculus
17	48	66.7	117	1 KVIJ_HUMAN	P01602 mus musculus
18	48	66.7	129	1 KV3H_HUMAN	P04207 homo sapien
19	47	65.3	107	1 KV04_RABIT	P01685 oryctolagus
20	47	65.3	108	1 KVIW_HUMAN	P01605 homo sapien
21	47	65.3	108	1 KVIH_HUMAN	P01606 homo sapien
22	46.5	64.6	109	1 KV3D_HUMAN	P01622 homo sapien
23	46	63.9	108	1 KV08_RABIT	P01689 oryctolagus
24	46	63.9	108	1 KVIQ_HUMAN	P01607 homo sapien
25	46	63.9	111	1 KVI2_RABIT	P01693 oryctolagus
26	45	62.5	107	1 KVIH_HUMAN	P01596 homo sapien
27	45	62.5	108	1 KV07_RABIT	P01688 oryctolagus
28	45	62.5	108	1 KV3V_MOUSE	P01674 mus musculus
29	45	62.5	109	1 KV03_RABIT	P01684 oryctolagus
30	44.5	61.8	109	1 KV3F_HUMAN	P01624 homo sapien
31	44	61.1	104	1 KVI7_RABIT	P01698 oryctolagus
32	44	61.1	108	1 KVIC_HUMAN	P01595 homo sapien
33	44	61.1	108	1 KVIH_HUMAN	P01597 homo sapien
34	44	61.1	108	1 KVIH_HUMAN	P01598 homo sapien

35	44	61.1	108	1 KVIK_HUMAN	P01603 homo sapien
36	44	61.1	108	1 KVIS_HUMAN	P01611 homo sapien
37	44	61.1	108	1 KVIY_HUMAN	P03622 homo sapien
38	44	61.1	108	1 KV5P_MOUSE	P01649 mus musculus
39	44	61.1	129	1 KVIH_HUMAN	P04432 homo sapien
40	43.5	60.4	109	1 KV3B_HUMAN	P01620 homo sapien
41	43	59.7	108	1 KVIQ_HUMAN	P01609 homo sapien
42	43	59.7	128	1 KV3K_HUMAN	P06311 homo sapien
43	43	59.7	283	1 LEG1_HAECO	O44126 haemonchus
44	43	59.7	521	1 COX1_APILI	P20374 apis mellif
45	42.5	59.0	108	1 KV3A_HUMAN	P01619 homo sapien

ALIGNMENTS

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RESULT 1
KVIW_HUMAN
ID KVIW_HUMAN STANDARD; PRT; 129 AA.
AC P04431;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION WALKER PRECURSOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85014148.
RA Klobbeck H.G., Combriato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human
RL lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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DR EMBL; X00965; CA25477.1; ALT_TERM.
DR PIR; A01883; K1HOWK.
DR HSSP; P01607; IREI.
DR PFAM; PF00047; Iq; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK 1.
FT DOMAIN 46 56 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 57 71 FRAMEWORK 2.
FT DOMAIN 72 78 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 79 110 FRAMEWORK 3.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 120 129 FRAMEWORK 4.
FT DISULFID 45 110 BY SIMILARITY.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;
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Query Match 80.6%; Score 58; DB 1; Length 129;
Best Local Similarity 76.9%; Pred. No. 0.0015;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QASQISINFLHWY 13
:|||||:|
Db 46 RASQISINFLNHWY 58

RESULT 2
KV09_RABIT

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ID KV09_RABIT STANDARD; PRT; 92 AA.
AC P01690;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V REGION 3381 (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE.
RX MEDLINE; 75176905.
RA Margolies M.N., Cannon L.E. III, Strosberg A.D., Haber E.;
RT "Diversity of light chain variable region sequences among rabbit
RT antibodies elicited by the same antigens.";
RL Proc. Natl. Acad. Sci. U.S.A. 72:2180-2184(1975).
CC -1- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM ANTIBODY TO TYPE III
CC PNEUMOCOCCI AND WAS ISOLATED FROM THE SERUM OF A SINGLE RABBIT.
DR PIR; A01953; KVRB38.
DR PFAM; PF00047; ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 >92
FT NON_TER 92 92
SQ SEQUENCE 92 AA; 9730 MW; 9A36B15913CB3BEE CRC64;

Query Match 75.0%; Score 54; DB 1; Length 92;
Best Local Similarity 76.9%; Pred. No. 0.0052;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
Db 24 QASESISNFWY 36

RESULT 3
KV5K_MOUSE STANDARD; PRT; 108 AA.
AC P01644;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-V REGION HP R16.7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RX STRAIN-A/J;
RC MEDLINE; 82150934.
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsonate antibodies differing
RT with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -1- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR; A01927; KVMASR.
DR PFAM; PF00047; ig; 1.
KW Immunoglobulin V region; Antiarsenate antibody.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFFF58E CRC64;

Query Match 75.0%; Score 54; DB 1; Length 108;
Best Local Similarity 69.2%; Pred. No. 0.0062;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
Db 24 RASQDISNFWY 36

RESULT 5
KV5M_MOUSE STANDARD; PRT; 108 AA.
AC P01646;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-V REGION HP 123E6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RX STRAIN-A/J;
RC MEDLINE; 82150934.
RA Siegelman M., Capra J.D.;
```

RT "Complete amino acid sequence of light chain variable regions derived
 RT from five monoclonal anti-p-azophenylarsonate antibodies differing
 RL with respect to a crossreactive idiotype.";
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
 CC -1- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
 DR PIR: A01927; KVMASR.
 DR PFAM: PF00047; Ig; 1.
 KW Immunoglobulin V region; Antiarsonate antibody.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49 FRAMEWORK 2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 108 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08EBA09A CRC64;
 Query Match 75.0%; Score 54; DB 1; Length 108;
 Best Local Similarity 69.2%; Pred. No. 0.0062;
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QASQSISNLFHWY 13
 Db :||| |||:|:|
 24 RASQDISYLNWY 36
 RESULT 6
 ID KV10_RABIT STANDARD; PRT; 117 AA.
 AC P01691;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V REGION 12F2 PRECURSOR (FRAGMENT).
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 83273646.
 RA Dreher K.L., Emorine L., Kindt T.J., Max E.E.;
 RT "cDNA clone encoding a complete rabbit immunoglobulin kappa light
 chain of b4 allotype.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:4489-4493(1983).
 CC -1- MISCELLANEOUS: THIS CLONE WAS DERIVED FROM THE RABBIT-MOUSE
 CC HYBRIDOMA 12F2; THE CHAIN PRODUCED IS A MONOCLONAL ANTIBODY
 CC AGAINST STREPTOCOCCAL GROUP C VACCINE.
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 CC -----
 DR EMBL; K01358; AAB59259.1; ALT_TERM.
 DR PIR; A01954; K4RBF2.
 DR PFAM: PF00047; Ig; 1.
 KW Immunoglobulin V region; Monoclonal antibody; Hybridoma; Signal.
 FT NON_TER 1 1
 FT SIGNAL <1 6
 FT CHAIN 7 117 IG KAPPA CHAIN V REGION 12F2.
 FT DOMAIN 7 29 FRAMEWORK 1.
 FT DOMAIN 30 40 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 41 55 FRAMEWORK 2.
 FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 63 94 FRAMEWORK 3.
 FT DOMAIN 95 106 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 107 116 FRAMEWORK 4.

FT DISULFID 29 86 BY SIMILARITY.
 FT NON_TER 117 117
 SQ SEQUENCE 117 AA; 12288 MW; E24A7582389E4439 CRC64;
 Query Match 75.0%; Score 54; DB 1; Length 117;
 Best Local Similarity 76.9%; Pred. No. 0.0067;
 Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 QASQSISNLFHWY 13
 Db :||| |||:|:|
 30 QASQSISYLSWY 42
 RESULT 7
 ID KV1B_HUMAN STANDARD; PRT; 108 AA.
 AC P01594;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG KAPPA CHAIN V-I REGION AU.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 72189444.
 RA Schiechi H., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal
 RT immunoglobulin L-chain of the kappa-type, subgroup I (Bence-Jones
 RT protein Au).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:345-370(1972).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY.
 RX MEDLINE; 77022433.
 RA Fehlhammer H., Schiffer M., Epp O., Colman P.M., Lattman E.E.,
 RA Schwager P., Steigemann W., Schramm H.J.;
 RT "The structure determination of the variable portion of the
 RT Bence-Jones protein Au.";
 RL Biophys. Struct. Mech. 1:139-146(1975).
 CC -1- MISCELLANEOUS: THE STRUCTURE OF THE V REGION WAS DETERMINED BY
 CC MOLECULAR REPLACEMENT METHODS USING THE KNOWN STRUCTURE OF THE V
 CC REGION OF THE KAPPA CHAIN REI.
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC PIR: A01862; K1HUAU.
 DR HSSP; P01607; 1REI.
 DR PFAM: PF00047; Ig; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK 1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
 FT DOMAIN 35 49 FRAMEWORK 2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
 FT DOMAIN 57 88 FRAMEWORK 3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
 FT DOMAIN 98 107 FRAMEWORK 4.
 FT DISULFID 23 88 BY SIMILARITY.
 FT NON_TER 108 108
 SQ SEQUENCE 108 AA; 11939 MW; E8011187E6F6FB9 CRC64;
 Query Match 73.6%; Score 53; DB 1; Length 108;
 Best Local Similarity 69.2%; Pred. No. 0.0053;
 Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 1 QASQSISNLFHWY 13
 Db :||| |||:|:|
 24 QASQDISYLNWY 36
 RESULT 8
 ID KV5U_MOUSE

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ID KV5U_MOUSE STANDARD; PRT; 108 AA.
AC P04946;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-V REGION NQ5-89.4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 83271467.
RA Kaartinen M., Griffiths G.M., Markham A.F., Milstein C.;
RT "mRNA sequences define an unusually restricted IgG response to 2-
RT phenylloxazalone and its early diversification.";
RL Nature 304:320-324(1983).
CC -1- MISCELLANEOUS: ANTI-2-PHENYL OXAZOLONE (PHOX) ANTIBODY.
CC -----
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CC -----
DR EMBL; K00745; AAA38690.1; -.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 FRAMEWORK 4.
FT DOMAIN 98 107 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 23 88 FRAMEWORK 4.
FT NON_TER 108 108 BY SIMILARITY.
SQ SEQUENCE 108 AA; 11866 MW; DB2C885920DC6DDDD CRC64;

Query Match 73.6%; Score 53; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. No. 0.0093;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ASQSTISNFWY 13
Db 25 ASQDISNFWY 36

RESULT 9
KVLP_HUMAN STANDARD; PRT; 108 AA.
AC P01608;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION ROY.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE; 68362076.
RA Hilschmann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT Cum.)";
FT Cum.);";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
RN [2]
RP REVISIONS TO 39 AND 41.
RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA Steinmetz-Kayne M., Suter L., Watanabe S.;
RA (In) Franek F., Shugar D. (eds.);
```

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RL Gamma globulins: structure and function, pp.57-74, Academic Press,
RL New York (1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01874; KIHURY.
DR HSSP; P80362; IWTL.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11782 MW; F5ACEDE5A313DF3A CRC64;

Query Match 72.2%; Score 52; DB 1; Length 108;
Best Local Similarity 76.9%; Pred. No. 0.014;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QASQISNFWY 13
Db 24 QASQDISNFWY 36

RESULT 10
KV5J_MOUSE STANDARD; PRT; 108 AA.
ID KV5J_MOUSE STANDARD; PRT; 108 AA.
AC P01643;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-V REGION MOPC 173.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RX MEDLINE; 76091934.
RA Schiff C., Fougereau M.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin. Amino-acid sequence of the light chain.";
RL Eur. J. Biochem. 59:525-537(1975).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01926; KVM573.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 108 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11819 MW; 2AD29D92A72AA0A3 CRC64;

Query Match 72.2%; Score 52; DB 1; Length 108;
Best Local Similarity 75.0%; Pred. No. 0.014;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ASQSTISNFWY 13
Db 25 ASQDISNFWY 36
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RESULT 11
KV1H_HUMAN
ID KV1H_HUMAN STANDARD; PRT; 108 AA.
AC P01600;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION HAU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE.
RX MEDLINE; 71032830.
RA Watanabe S., Hilschmann N.;
RT "The primary structure of a monoclonal kappa-type immunoglobulin L-
RT chain of subgroup I (Bence-Jones Protein HAU): subdivision within
RT subgroups."
RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295(1970).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01868: K1HUHU.
DR HSSP; P80362; LWTU.
DR PFW; PF00047; Ig; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160B0D0618 CRC64;

Query Match 70.8%; Score 51; DB 1; Length 108;
Best Local Similarity 69.2%; Pred. No. 0.021;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNLFHWY 13
:|||||:|
Db 24 RASQSISSVLSWY 36

RESULT 12
KV5N_MOUSE
ID KV5N_MOUSE STANDARD; PRT; 108 AA.
AC P01647;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-V REGION HP 124E1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RX MEDLINE; 82150934.
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsonate antibodies differing
RT with respect to a crossreactive idiotype."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR; A01927; KVMASR.
DR PFW; PF00047; Ig; 1.
KW Immunoglobulin V region; Antiarsonate antibody.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 108 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11961 MW; D52EDA5E9A45291C CRC64;

Query Match 70.8%; Score 51; DB 1; Length 108;
Best Local Similarity 61.5%; Pred. No. 0.021;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNLFHWY 13
:|||||:|
Db 24 RASQDINNVLNWKY 36

RESULT 14
KV1A_HUMAN
ID KV1A_HUMAN STANDARD; PRT; 108 AA.
AC P01593;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-I REGION AG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

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FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 108 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11965 MW; 39971BC653EFEFA2 CRC64;

Query Match 70.8%; Score 51; DB 1; Length 108;
Best Local Similarity 61.5%; Pred. No. 0.021;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNLFHWY 13
:|||||:|
Db 24 RASQDINNVLNWKY 36

RESULT 13
KV5Q_MOUSE
ID KV5Q_MOUSE STANDARD; PRT; 108 AA.
AC P01648;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-V REGION HP 91A3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE.
RX STRAIN-A/J;
RC MEDLINE; 82150934.
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsonate antibodies differing
RT with respect to a crossreactive idiotype."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: ANTI-ARSONATE HYBRIDOMA PROTEIN.
DR PIR; A01927; KVMASR.
DR PFW; PF00047; Ig; 1.
KW Immunoglobulin V region; Antiarsonate antibody.
FT DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 108 FRAMEWORK 4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11961 MW; D52EDA5E9A45291C CRC64;

Query Match 70.8%; Score 51; DB 1; Length 108;
Best Local Similarity 61.5%; Pred. No. 0.021;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNLFHWY 13
:|||||:|
Db 24 RASQDINNVLNWKY 36

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OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE.
RX Titani K., Shinoda T., Putnam F.W.;
RA "The amino acid sequence of a kappa type Bence-Jones protein. 3. The
RT complete sequence and the location of the disulfide bridges.";
RL J. Biol. Chem. 244:3550-3560(1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -1- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
DR PIR; A01861; K1HUAG.
DR HSP; P01607; IREI.
DR PFAM; PF00047; Ig; 1.
DR Immunoglobulin V region; Bence-Jones protein.
KW DOMAIN 1 23 FRAMEWORK 1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 35 49 FRAMEWORK 2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 57 88 FRAMEWORK 3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING 3.
FT DOMAIN 98 107 FRAMEWORK 4.
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11992 MW; E3B3B246C18F0C4F CRC64;

Query Match 69.4%; Score 50; DB 1; Length 108;
Best Local Similarity 61.5%; Pred. No. 0.031;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSIISNLFHWY 13
Db 24 QASQDINHLYNWY 36
|||||:::|

RESULT 15
KV3I_HUMAN
ID KV3I_HUMAN STANDARD; PRT; 115 AA.
AC P04433.
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-III REGION VG PRECURSOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85087932.
RA Pech M., Zachau H.G.;
RT "Immunoglobulin genes of different subgroups are interdigitated
RL within the VK locus.";
RL Nucleic Acids Res. 12:9229-9236(1984).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X01668; -; NOT_ANNOTATED_CDS.
DR PIR; A01900; K3HUVG.
DR PFAM; PF00047; Ig; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-III REGION VG.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT *DOMAIN 77 108 FRAMEWORK 3.
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FT DOMAIN 109 115 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115
SQ SEQUENCE 115 AA; 12575 MW; 2DE47CDA3A17D555 CRC64;

Query Match 68.1%; Score 49; DB 1; Length 115;
Best Local Similarity 61.5%; Pred. No. 0.05;
Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSIISNLFHWY 13
Db 44 RASQSVSSYLAWY 56
|||||:::|

Search completed: May 27, 2000, 20:07:20
Job time: 992 sec
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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:38:42 ; Search time 199.56 Seconds
(without alignments)
4.517 Million cell updates/sec

Title: US-09-016-061-82

Perfect score: 72

Sequence: 1 QASQISNPLHWY 13

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 225878 segs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPTREMBL_12.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phase.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	47	65.3	307	3	059680 schizosacch
2	43	59.7	130	8	080033 exoneurella
3	43	59.7	130	8	080034 exoneurella
4	43	59.7	131	8	079124 braunsapis
5	43	59.7	131	8	079125 exoneurella
6	43	59.7	131	8	079126 exoneurella
7	42	58.3	873	5	001424 caenorhabdi
8	42	58.3	897	5	09X280 caenorhabdi
9	41	56.9	400	5	017674 caenorhabdi
10	40	55.6	166	5	096211 plasmodium
11	39	54.2	130	8	080035 exoneurella
12	39	54.2	185	8	063601 drosophila
13	39	54.2	187	10	092WD1 arabisopsis
14	39	54.2	334	2	Q9Z785 chlamydia p
15	39	54.2	399	4	Q16529 homo sapien
16	39	54.2	736	10	082754 arabisopsis
17	38	52.8	98	2	066132 buchnera ap
18	38	52.8	162	5	Q17590 caenorhabdi
19	38	52.8	219	2	P73967 synechocyst
20	38	52.8	265	8	047565 agrocye ae

21	38	52.8	285	5	Q18853	Q18853 caenorhabdi
22	38	52.8	324	8	Q9XKG9	Q9XKG9 oecophylla
23	38	52.8	341	5	Q61921	Q61921 caenorhabdi
24	38	52.8	487	2	Q30651	Q30651 vibrio chol
25	38	52.8	814	4	Q13444	Q13444 homo sapien
26	38	52.8	814	4	Q13493	Q13493 homo sapien
27	38	52.8	887	4	Q15134	Q15134 homo sapien
28	38	52.8	887	11	Q88763	Q88763 rattus norv
29	38	52.8	1670	5	Q23901	Q23901 dictyostell
30	37.5	52.1	723	5	Q17748	Q17748 caenorhabdi
31	37	51.4	17	8	Q9ZYX4	Q9ZYX4 xorides pra
32	37	51.4	240	2	P73054	P73054 synechocyst
33	37	51.4	304	2	Q9WY40	Q9WY40 thermotoga
34	37	51.4	310	1	Q58038	Q58038 pyrococcus
35	37	51.4	324	8	Q63272	Q63272 polyergus r
36	37	51.4	397	6	Q29458	Q29458 bos taurus
37	37	51.4	470	4	Q15204	Q15204 homo sapien
38	37	51.4	509	5	Q76924	Q76924 drosophila
39	37	51.4	601	8	Q9XPH6	Q9XPH6 chelonla my
40	36	50.0	43	9	Q38227	Q38227 bacterioph
41	36	50.0	51	5	Q27062	Q27062 trypanosoma
42	36	50.0	55	9	Q21921	Q21921 bacterioph
43	36	50.0	55	9	Q80163	Q80163 bacterioph
44	36	50.0	68	10	Q41946	Q41946 arabidopsis
45	36	50.0	71	10	Q96415	Q96415 daucus caro

ALIGNMENTS

RESULT 1
059680
ID 059680 PRELIMINARY; PRT; 307 AA.
AC 059680;
DT 01-JAN-1999 (TREMBlrel. 09, Created)
DT 01-JAN-1999 (TREMBlrel. 09, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE PROBABLE CYTOCHROME C1, HEME PROTEIN PRECURSOR.
GN SPC29A3.18.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Archiascomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RA LYNE M., RAJANDREAM M.A., BARRELL B.G., VOLCKAERT G.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IS THE HEME-CONTAINING COMPONENT OF THE CYTOCHROME
CC B-C1 COMPLEX, WHICH ACCEPTS ELECTRONS FROM RIESKE PROTEIN AND
CC TRANSFERS ELECTRONS TO CYTOCHROME C IN THE MITOCHONDRIAL
CC RESPIRATORY CHAIN.
CC -!- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN.
CC -!- SUBCELLULAR LOCATION: ANCHORED IN THE INNER MITOCHONDRIAL MEMBRANE
CC WITH ITS N-TERMINUS PROTRUDING INTO THE MITOCHONDRIAL
CC INTERMEMBRANE SPACE (BY SIMILARITY).
DR EMBL; AL022299; CAA18395.1; -
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PRINTS; PR00603; CYTOCHROME_C1.
KW Electron transport; Respiratory chain; Oxidative phosphorylation;
KW Heme; Mitochondrion; Transmembrane; Transit peptide.
FT TRANSIT 1 62 MITOCHONDRION (BY SIMILARITY).
FT CHAIN 63 307 PROBABLE CYTOCHROME C1, HEME PROTEIN.
FT BINDING 102 102 HEME (COVALENT) (BY SIMILARITY).
FT BINDING 105 105 HEME (COVALENT) (BY SIMILARITY).
FT METAL 106 106 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT METAL 225 225 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT TRANSMEM 273 287 ANCHORS TO THE MEMBRANE (BY SIMILARITY).
SQ SEQUENCE 307 AA; 34340 MW; 8B01AB57 CRC32;

Query Match

65.3%; Score 47; DB 3; Length 307;

Best Local Similarity 58.3%; Pred. No. 0.85;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 QASQISNFWLW 12
||.:.:|||||
Db 246 QAAKDVNFWLW 257

RESULT 2
O80033 PRELIMINARY; PRT; 130 AA.
AC O80033;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE CYTOCHROME OXIDASE I (FRAGMENT).
OS Exoneurella lawsoni.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Exoneurella.
RN [1]
RP SEQUENCE FROM N.A.
RA REYES S.G., COOPER S.J.B., SCHWARZ M.P.;
RT "Species phylogeny of the bee genus Exoneurella Michener (Hymenoptera:
RT Apidae: Allodapini): evidence from molecular and morphological data
RT sets.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF072661; AAC24880.1; -.
DR PFAM; PF00115; COX1; 1.
KW Mitochondrion.
FT NON_TER 1 1
FT NON_TER 130 130
SQ SEQUENCE 130 AA; 15339 MW; 76C2FAFF CRC32;

Query Match 59.7%; Score 43; DB 8; Length 130;
Best Local Similarity 75.0%; Pred. No. 1.9;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 ISNFWLW 13
||.:.:|||||
Db 19 ISSFWW 26

RESULT 3
O80034 PRELIMINARY; PRT; 130 AA.
AC O80034;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE CYTOCHROME OXIDASE I (FRAGMENT).
OS Exoneurella tridentata.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Exoneurella.
RN [1]
RP SEQUENCE FROM N.A.
RA REYES S.G., COOPER S.J.B., SCHWARZ M.P.;
RT "Species phylogeny of the bee genus Exoneurella Michener (Hymenoptera:
RT Apidae: Allodapini): evidence from molecular and morphological data
RT sets.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF072663; AAC24882.1; -.
DR PFAM; PF00115; COX1; 1.
KW Mitochondrion.
FT NON_TER 1 1
FT NON_TER 130 130
SQ SEQUENCE 130 AA; 15438 MW; 429B063B CRC32;

Query Match 59.7%; Score 43; DB 8; Length 130;
Best Local Similarity 75.0%; Pred. No. 1.9;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 ISNFWLW 13
||.:.:|||||
Db 19 ISSFWW 26

RESULT 4
O79124 PRELIMINARY; PRT; 131 AA.
AC O79124;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE CYTOCHROME OXIDASE I (FRAGMENT).
OS Braunsapis unicolor.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Braunsapis.
RN [1]
RP SEQUENCE FROM N.A.
RA REYES S.G., COOPER S.J.B., SCHWARZ M.P.;
RT "Species phylogeny of the bee genus Exoneurella Michener (Hymenoptera:
RT Apidae: Allodapini): evidence from molecular and morphological data
RT sets.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF072659; AAC24878.1; -.
DR PFAM; PF00115; COX1; 1.
KW Mitochondrion.
FT NON_TER 1 1
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 15603 MW; 7764748E CRC32;

Query Match 59.7%; Score 43; DB 8; Length 131;
Best Local Similarity 75.0%; Pred. No. 1.9;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 ISNFWLW 13
||.:.:|||||
Db 19 ISSFWW 26

RESULT 5
O79125 PRELIMINARY; PRT; 131 AA.
AC O79125;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE CYTOCHROME OXIDASE I (FRAGMENT).
OS Brevineura xanthoclypeata.
OG Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Apoidea; Apidae; Brevineura.
RN [1]
RP SEQUENCE FROM N.A.
RA REYES S.G., COOPER S.J.B., SCHWARZ M.P.;
RT "Species phylogeny of the bee genus Exoneurella Michener (Hymenoptera:
RT Apidae: Allodapini): evidence from molecular and morphological data
RT sets.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF072660; AAC24879.1; -.
DR PFAM; PF00115; COX1; 1.
KW Mitochondrion.
FT NON_TER 1 1
FT NON_TER 131 131
SQ SEQUENCE 131 AA; 15508 MW; 6FAB2172 CRC32;

Query Match 59.7%; Score 43; DB 8; Length 131;
 Best Local Similarity 75.0%; Pred. No. 1.9;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ISNFIHWY 13
 ||:||||
 Db 19 ISSFIHWY 26

RESULT 6
 079126 PRELIMINARY; PRT; 131 AA.
 AC 079126;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE CYTOCHROME OXIDASE I (FRAGMENT).
 OS Exoneurella eremophila.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Apoidea; Apidae; Exoneurella.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA REYES S.G., COOPER S.J.B., SCHWARZ M.P.;
 RT "Species phylogeny of the bee genus Exoneurella Michener (Hymenoptera:
 RT Apidae: Allodapini): evidence from molecular and morphological data
 RT sets";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF072662; AAC24881.1; -;
 DR PFAM; PF00115; COX1; 1.
 KW Mitochondrion.
 FT NON_TER 1 1
 FT NON_TER 131 131
 SQ SEQUENCE 131 AA; 15531 MW; 59E15055 CRC32;

Query Match 59.7%; Score 43; DB 8; Length 131;
 Best Local Similarity 75.0%; Pred. No. 1.9;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 ISNFIHWY 13
 ||:||||
 Db 19 ISSFIHWY 26

RESULT 7
 001424 PRELIMINARY; PRT; 873 AA.
 AC 001424;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE SIMILARITY TO PHOSPHATIDYLINOSITOL 3-KINASES.
 GN B0025.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
 OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE; 94150718.
 RA WILSON R., AINSKOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU 2., DUREIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMANN P.;

RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA DAVIDSON S., WOHLDMANN P.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA WATERSTON R.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U97190; AAB52364.1; -;
 DR PFAM; PF00454; PI3_P14_kinase; 1.
 DR PFAM; PF00792; PI3K_C2; 1.
 DR PFAM; PF00613; PI3Ka; 1.
 SQ SEQUENCE 873 AA; 99766 MW; 34B5E25F CRC32;

Query Match 58.3%; Score 42; DB 5; Length 873;
 Best Local Similarity 50.0%; Pred. No. 18;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ASQISISNFIHWY 13
 ||:||||:
 Db 463 ASPKVSNIYWH 474

RESULT 8
 09XZRO PRELIMINARY; PRT; 897 AA.
 ID 09XZRO
 AC 09XZRO;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE VPS34 HOMOLOGUE.
 GN VPS34.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
 OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA BERNARD V., ROGGO L., MLLER F., WYMAN M.P.;
 RT "The VPS34 gene from C. elegans";
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; Y12543; CAA73142.1; -;
 SQ SEQUENCE 897 AA; 102656 MW; E8A4ABE4 CRC32;

Query Match 58.3%; Score 42; DB 5; Length 897;
 Best Local Similarity 50.0%; Pred. No. 18;
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ASQISISNFIHWY 13
 ||:||||:
 Db 487 ASPKVSNIYWH 498

RESULT 9
 017674 PRELIMINARY; PRT; 400 AA.
 ID 017674
 AC 017674; 046026;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE C49A1.2 PROTEIN.
 GN C49A1.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
 OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.


```

RESULT 13
Q9ZWD1
ID Q9ZWD1 PRELIMINARY; PRT; 187 AA.
AC Q9ZWD1;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE F202.21.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC eudicotyledons; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RP SEQUENCE FROM N.A.
RA SHINN P., BUEHLER E., DEWAR K., DUNN P., FENG J., KIM C., WALKER M.,
RA CONWAY A.B., CONWAY A.R., KURTZ D., OJI O., SHEN Y.K., TORIUMI M.,
RA VISOTSKAIA V., YU G., DAVIS R.W., FEDERSPIEL N.A., THEOLOGIS A.,
RA ECKER J.R.;
RT "Genomic sequence for Arabidopsis thaliana BAC F20N2.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC002328; AAC83072.1; -.
SQ SEQUENCE 187 AA; 20782 MW; 6F4593D5 CRC32;

Query Match 54.2%; Score 39; DB 10; Length 187;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SNFLHW 12
| | | | |
Db 181 SNFLHW 186

RESULT 14
Q9Z785
ID Q9Z785 PRELIMINARY; PRT; 334 AA.
AC Q9Z785;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE CT566 HYPOTHETICAL PROTEIN.
GN CPN0821.
OS Chlamydia pneumoniae.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydothi.
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CWL029;
RA KALMAN S., MITCHELL W., MARATHE R., LAMMEL C., FAN J., OLINGER L.,
RA GRIMWOOD J., DAVIS R.W., STEPHENS R.S.;
RT "Comparative Genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF001662; AAD18959.1; -.
SQ SEQUENCE 334 AA; 38107 MW; 4100077E CRC32;

Query Match 54.2%; Score 39; DB 2; Length 334;
Best Local Similarity 70.0%; Pred. No. 23;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 SQSISNFW 12
| | | | |
Db 197 SQSLLNFW 206

RESULT 15
Q16529
ID Q16529 PRELIMINARY; PRT; 399 AA.
AC Q16529;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

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DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE LYSOSOMAL ACID LIPASE PRECURSOR.
GN LAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RA DU H., GREGORY G.A.;
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z31690; CAA83495.1; -.
DR EMBL; U08464; AAB60328.1; -.
DR PROSITE; PS00120; LIPASE_SER; 1.
DR PFAM; PF00561; abhydrolase; 1.
KW Signal.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 399 LYSOSOMAL ACID LIPASE.
FT VARIANT 16 16 T -> P (IN REF. 1).
FT VARIANT 23 23 R -> G (IN REF. 1).
SQ SEQUENCE 399 AA; 45518 MW; 1A970E61 CRC32;

Query Match 54.2%; Score 39; DB 4; Length 399;
Best Local Similarity 54.5%; Pred. No. 28;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 ASQISNFW 12
| | | | |
Db 286 AGTSVQNNLHW 296

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Search completed: May 27, 2000, 19:38:43
Job time: 2376 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:21:37 ; Search time 148.45 Seconds
(without alignments)
2.074 Million cell updates/sec

Title: US-09-016-061-82
Perfect score: 72
Sequence: 1 QASQSISNFWLHWY 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	72	100.0	13	W76031	LM609 grafted anti
2	65	90.3	13	W76011	LM609 grafted anti
3	65	90.3	107	W76006	LM609 grafted anti
4	65	90.3	107	W76002	Vitaxin antibody 1
5	65	90.3	107	W76004	LM609 antibody lig
6	61	84.7	105	W87456	Jk gene product. N
7	61	84.7	105	W87458	Humanised anti-alp
8	61	84.7	107	W84098	Humanised anti-alp
9	61	84.7	108	W84094	Murine vitronectin
10	61	84.7	112	W84100	Vitronectin alpha-
11	60	83.3	108	W00241	EGF receptor chime
12	59	81.9	107	R25729	Humanised VL regio
13	59	81.9	108	R15438	Light chain variab
14	59	81.9	109	W89176	Anti-p53 monoclon
15	59	81.9	127	R54093	Sequence of mouse
16	59	81.9	240	R15443	Single chain Fv fr
17	58	80.6	75	W62818	Amino acid sequenc
18	58	80.6	75	W62802	Amino acid sequenc
19	58	80.6	76	W80980	Variable kappa lig
20	58	80.6	86	W62806	Amino acid sequenc
21	58	80.6	101	R22577	Light chain VK10.1
22	58	80.6	104	W62821	Amino acid sequenc
23	58	80.6	104	W62822	Amino acid sequenc
24	58	80.6	104	W62804	Amino acid sequenc
25	58	80.6	105	W80968	Kappa light chain
26	58	80.6	105	W80974	Kappa light chain
27	58	80.6	105	W80978	Kappa light chain
28	58	80.6	108	R54258	Anti-HIV gp120 imm
29	58	80.6	108	W01281	VL region of HIV n
30	58	80.6	122	W24538	Immunoglobulin rB6
31	57	79.2	108	R50219	HSV glycoprotein F
32	57	79.2	108	W04333	Light chain of mon
33	57	79.2	124	W59620	Anti-RSV F protein
34	57	79.2	127	W59621	Anti-RSV F protein

35	56	77.8	40	1	P60258	N-terminal sequenc
36	56	77.8	105	1	W80976	Kappa light chain
37	55	76.4	107	1	R30770	Consensus humanise
38	55	76.4	107	1	R38601	HYH light chain A
39	55	76.4	107	1	W58482	Murine HYH antibody
40	55	76.4	108	1	W54012	Anti-CD4 antibody
41	55	76.4	108	1	W70622	Human consensus fr
42	55	76.4	109	1	R52033	Light chain variab
43	54	75.0	55	1	W99076	Immunoglobulin lik
44	54	75.0	107	1	R54319	Anti-HIV gp120 imm
45	54	75.0	107	1	W01287	VL region of HIV n

ALIGNMENTS

RESULT 1

W76031
ID W76031 standard; Protein; 13 AA.
AC W76031;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-L region CDRL protein fragment #2.
KW Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;
KW LM609; inhibitor; Integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-L region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49868.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
Integrin - and related grafted antibodies based on murine monoclonal
LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
LM609 heavy and light chain variable region. LM609 and the antibody
vitaxin bind selectively to Integrin alphavbeta3 and can be used to
inhibit binding of alphavbeta3 to a ligand and thus block
Integrin-mediated signal transduction. This is useful in the treatment,
prevention and diagnosis of alphavbeta3-mediated disease, specifically,
angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
arthritis, macular degeneration, osteoporosis etc.). The antibodies
contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
that of parent the parent antibody.
CC Sequence 13 AA;
SQ

Query Match 100.0%; Score 72; DB 1; Length 13;

Best Local Similarity 100.0%; Pred. No. 7.9e-06;

Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QASQSISNFWLHWY 13

Db 1 QASQSISNFWLHWY 13

RESULT 2

W76011
ID W76011 standard; Protein; 13 AA.
AC W76011;
DT 02-NOV-1998 (first entry)

DE LM609 grafted antibody V-L region CDRL protein fragment #1.
KW Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DT N-PSDB; V49843.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Disclosure: Page 40; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 13 AA;

Query Match 90.3%; Score 65; DB 1; Length 13;
 Best Local Similarity 92.3%; Pred. No. 0.0001;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQTSNLFHWY 13
 ||||| ||||
 DB 1 QASQTSNHLHWY 13

RESULT 3
 W76006
 ID W76006 standard; Protein; 107 AA.

AC W76006;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody light chain variable region protein fragment.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

OS Mus sp.
 FH Key Location/Qualifiers
 FT Misc_difference 49 /label= Arg, Met
 FT PN WO9833919-A2.

PN 06-AUG-1998.

PD 30-JAN-1998; U01826.

PR 30-JAN-1997; US-791391.

PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

DR WPI: 98-437472/37.

DT N-PSDB; V49843.

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

PS Claim 19; Fig 7; 129pp; English.

CC This sequence represents a LM609 grafted antibody variable light chain

CC region. LM609 and the antibody vitaxin bind selectively to integrin

CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand
 CC and thus block integrin-mediated signal transduction. This is useful in
 CC the treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 SQ Sequence 107 AA;

Query Match 90.3%; Score 65; DB 1; Length 107;
 Best Local Similarity 92.3%; Pred. No. 0.00097;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQTSNLFHWY 13
 ||||| ||||
 DB 24 QASQTSNHLHWY 36

RESULT 4
 W76002
 ID W76002 standard; Protein; 107 AA.

AC W76002;
 DT 02-NOV-1998 (first entry)
 DE Vitaxin antibody light chain variable region protein fragment.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

OS Mus sp.

PN WO9833919-A2.

PD 06-AUG-1998.

PF 30-JAN-1998; U01826.

PR 30-JAN-1997; US-791391.

PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

DR WPI: 98-437472/37.

DT N-PSDB; V49821.

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

PS Claim 1; Fig 1b; 129pp; English.

CC This sequence represents the vitaxin antibody variable light chain
 CC region. Vitaxin and the antibody LM609 bind selectively to integrin
 CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a
 CC ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions

CC so are suitable for use in humans. Enhanced types of LM609 have affinity

CC more than 90 times greater than that of parent the parent antibody.

CC Sequence 107 AA;

Query Match 90.3%; Score 65; DB 1; Length 107;
 Best Local Similarity 92.3%; Pred. No. 0.00097;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQTSNLFHWY 13
 ||||| ||||
 DB 24 QASQTSNHLHWY 36

RESULT 5
 W76004
 ID W76004 standard; Protein; 107 AA.

AC W76004;

DT 02-NOV-1998 (first entry)
 DE LM609 antibody light chain variable region protein fragment.
 KW vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB: W76004.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 46; Fig 2b; 129pp; English.
 CC This sequence represents the LM609 antibody variable light chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 CC Sequence 107 AA;
 SQ

Query Match 90.3%; Score 65; DB 1; Length 107;
 Best Local Similarity 92.3%; Pred. No. 0.00097;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNHLHWY 13
 :|||||
 Db 24 QASQSISNHLHWY 36

RESULT 6
 W87456
 ID W87456 standard; Protein; 105 AA.
 AC W87456;
 DT 15-MAR-1999 (first entry)
 DE Jk gene product.
 KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
 KW D12H2LCREI; Jk protein.
 OS Mus sp.
 PN WO9840488-A1.
 PD 17-SEP-1998.
 PF 12-MAR-1998; U04987.
 PR 12-MAR-1997; US-039609.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PI Johanson KO, Jonak ZL, Taylor AH;
 DR WPI: 99-034590/03.
 DR N-PSDB: V71803.
 PT New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis
 PS Example 14; Page 66; 97pp; English.
 CC This polypeptide is encoded by a Jk synthetic gene segment (see
 CC V71803). It was utilising in novel D12H2REI humanised light chain

CC variable region (see W87458), which comprises a human REI framework
 CC and complementarity determining regions from the anti-human alpha-v
 CC beta-3 vitronectin receptor monoclonal antibody D12. Humanised D12
 CC antibodies can be used for passive immunotherapy of disorders
 CC mediated by the alpha-v beta-3 vitronectin receptor, e.g. restenosis
 CC and angiogenic associated diseases.
 SQ Sequence 105 AA;

Query Match 84.7%; Score 61; DB 1; Length 105;
 Best Local Similarity 84.6%; Pred. No. 0.0041;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNHLHWY 13
 :|||||
 Db 24 RASQSISNHLHWY 36

RESULT 7
 W87458
 ID W87458 standard; Protein; 105 AA.
 AC W87458;
 DT 15-MAR-1999 (first entry)
 DE Humanised anti-alpha-v beta-3 MAB D12H2LCREI VL.
 KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;
 KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
 KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
 KW angiogenesis; diabetic retinopathy; inflammation;
 KW macular degeneration; osteoporosis; Paget's disease;
 KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
 KW D12H2LCREI.
 OS Homo sapiens.
 OS Synthetic.
 PN WO9840488-A1.
 PD 17-SEP-1998.
 PF 12-MAR-1998; U04987.
 PR 12-MAR-1997; US-039609.
 PA (SMIK) SMITHKLINE BEECHAM CORP.
 PI Johanson KO, Jonak ZL, Taylor AH;
 DR WPI: 99-034590/03.
 DR N-PSDB: V71805.
 PT New anti alpha_v beta_3 vitronectin receptor antibodies - used for
 PT immunotherapeutic treatment of e.g. diabetic retinopathy,
 PT inflammatory disorders, atherosclerosis, restenosis, cancers or
 PT osteoporosis
 PS Example 14; Page 68-69; 97pp; English.
 CC This is the amino acid sequence of the light chain variable region
 CC (VL) of humanised anti-alpha-v beta-3 vitronectin receptor
 CC monoclonal antibody D12H2LCREI. It is based on a synthetic
 CC humanised kappa chain based on a modified human REI kappa
 CC framework and complementarity determining regions from the murine
 CC anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody
 CC D12 (see W84094). Humanised antibodies of the invention can be used
 CC for passive immunotherapy of a disorder mediated by the alpha-v
 CC beta-3 receptor, e.g. cardiovascular disorders or angiogenic-
 CC related disorders, such as angiogenesis associated with diabetic
 CC retinopathy, atherosclerosis and restenosis, chronic inflammatory
 CC disorders, macular degeneration, rheumatoid arthritis and cancer,
 CC e.g. solid tumour metastasis, and diseases where bone resorption is
 CC associated with pathology such as osteoporosis, hyperparathyroidism,
 CC Paget's disease, hypercalcaemia of malignancy, osteolytic lesions
 CC produced by bone metastasis, bone loss due to immobilisation or sex
 CC hormone deficiency. They can also be used for targeted drug
 CC therapy, and for detection and diagnosis.
 SQ Sequence 105 AA;

Query Match 84.7%; Score 61; DB 1; Length 105;
 Best Local Similarity 84.6%; Pred. No. 0.0041;
 Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQSISNHLHWY 13
 :|||||


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Db      24 RASQSTSNHLHWY 36

RESULT      8
W84098
ID      W84098 standard; Protein; 107 AA.
AC      W84098;
DE      Humanised anti-alpha-v beta-3 MAb D12HZHC 1-0 VL.
KW      Humanised antibody; monoclonal antibody; MAb; antibody engineering;
KW      mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
KW      cancer; metastasis; rheumatoid arthritis; atherosclerosis;
KW      angiogenesis; diabetic retinopathy; inflammation;
KW      macular degeneration; osteoporosis; Paget's disease;
KW      hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
KW      D12HZHC-10.
OS      Homo sapiens.
OS      Synthetic.
FH      Key
FT      Region
FT      Location/Qualifiers
FT      24..34
FT      /label= CDR1
FT      Region
FT      50..56
FT      /label= CDR2
FT      Region
FT      89..97
FT      /label= CDR3
FT
PN      W09840488-A1.
PD      17-SEP-1998.
PF      12-MAR-1998; U04987.
PR      12-MAR-1997; US-039609.
PA      (SMIK ) SMITHKLINE BEECHAM CORP.
PI      Johanson KO, Jonak ZL, Taylor AH;
DR      WPI: 99-034590/03.
DR      N-PSDB: V71800.
PT      New anti alpha_v beta_3 vitronectin receptor antibodies - used for
PT      immunotherapeutic treatment of e.g. diabetic retinopathy,
PT      inflammatory disorders, atherosclerosis, restenosis, cancers or
PT      osteoporosis
PS      Claim 2; Page 61-62: 97pp; English.
CC      This is the amino acid sequence of the light chain variable region
CC      (VL) of humanised anti-alpha-v beta-3 vitronectin receptor
CC      monoclonal antibody D12HZHC 1-0. It is based on the VL sequence
CC      (see W84096) of human Kabat subgroup III kappa chain, with
CC      complementarity determining regions (CDRs) from the murine
CC      anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody
CC      D12 (see W84093). 3 Murine framework residues (1, 49 and 60)
CC      are retained. The humanised light chain can be expressed in host
CC      cells using nucleic acid molecules (see V71800) of the invention.
CC      Humanised D12 VH is also provided (see W84097). The humanised
CC      antibodies can be used for passive immunotherapy of disorders
CC      mediated by the alpha-v beta-3 receptor, e.g. cardiovascular or
CC      angiogenic-related disorders, such as angiogenesis associated
CC      with diabetic retinopathy, atherosclerosis and restenosis, chronic
CC      inflammatory disorders, macular degeneration, rheumatoid arthritis
CC      and cancer, e.g. solid tumour metastasis, and diseases where bone
CC      resorption is associated with pathology such as osteoporosis.
CC      hyperparathyroidism, Paget's disease, hypercalcaemia of malignancy,
CC      osteolytic lesions produced by bone metastasis, bone loss due to
CC      immobilisation or sex hormone deficiency. They can also be used for
CC      targeted drug therapy, and for detection and diagnosis.
CC      Sequence 107 AA;
SQ

Query Match      84.7%; Score 61; DB 1; Length 107;
Best Local Similarity 84.6%; Pred. No. 0.0042;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 QASQSTSNFLHWY 13
      :|:|:|:|:|:|:|:|:|
Db      24 RASQSTSNHLHWY 36

RESULT      10
W84100
ID      W84100 standard; Protein; 112 AA.
AC      W84100;
DE      15-MAR-1999 (first entry)
DT      Vitronectin alpha-v beta-3 MAb VL.
DE      Vitronectin alpha-v beta-3
KW      Humanised antibody; monoclonal antibody; MAB; antibody engineering;
KW      mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;

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ID      W84094 standard; Protein; 108 AA.
AC      W84094;
DE      15-MAR-1999 (first entry)
DE      Murine vitronectin alpha-v beta-3 receptor MAB VL region.
KW      Humanised antibody; monoclonal antibody; MAB; antibody engineering;
KW      mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
KW      cancer; metastasis; rheumatoid arthritis; atherosclerosis;
KW      angiogenesis; diabetic retinopathy; inflammation;
KW      macular degeneration; osteoporosis; Paget's disease;
KW      hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.
OS      Mus sp.
OS      Location/Qualifiers
FH      Key
FT      Region
FT      24..34
FT      /label= CDR1
FT      Region
FT      50..56
FT      /label= CDR2
FT      Region
FT      89..97
FT      /label= CDR3
FT
PN      W09840488-A1.
PD      17-SEP-1998.
PF      12-MAR-1998; U04987.
PR      12-MAR-1997; US-039609.
PA      (SMIK ) SMITHKLINE BEECHAM CORP.
PI      Johanson KO, Jonak ZL, Taylor AH;
DR      WPI: 99-034590/03.
DR      N-PSDB: V71798.
PT      New anti alpha_v beta_3 vitronectin receptor antibodies - used for
PT      immunotherapeutic treatment of e.g. diabetic retinopathy,
PT      inflammatory disorders, atherosclerosis, restenosis, cancers or
PT      osteoporosis
PS      Example 13; Page 59-60: 97pp; English.
CC      This is the amino acid sequence of the light chain variable region
CC      (VL) of the anti-human alpha-v beta-3 vitronectin receptor murine
CC      monoclonal antibody D12, as deduced from isolated cDNA (see
CC      V71798). D12 VH (see W84093) and VL show sequence similarity to
CC      Kabat VH subgroup I (see W84095) and Kabat VK subgroup III (see
CC      W84096), respectively. Humanised VH (see W84097) and VL (see
CC      W84098) were constructed by combining the framework regions of the
CC      human V region consensus sequences with complementarity determining
CC      regions of D12 (keeping some preferred murine framework residues).
CC      The humanised antibodies are specifically reactive with the human
CC      alpha-v beta-3 protein receptor and capable of neutralising the
CC      receptor. They can be used for passive immunotherapy of a disorder
CC      mediated by the alpha-v beta-3 receptor, e.g. cardiovascular
CC      disorders or angiogenic-related disorders, such as angiogenesis
CC      associated with diabetic retinopathy, atherosclerosis and
CC      restenosis, chronic inflammatory disorders, macular degeneration,
CC      rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and
CC      diseases where bone resorption is associated with pathology such as
CC      osteoporosis, hyperparathyroidism, Paget's disease, hypercalcaemia
CC      of malignancy, osteolytic lesions produced by bone metastasis, bone
CC      loss due to immobilisation or sex hormone deficiency. They can also
CC      be used for targeted drug therapy, and for detection and diagnosis.
CC      Sequence 108 AA;
SQ

Query Match      84.7%; Score 61; DB 1; Length 108;
Best Local Similarity 84.6%; Pred. No. 0.0043;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 QASQSTSNFLHWY 13
      :|:|:|:|:|:|:|:|:|
Db      24 RASQSTSNHLHWY 36

RESULT      10
W84100
ID      W84100 standard; Protein; 112 AA.
AC      W84100;
DE      15-MAR-1999 (first entry)
DT      Vitronectin alpha-v beta-3 MAB VL.
DE      Vitronectin alpha-v beta-3
KW      Humanised antibody; monoclonal antibody; MAB; antibody engineering;
KW      mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;

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KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
KW angiogenesis; diabetic retinopathy; inflammation;
KW macular degeneration; osteoporosis; Paget's disease;
KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.
OS Mus sp.
PN W09840488-A1.
PD 17-SEP-1998.
PF 12-MAR-1998; U04987.
PR 12-MAR-1997; US-039609.
PA (SMIK) SMITHKLINE BEECHAM CORP.
PI Johanson KO, Jonak ZL, Taylor AH;
DR WPI; 99-034590/03.
DR N-PSDB; V71802.
PT New anti alpha_v beta_3 vitronectin receptor antibodies - used for
PT immunotherapeutic treatment of e.g. diabetic retinopathy,
PT inflammatory disorders, atherosclerosis, restenosis, cancers or
PT osteoporosis
PS Example 13; Page 64; 97pp; English.
CC This is the amino acid sequence of the region of the murine
CC monoclonal antibody (MAB) D12 light chain variable region (VL)
CC that is altered in humanised D12 VL (see also W84098). A
CC synthetic gene (see V81902) encoding the protein was prepared
CC from synthetic oligonucleotides and used to prepare an expression
CC vector for humanised D12 VL. D12 is an anti-human alpha-v beta-3
CC vitronectin receptor MAB. Humanised D12 MABs can be used for
CC passive immunotherapy of disorders mediated by the alpha-v beta-3
CC vitronectin receptor, e.g. restenosis and angiogenic associated
CC diseases.
SQ Sequence 112 AA;

Query Match 84.7%; Score 61; DB 1; Length 112;
Best Local Similarity 84.6%; Pred. No. 0.0044;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNPLHWY 13
:||||| |
Db 24 RASQISNHLHWY 36

RESULT 11
W00241
ID W00241 standard; Protein; 108 AA.
AC W00241;
DT 22-NOV-1996 (first entry)
DE EGF receptor chimeric MAB chMint5 VL chain.
KW Mouse-human chimeric antibody; monoclonal antibody; chMint5;
KW epidermal growth factor receptor; EGF-R; diagnosis; therapy;
KW immunotoxin; immunocytokine; tumour; cancer.
OS Mus musculus.
FH Key Location/Qualifiers
FT region 24..34
FT /label= CDR1
FT region 50..56
FT /label= CDR2
FT region 89..97
FT /label= CDR3

PN W09627010-A1.
PD 06-SEP-1996.
PF 01-MAR-1996; E00805.
PR 01-MAR-1995; IT-FI0036.
PA (ITU-) ITAL MIN UNIV RICERCA SCI & TECNOLOGICA.
PI Anastasi AM, Colnaghi MI, De Santis R, Di Massimo AM;
PI Ferrer Marsal C, Mele A;
DR WPI; 96-412776/41.
DR N-PSDB; T33446.
PT Murine/human chimeric monoclonal antibody, chMint5 specific for
PT EGF-R - shows a lower immunogenicity when administered to humans
PS Claim 7; Page 18; 28pp; English.
CC The amino acid sequence (W00241) of the light chain variable region
CC (VL) of the epidermal growth factor receptor (EGF-R)-specific mouse-
CC human chimeric antibody chMint5 was deduced from a cDNA clone
CC (T33446) obtd. by PCR amplification of murine Mint5 hybridoma DSM

CC ACC2150 cDNA. chMint5 comprises Mint5 VH and VL regions fused
CC to human C-gamma1 and CK regions. Constructs were expressed in
CC CHO cell transfectants. chMint5 shows lower immunogenicity than
CC Mint5 when administered to humans. It can be used in diagnostic
CC assays or used to produce immunotoxins or immunocytokines useful
CC for tumour therapy.
SQ Sequence 108 AA;

Query Match 83.3%; Score 60; DB 1; Length 108;
Best Local Similarity 84.6%; Pred. No. 0.0062;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNPLHWY 13
:||||| |
Db 24 RASQISNHLHWY 36

RESULT 12
R25729
ID R25729 standard; Protein; 107 AA.
AC R25729;
DT 13-JAN-1993 (first entry)
DE Humanised VL region of the mouse CMV5 antibody.
KW Murine; immunoglobulin; CDR; non immunogenic; cytomegalovirus;
KW gH; light chain; variable region; framework; human; Wol.
OS Mus musculus.
FH Key Location/Qualifiers
FT region 24..34
FT /note= "CDR"
FT region 50..56
FT /note= "CDR"
FT region 89..97
FT /note= "CDR"
FT misc_difference 49
FT /note= "mutated residue"

PN W09211018-A.
PD 09-JUL-1992.
PF 19-DEC-1991; U09711.
PR 19-DEC-1990; US-634278.
PA (PROT-) PROTEIN DESIGN LABS INC.
PI Co MS, Coeligh KL, Landolfi NF, Queen CL, Schneider WP;
DR WPI; 92-249842/30.
PT New immunoglobulin(s) having murine CDRs in human framework
PT regions - have lower antigenicity; useful for treating e.g. HSV,
PT CMV, T-cell disorders, myeloid disorders and auto-immune
PT conditions
PS Claim 40; Fig 27A; 141pp; English.
CC The sequence shows the humanised mature light chain variable
CC region of the mouse CMV5 antibody. Murine CDRs were used
CC in a human Wol framework to produce a pure humanised immunoglobulin
CC (Ig) which is capable of binding to the gH glycoprotein of
CC cytomegalovirus. The Ig is non immunogenic, due to the human
CC framework, and has a strong affinity for its predetermined
CC antigen. They can be produced in large quantities via recombinant
CC DNA and monoclonal antibody technology. The humanised Igs may be
CC used alone or in combination with chemotherapeutic agents such as
CC non-steroidal anti-inflammatory drugs or immunosuppressants.
CC See also R25721-32.
SQ Sequence 107 AA;

Query Match 81.9%; Score 59; DB 1; Length 107;
Best Local Similarity 84.6%; Pred. No. 0.0088;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNPLHWY 13
:||||| |
Db 24 RASQISNHLHWY 36

RESULT 13
R15438

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ID R15438 standard; Protein; 108 AA.
AC R15438;
DE 25-FEB-1992 (first entry)
DE Light chain variable region of MAB 1A6.
KW HRV; ICAM-1; antigen-binding fragment; inflammation;
KW auto-immune disease.
OS Homo sapiens.
PN EP-459577-A.
PD 04-DEC-1991.
PF 25-MAY-1991; 201243.
PR 01-JUN-1990; US-532001.
PA (MERI ) MERCK & CO INC.
PI Colonna RJ, Condra JH, Tomassini JE, Sardana VV;
PI WPI: 91-355850/49.
PT Microbially expressed portions of monoclonal antibody - can block
PT attachment of rhinovirus ligands to inter-cellular adhesion
PT molecule (ICAM-1)
PS Claim 1; Page 19; 28pp; English.
CC This is one of six antibody fragments from MAB's specific for domain
CC 1 of ICAM-1. MAB 1A6 also specifically blocks the major group of
CC human rhinovirus from binding to and infecting HeLa cells. The
CC peptide fragments can be used to treat or prevent rhinovirus
CC infection. See R15437-R15443.
SQ Sequence 108 AA;

Query Match 81.9%; Score 59; DB 1; Length 108;
Best Local Similarity 84.6%; Pred. No. 0.0089;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
Db 24 RASQISNNLHWY 36
:||||| ||||

RESULT 14
W89176
ID W89176 standard; peptide; 109 AA.
AC W89176;
DE 25-MAR-1999 (first entry)
DE Anti-p53 monoclonal antibody 248 variable light chain sequence.
KW Anti-p53; monoclonal antibody 240; immunogen; anti-tumour; immunity;
KW immune response; tumour associated antigen; metastatic cancer.
OS Mus sp.
OS Synthetic.
PN WO9856416-A1.
PD 17-DEC-1998.
PF 09-JUN-1998; IL0266.
PR 09-JUN-1997; IL-121041.
PA (YEDA ) YEDA RES & DEV CO LTD.
PI Cohen IR, Erez-Alon N, Herkel J, Rotter V, Ruiz PJ,
PI Wolkowicz R;
DR WPI: 99-070296/06.
PT Use of a monoclonal antibody to a tumour-associated antigen - to
PT induce anti-tumour immunity or elicit an increased immune response
PT to the antigen
PS Example 3; Fig 3; 47pp; English.
CC The present invention describes the use of an immunogen (A) to induce
CC anti-tumour immunity; to elicit an increased immune response to tumour
CC associated antigen (TAA) and/or to induce an immune response to mutant
CC or wild-type forms of TAA in mammals. (A) is: (i) a monoclonal antibody
CC (MAB) to TAA, or its fragment; (ii) a peptide based on a CDR
CC (complementarity determining region) on the heavy or light chain of MAB
CC (able to elicit antibodies to TAA); or (iii) a DNA that encodes the
CC variable (V) region of MAB, in a gene delivery vehicle. The present
CC sequence represents the variable light chain sequence from anti-p53 MAB
CC 248. Also described is a method for generating sequence-specific,
CC anti-DNA antibodies (AB) by immunising a mammal with a MAB directed to a
CC domain containing a DNA-binding site of a DNA-binding protein. (A) is
CC used to treat a wide variety of primary and metastatic cancers,
CC particularly those where p53 is involved. Ab are used for diagnosis (e.g
CC to determine critical sequences in animal or plant breeding); to
CC identify bacteria and other parasites; to determine parentage; in

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CC forensic science; to isolate specific genes for DNA vaccination; in gene
CC sequencing and cloning; also possibly for activation of selected
CC therapeutic genes in plants, animals and humans. (A) induce an effective
CC anti-tumour response without causing harm to the patient. The method
CC uses (A) to generate anti-TAA by exploiting the anti-idiotype network.
SQ Sequence 109 AA;

Query Match 81.9%; Score 59; DB 1; Length 109;
Best Local Similarity 84.6%; Pred. No. 0.009;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
Db 25 RASQISNNLHWY 37
:||||| ||||

RESULT 15
R54093
ID R54093 standard; Protein; 127 AA.
AC R54093;
DE 29-DEC-1994 (first entry)
DE Sequence of mouse V-kappa showing the sequences of recombinant
DE anti-FHV-1 antibody CDRs 1, 2 and 3.
KW Feline herpes virus; FHV-1; monoclonal antibody; CDR;
KW complementarity determining region.
OS Mus musculus.
FH Key Location/Qualifiers
FT peptide 1..20
FT /label= leader
FT region 21..43
FT /label= FR1
FT region 44..54
FT /label= CDR1
FT region 55..70
FT /label= FR2
FT region 71..76
FT /label= CDR2
FT region 77..108
FT /label= FR3
FT region 109..117
FT /label= CDR3
FT region 118..127
FT /label= FR4
PN WO9412661-A.
PD 09-JUN-1994.
PF 25-NOV-1993; J01724.
PR 28-NOV-1992; JP-341255.
PA (KAGA ) CEMO SERO THERAPEUTIC RES INST.
PI Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;
PI WPI: 94-200288/24.
DR N-PSDB; Q64167.
PT Feline monoclonal antibody and recombinant antibodies specific
PT for FHV-1 - for detection, treatment and prevention of FHV-1
PT infection.
PS Disclosure; Page 18-19; 53pp; Japanese.
CC The inventors claim a monoclonal antibody against feline herpes
CC virus (FHV-1). They also claim a recombinant antibody against FHV-1
CC and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are
CC used in the detection, treatment and prevention of FHV-1. The
CC sequences of the CDRs in the VH of the recombinant anti-FHV-1
CC antibody are given in R54092. The sequences of the CDRs in the VL of
CC the recombinant anti-FHV-1 antibody are given in R54093. These CDR
CC sequences are claimed.
SQ Sequence 127 AA;

Query Match 81.9%; Score 59; DB 1; Length 127;
Best Local Similarity 84.6%; Pred. No. 0.011;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QASQISNLFHWY 13
:||||| ||||

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Db 44 RASOSISNNLHWY 56

Search completed: May 27, 2000, 19:21:38
Job time: 1592 sec

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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:26:46 ; Search time 163.56 Seconds
(without alignments)
3.226 Million cell updates/sec

Title: US-09-016-061-88
Perfect score: 54
Sequence: 1 QQSTSWPHT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_63:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	49	90.7	107	2 A45722	anti-glycoprotein
2	49	90.7	123	2 S35479	Ig kappa chain pre
3	46	85.2	107	2 B45722	anti-glycoprotein
4	43	79.6	106	2 PL0267	Ig kappa chain v r
5	41	75.9	67	2 PH1081	Ig light chain v r
6	41	75.9	69	2 PH1080	Ig light chain v r
7	40	74.1	102	2 S26346	Ig kappa chain v r
8	38	70.4	104	2 B43413	Ig kappa chain v r
9	38	70.4	108	2 C30502	Ig kappa chain v r
10	38	70.4	138	2 A26471	Ig kappa chain pre
11	38	70.4	235	1 SQMS	parotid secretory
12	37	68.5	739	2 S47772	biotin sulfoxide r
13	36	66.7	87	2 PH1082	Ig light chain v r
14	36	66.7	100	2 S69860	hypothetical prote
15	36	66.7	115	1 KVM5L7	Ig kappa chain pre
16	36	66.7	128	2 PN0445	Ig kappa chain pre
17	36	66.7	133	2 S69224	aromatase snoE - s
18	35	64.8	235	2 B42337	parotid secretory
19	35	64.8	400	1 JC1428	ketol-acid reducto
20	35	64.8	770	2 S76095	hypothetical prote
21	35	64.8	774	1 JQ0550	1,4-alpha-glucan b
22	35	64.8	4845	2 T31067	BIR repeat contain
23	34	63.0	96	2 JC5945	regulatory protein
24	34	63.0	118	2 S40374	Ig kappa chain - h
25	34	63.0	122	2 S40338	Ig kappa chain - h
26	34	63.0	128	2 S40338	Ig kappa chain v-j
27	34	63.0	133	2 S23230	Ig kappa chain pre
28	34	63.0	254	2 S30957	gene 12 protein -
29	34	63.0	448	2 T17290	hypothetical prote
30	34	63.0	452	1 WZBE4	gene 4 protein - h

31 34 63.0 608 2 I53269 prolactin receptor
32 34 63.0 613 4 C40201 artifact-warning s
33 34 63.0 640 2 T26820 hypothetical prote
34 34 63.0 815 2 H64949 biotin sulfoxide r
35 34 63.0 817 2 A47716 dolichyl-phosphate
36 34 63.0 848 2 C64841 trimethylamine-N-o
37 34 63.0 1045 2 T16275 hypothetical prote
38 34 63.0 1189 1 JC2366 protein-tyrosine-p
39 34 63.0 1918 2 S43719 lactase (EC 3.2.1.
40 34 63.0 1920 2 S43720 lactase (EC 3.2.1.
41 34 63.0 1926 2 S01169 beta-glycosidase c
42 33 61.1 92 2 S37506 Ig kappa chain v r
43 33 61.1 106 2 FC4282 Ig kappa chain (an
44 33 61.1 107 2 C45722 anti-glycoprotein
45 33 61.1 255 2 T36749 hypothetical prote

ALIGNMENTS

RESULT 1

A45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (C;Species: Mus musculus (house mouse)
C;Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C;Accession: A45722
R;Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va J. Virol. 67, 489-496, 1993
A;Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on A;Reference number: A45722; MUID:93100833
A;Accession: A45722
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-107 <SW>
A;Note: sequence extracted from NCBI backbone (NCBIP:120589)
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: glycoprotein

Query Match 90.7%; Score 49; DB 2; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.053;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSTSWPHT 9
Db 89 QQSNSWPHT 97

RESULT 2

S35479
Ig kappa chain precursor V region - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 23-Jul-1999
C;Accession: S35479
R;Takeda, Y.; Wise, K.S.; Hoffman, R.W.
Nucleic Acids Res. 20, 4099, 1992
A;Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from A;Reference number: S35479; MUID:92375706
A;Accession: S35479
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-123 <TAK>
A;Cross-references: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148
C;Genetics:
A;Map position: 6
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotrimer; immunoglobulin
F;1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F;13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAT>

Query Match 90.7%; Score 49; DB 2; Length 123;
Best Local Similarity 88.9%; Pred. No. 0.062;

Matches 8: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9
||| |||||

Db 101 QQSNSWPHT 109

RESULT 3

B45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C:Accession: B45722
R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasquez, J.; Virol, 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on human anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 33) - mouse (fragment)
A:Reference number: B45722; MUID:93100833
A:Accession: B45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-107 <STM>
A:Note: sequence extracted from NCBI backbone (NCBIP:120590)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein

Query Match 85.2%; Score 46; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 0.18;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9
||| |||||

Db 89 QOSTSWPHT 97

RESULT 4

PL0267
Ig kappa chain V region (anti-DNA, DP12VK) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996
C:Accession: PL0267
R:Shlomchik, M.; Mascelli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A.
J. Exp. Med. 171, 265-297, 1990
A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic hypermutation
A:Reference number: PL0231; MUID:90111618
A:Accession: PL0267
A:Molecule type: mRNA
A:Residues: 1-106 <SHL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-23/Region: framework 1
F:24-34/Region: complementarity-determining 1
F:35-49/Region: framework 2
F:50-56/Region: complementarity-determining 2
F:57-88/Region: framework 3
F:89-97/Region: complementarity-determining 3
F:98-106/Region: framework 4

Query Match 79.6%; Score 43; DB 2; Length 106;
Best Local Similarity 77.8%; Pred. No. 0.59;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9
||| |||||

Db 89 QQSNSWPHT 97

RESULT 5

PH1081
Ig light chain V region (clone 165.6) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
C:Accession: PH1081
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective hypermutation
A:Reference number: PH0971; MUID:92381444
A:Accession: PH1081
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-67 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 75.9%; Score 41; DB 2; Length 67;
Best Local Similarity 77.8%; Pred. No. 0.82;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9
||| |||||

Db 58 QQSNSWPHT 66

RESULT 6

PH1080
Ig light chain V region (clone 165.60) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
C:Accession: PH1080
R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective hypermutation
A:Reference number: PH0971; MUID:92381444
A:Accession: PH1080
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-69 <TIL>
A:Experimental source: B cell, strain [NZB x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 75.9%; Score 41; DB 2; Length 69;
Best Local Similarity 77.8%; Pred. No. 0.84;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9
||| |||||

Db 60 QQSNSWPHT 68

RESULT 7

S26346
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26346
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protein
A:Reference number: S26309; MUID:91341421
A:Accession: S26346
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-102 <STA>
A:Cross-references: EMBL:X59211; NID:g52338; PIDN:CAA41921.1; PID:s36191; PID:g133407
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 74.1%; Score 40; DB 2; Length 102;
Best Local Similarity 66.7%; Pred. No. 1.9;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
||| :|||
Db 87 QOSTWPT 95

RESULT 8
B43413
Ig kappa chain V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-May-1997
C:Accession: B43413
R:Tomiyama, Y.; Brojer, E.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.; Kum
J. Biol. Chem. 267, 18085-18092, 1992
A:Title: A molecular model of RGD ligands. Antibody D gene segments that direct specific
A:Reference number: A43413; MUID:92388177
A:Accession: B43413
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-104 <TOM>
A:Note: sequence extracted from NCBI backbone (NCBIP:112818)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.4%; Score 38; DB 2; Length 104;
Best Local Similarity 77.8%; Pred. No. 4.3;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
||| |||
Db 86 QOSTSWPHT 94

RESULT 9
C30502
Ig kappa chain V region (D444) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 03-Nov-1988 #sequence_revision 03-Nov-1988 #text_change 23-Jul-1999
C:Accession: C30502
R:Billat, D.; Webster, D.M.; Rees, A.R.
J. Immunol. 141, 1745-1753, 1988
A:Title: V region sequences of anti-DNA and anti-RNA autoantibodies from NZB/NZW F-1 m
A:Reference number: A30502; MUID:88315787
A:Accession: C30502
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-108 <BIL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 70.4%; Score 38; DB 2; Length 108;
Best Local Similarity 66.7%; Pred. No. 4.5;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
||| :|||
Db 89 QOSTSWPHT 97

RESULT 10
A26471
Ig kappa chain precursor V region (MAK33) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999
C:Accession: A26471
R:Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.
Gene 51, 13-19, 1987
A:Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creatine
A:Reference number: A91572; MUID:87248058
A:Accession: A26471

A:Molecule type: mRNA
A:Residues: 1-138 <BUC>
A:Cross-references: GB:M16162; NID:g196893; PIDN:AAA38823.1; PID:g196894
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-138/Product: Ig kappa chain V region #status predicted <MAT>

Query Match 70.4%; Score 38; DB 2; Length 138;
Best Local Similarity 77.8%; Pred. No. 5.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
||| |||
Db 109 QOSTSWPHT 117

RESULT 11
S0M5
parotid secretory protein precursor - mouse
N:Alternate names: PSP
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 22-Jun-1999
C:Accession: A23031; I53236
R:Madsen, H.O.; Hjorth, J.P.
Nucleic Acids Res. 13, 1-13, 1985
A:Title: Molecular cloning of mouse PSP mRNA.
A:Reference number: A23031; MUID:85215456
A:Accession: A23031
A:Molecule type: mRNA
A:Residues: 1-235 <MAD>
A:Cross-references: GB:X01697; NID:g53810; PIDN:CAA35846.1; PID:g758163
R:Poulsen, K.; Jakobsen, B.K.; Mikkelsen, B.M.; Harmark, K.; Nielsen, J.T.; Hjorth, J
EMBO J. 5, 1891-1896, 1986
A:Title: Coordination of murine parotid secretory protein and salivary amylase expres
A:Reference number: I53236; MUID:87004556
A:Accession: I53236
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-87 <RES>
A:Cross-references: GB:M26807; NID:g200556; PIDN:AAA40009.1; PID:g554264
C:Comment: PSP is the most abundant protein in the parotid gland. Its function is not
C:Genetics:
A:Gene: Psp
A:Map position: 2
A:Introns: 41/1
A:Note: list of introns may be incomplete
C:Superfamily: parotid secretory protein
C:Keywords: parotid gland; saliva
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-235/Product: parotid secretory protein #status predicted <MAT>

Query Match 70.4%; Score 38; DB 1; Length 235;
Best Local Similarity 85.7%; Pred. No. 10;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSTSWP 7
||:||||
Db 54 QOSTSWP 60

RESULT 12
S47772
biotin sulfoxide reductase (EC 1.-.-) 1 - Escherichia coli
C:Species: Escherichia coli
C:Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 24-Sep-1999
C:Accession: S47772; JVO071; A65154
R:Plunkett, G.
submitted to the EMBL Data Library, March 1994
A:Reference number: S47666
A:Accession: S47772

A:Molecule type: DNA
A:Residues: 1-739 <PLU>
A:Cross-references: EMBL:U00039; NID:g46582; PIDN:AAB18528.1; PID:g46689
R:Pierion, D.E.; Campbell, A.
J. Bacteriol. 172, 2194-2198, 1990
A:Title: Cloning and nucleotide sequence of bIsC, the structural gene for biotin sulfoxide sulfoxidase from *Escherichia coli* K-12.
A:Reference number: JVO071; MUID:90202748
A:Accession: JVO071
A:Molecule type: DNA
A:Residues: 1-544 'AFLPSAGD', 554-557 'OR', 561-708 'MAVRVIRRHGWKNTTVRN' <PIE>
A:Cross-references: GB:M34827; NID:g145435; PIDN:AA23522.1; PID:g145436
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, D.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of *Escherichia coli* K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: A65154
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-739 <BLAT>
A:Cross-references: GB:AE000432; GB:U00096; NID:g2367241; PIDN:AAC76575.1; PID:g1789973;
A:Experimental source: strain K-12, substrain MG1655
C:Comment: This enzyme may serve as a scavenger, allowing the cell to utilize biotin sulfoxide sulfoxidase.
C:Genetics:
A:Gene: bIsC
A:Map position: 79 min
C:Superfamily: trimethylamine-N-oxide reductase
C:Keywords: ATP; molybdenum; P-loop; oxidoreductase
F:486-493/Region: nucleotide-binding motif A (P-loop)

Query Match 68.5%; Score 37; DB 2; Length 739;
Best Local Similarity 85.7%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 QOSTSWP 7
| | | | |
Db 129 QOSTSWP 135

RESULT 13
PH1082
Ig light chain V region (clone 165.54) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996
C:Accession: PH1082
R:Fillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.
J. Exp. Med. 176, 761-779, 1992
A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective B cell clones.
A:Reference number: PH0971; MUID:92381444
A:Accession: PH1082
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-87 <TIL>
A:Experimental source: B cell, strain [N2B x NZW]F1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 66.7%; Score 36; DB 2; Length 87;
Best Local Similarity 85.7%; Pred. No. 8.1;
Matches 6; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 QOSTSWP 7
| | | | |
Db 79 QOSTSWP 85

RESULT 14
S69860
hypothetical protein YML116w-a - yeast (Saccharomyces cerevisiae)
C:Species: "Saccharomyces cerevisiae"
C:Date: 23-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 05-Nov-1999

C:Accession: S69860
R:Skelton, J.; Churcher, C.M.
submitted to the EMBL Data Library, May 1995
A:Reference number: S53954
A:Accession: S69860
A:Molecule type: DNA
A:Residues: 1-100 <SKE>
A:Cross-references: EMBL:Z49210; GSPDB:GN00013; MIPS:YML116w-a
C:Genetics:
A:Gene: MIPS:YML116w-a
A:Map position: 13L
C:Superfamily: Saccharomyces hypothetical protein YML116w-a

Query Match 66.7%; Score 36; DB 2; Length 100;
Best Local Similarity 66.7%; Pred. No. 9.3;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSTSWP 9
| | | | |
Db 22 QOSTSWP 30

RESULT 15
KVMSL7
Ig kappa chain precursor V region (L7) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 22-Jun-1999
C:Accession: A01925
R:Pech, M.; Hochtl, J.; Schnell, H.; Zachau, H.G.
Nature 291, 668-670, 1981
A:Title: Differences between germ-line and rearranged immunoglobulin V-kappa coding sequences.
A:Reference number: A93259; MUID:81220975
A:Accession: A01925
A:Molecule type: DNA
A:Residues: 1-115 <PEC>
A:Cross-references: GB:V01564; GB:J00574; NID:g51718; PIDN:CAA24884.1; PID:g758153
A:Note: the sequence was determined from the germline gene
A:Note: there appear to be two possible splice junctions at the 3' end of the intron;
C:Genetics:
A:Introns: 17/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a dimer.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-115/Product: Ig kappa chain V region (L7) #status predicted <MAT>
F:36-110/Domain: immunoglobulin homology <IMM>
F:43-108/Disulfide bonds: #status predicted

Query Match 66.7%; Score 36; DB 1; Length 115;
Best Local Similarity 85.7%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWP 7
| | | | |
Db 109 QOSTSWP 115

Search completed: May 27, 2000, 19:26:47
Job time: 1770 sec

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OM protein - protein search, using sw model

Run on: May 27, 2000, 20:07:20 ; Search time 69.28 Seconds
(without alignments)
3.956 Million cell updates/sec

Title: US-09-016-061-88
Perfect score: 54
Sequence: 1 QOSTSWPHT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	70.4	235	1 PSP_MOUSE	P07743 mus musculus
2	37	68.5	777	1 BISC_ECOLI	P20099 escherichia
3	36	66.7	115	1 KV51_MOUSE	P01642 mus musculus
4	35	64.8	400	1 ILV5_NEUCR	P38674 neurospora
5	35	64.8	734	1 GLGB_AGRU	P52979 agrobacteri
6	35	64.8	770	1 GLGB_SNY3	P52981 synecocyst
7	35	64.8	773	1 GLGB_STNP7	P16954 synecococc
8	34	63.0	96	1 CTC1_ACILW	O33947 acinetobact
9	34	63.0	178	1 ATPQ_DROME	Q24251 drosophila
10	34	63.0	254	1 VG12_BPML5	Q05328 mycobacteri
11	34	63.0	452	1 IE63_VZVD	P09269 varicella-z
12	34	63.0	608	1 PRUN_MOUSE	Q08501 mus musculus
13	34	63.0	809	1 B1SZ_ECOLI	P46923 escherichia
14	34	63.0	817	1 PMT1_YEAST	P33775 saccharomyc
15	34	63.0	848	1 TORA_ECOLI	P33225 escherichia
16	34	63.0	1189	1 PTNE_MOUSE	O62130 mus musculus
17	34	63.0	1326	1 LPH_RABIT	P09849 oryctolagus
18	33	61.1	591	1 LACL_CRYPA	Q03966 cryptoneutr
19	33	61.1	605	1 VP40_VZVD	P09286 varicella-z
20	33	61.1	668	1 MTMW_MFTWO	O59647 methanobact
21	33	61.1	765	1 YF63_MYCTU	O10768 mycobacteri
22	33	61.1	810	1 ILAR_MOUSE	P16382 mus musculus
23	33	61.1	862	1 PGCV_MACNE	Q28858 macaca neme
24	33	61.1	1417	1 BLM_HUMAN	P54132 homo sapien
25	33	61.1	1517	1 YD22_SCHPO	O10250 schizosacch
26	33	61.1	3396	1 PGCV_HUMAN	P13611 homo sapien
27	32	59.3	105	1 RNF1_GIBBA	P16411 gibberella
28	32	59.3	105	1 RNF2_GIBBA	P16412 gibberella
29	32	59.3	106	1 RNF1_GIBFU	P10282 gibberella
30	32	59.3	175	1 VPG_BWTVF	P09511 beet wester
31	32	59.3	175	1 VPG_BWVVG	P09512 beet wester
32	32	59.3	179	1 R1ML_ECOLI	P13857 escherichia
33	32	59.3	211	1 UL45_HSVMB	P22652 marek's dis
34	32	59.3	211	1 UL45_HSVMM	P22653 marek's dis

ALIGNMENTS

RESULT 1

ID	PSP_MOUSE	STANDARD	PRT	235 AA
AC	P07743;			
DT	01-AUG-1988 (Rel. 08, Created)			
DT	01-AUG-1988 (Rel. 08, Last sequence update)			
DT	01-NOV-1997 (Rel. 35, Last annotation update)			
DE	PAROTID SECRETORY PROTEIN PRECURSOR (PSP).			
GN	PSP.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
[1]				
RP	SEQUENCE FROM N.A.			
RC	TISSUE-PAROTID GLAND;			
RX	MEDLINE: 85215456			
RA	Madsen H.O., Hjorth J.P.;			
RT	"Molecular cloning of mouse PSP mRNA.";			
RL	Nucleic Acids Res. 13:1-13(1985).			
[2]				
RP	SEQUENCE OF 1-87 FROM N.A.			
RC	STRAIN-C3H; TISSUE-SPLEEN;			
RX	MEDLINE: 87004556			
RA	Poulsen K., Jakobsen B.K., Mikkelsen B.M., Harmark K.,			
RT	Nielsen J.T., Hjorth J.P.;			
RT	"Coordination of murine parotid secretory protein and salivary			
RL	amylase expression.";			
EMBO	J. 5:1891-1896(1986)			
CC	-1- FUNCTION: PSP IS THE MOST ABUNDANT PROTEIN IN THE PAROTID GLAND.			
CC	ITS FUNCTION IS NOT KNOWN; HOWEVER, ITS PRODUCTION IS COORDINATED			
CC	WITH THAT OF SALIVARY AMYLASE.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: X01697; CAA25846.1; -			
DR	EMBL: M26807; AAA40009.1; -			
DR	EMBL: M26806; AAA40009.1; JOINED.			
DR	PIR: A23031; SQMS			
DR	MGI:97787; PSP.			
KW	Parotid gland; Signal.			
FT	CHAIN 1 20			
FT	CHAIN 21 235			
SQ	SEQUENCE 235 AA; 24753 MW; 23311BAE1E6E2EF3 CRC64;			

Query Match 70.4%; Score 38; DB 1; Length 235;
Best Local Similarity 85.7%; Pred. No. 3.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QOSTSWP 7
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Db 54 QOATSWP 60

RESULT 2
BISC_ECOLI
ID BISC_ECOLI STANDARD; PRT; 777 AA.
AC P20099;
DT 01-FEB-1991 (Rel. 17, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE BIOTIN SULFOXIDE REDUCTASE 1 (EC 1.-.-.-) (BDS REDUCTASE 1) (BDS
DE REDUCTASE 1).
GN BISC.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90202748.
RA Pierson D.E., Campbell A.;
RT "Cloning and nucleotide sequence of bisc, the structural gene for
RT biotin sulfoxide reductase in Escherichia coli.";
RL J. Bacteriol. 172:2194-2198(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE; 94316500.
RA Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
RT "Analysis of the Escherichia coli genome. V. DNA sequence of the
RT region from 76.0 to 81.5 minutes.";
RL Nucleic Acids Res. 22:2576-2586(1994).
CC -1- FUNCTION: THIS ENZYME MAY SERVE AS A SCAVENGER, ALLOWING THE CELL
CC TO UTILIZE BIOTIN SULFOXIDE AS A BIOTIN SOURCE.
CC -1- CATALYTIC ACTIVITY: REDUCES A SPONTANEOUS OXIDATION PRODUCT OF
CC BIOTIN, D-BIOTIN D-SULFOXIDE (BSO OR BDS), BACK TO BIOTIN.
CC -1- COFACTOR: MOLYBDENUM (MOLYBDOPTERIN).
CC -1- MISCELLANEOUS: REQUIRES A SMALL THIOREDUXIN-LIKE PROTEIN FOR
CC ACTIVITY.
CC -1- SIMILARITY: BELONGS TO THE PROKARYOTIC MOLYBDOPTERIN-CONTAINING
CC OXIDOREDUCTASE FAMILY.
CC
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CC
CC -----
CC EMBL; M34827; AAA23522.1; ALT_FRAME.
CC EMBL; U00039; AAB18528.1; ALT_INIT.
CC EMBL; AE000432; AAC76575.1; ALT_INIT.
CC PIR; JV0071; JV0071.
CC HSP; Q57366; 1CXT.
CC ECGENE; EG10124; BISC.
CC PROSITE; PS00551; MOLYBDOPTERIN_PROK_1; FALSE_NEG.
CC PROSITE; PS00490; MOLYBDOPTERIN_PROK_2; 1.
CC PROSITE; PS00932; MOLYBDOPTERIN_PROK_3; 1.
CC PFAM; PF00384; molybdopterin; 1.
CC PFAM; PF01568; molybdop_binding; 1.
CC Oxidoreductase; Molybdenum.
FT CONFLICT 583 591 DFCRDPLAH -> AFLPRSAGD (IN REF. 1).
FT CONFLICT 596 598 ASG -> QR (IN REF. 1).
FT CONFLICT 747 777 NGCAGTALAWLRYNGPELTAFEPASS ->
FT MAVRVRHWGKNTVRN (IN REF. 1).
FT SEQUENCE 777 AA; 85850 MW; 51087D957E4FB38B CRC64;

Query Match 68.5%; Score 37; DB 1; Length 777;
Best Local Similarity 85.7%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOATSWP 7

Db 167 QOATSWP 173

RESULT 3
KV51_MOUSE
ID KV51_MOUSE STANDARD; PRT; 115 AA.
AC P01642;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-V REGION L7 PRECURSOR (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81220975.
RA Pech M., Hochtl J., Schnell H., Zachau H.G.;
RT "Differences between germ-line and rearranged immunoglobulin V kappa
RT coding sequences suggest a localized mutation mechanism.";
RL Nature 291:668-670(1981).
CC -1- MISCELLANEOUS: THERE APPEAR TO BE TWO POSSIBLE SPLICE JUNCTIONS AT
CC THE 3' END OF THE INTRON. THE ALTERNATE WOULD CODE FOR A PROTEIN
CC LACKING RESIDUES 17-19.
CC PIR; A01925; KVMSL7.
CC PFAM; PF00047; ig; 1.
CC Immunoglobulin V region; Signal.
FT CHAIN 1 20
FT DOMAIN 21 >115 IG KAPPA CHAIN V-V REGION L7.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 >115 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
FT SEQUENCE 115 AA; 12615 MW; C17BEC758C577E00 CRC64;

Query Match 66.7%; Score 36; DB 1; Length 115;
Best Local Similarity 85.7%; Pred. No. 4.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOATSWP 7

Db 109 QOATSWP 115

RESULT 4
ILV5_NEUCR
ID ILV5_NEUCR STANDARD; PRT; 400 AA.
AC P38674;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE KETOL-ACID REDUCTOISOMERASE PRECURSOR (EC 1.1.1.86) (ACETOHYDROXY-ACID
DE REDUCTOISOMERASE) (ALPHA-KETO-BETA-HYDROXYLACIL REDUCTOISOMERASE).
GN ILV-2.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pyrenomycetes; Sordariales;
OC Sordariaceae; Neurospora.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93013010.
RA Sista H., Bowman B.;
RT "Characterization of the ilv-2 gene from Neurospora crassa encoding
RT alpha-keto-beta-hydroxylacyl reductoisomerase.";
RL Gene 120:115-118(1992).
CC -1- CATALYTIC ACTIVITY: 2,3-DIHYDROXYISOVALERATE + NADP(+) =
CC 2-ACETOLACTATE + NADPH (ALSO: 2,3-DIHYDROXYACID-3-METHYLVALERATE
CC + NADP(+)) = 2-ACETO-2-HYDROXYBUTYRATE + NADPH).

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CC -1- COPACTOR: REQUIRES MAGNESIUM.
CC -1- PATHWAY: SECOND STEP IN VALINE AND ISOLEUCINE BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
CC -1- SIMILARITY: BELONGS TO THE KETOL-ACID REDUCTOISOMERASE FAMILY.
-----
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-----
DR EMBL; M84189; AAB00797.1; -.
DR PIR; JC1428; JC1428.
DR HSSP; Q01292; 1YVE.
DR PFAM; PF01450; ILVC; 1.
KW Oxidoreductase; Branched-chain amino acid biosynthesis; Magnesium;
KW NADP; Mitochondrion; Transit peptide.
KW TRANSIT 1 26 MITOCHONDRION (POTENTIAL).
FT CHAIN 27 400 KETOL-ACID REDUCTOISOMERASE.
FT NP_BIND 90 99 NADPH (POTENTIAL).
FT ACT_SITE 177 177 POTENTIAL.
SQ SEQUENCE 400 AA; 44508 MW; DBAA4C0A3F4BD7CB CRC64;

Query Match 64.8%; Score 35; DB 1; Length 400;
Best Local Similarity 71.4%; Pred. No. 23;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSTSWP 8
Db 156 QSETWP 162

RESULT 5
GLGB_AGRTU
ID GLGB_AGRTU STANDARD; PRT; 734 AA.
AC P52979;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE 1.4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYCOPEN BRANCHING
DE ENZYME).
GN GLGB.
OS Agrobacterium tumefaciens.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Agrobacterium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A348;
RX MEDLINE; 99069330.
RA Ugaldé J.E., Lepek V., Uttaro A.D., Estrella J., Iglesias A.,
RA Ugaldé R.A.;
RT "Gene organization and transcription analysis of the Agrobacterium
RT tumefaciens glycogen (glg) operon: two transcripts for the single
RT phosphoglucomutase gene.";
RL Bacteriol. 180:6557-6564(1998).
CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF
CC GLYCOPEN.
CC -1- PATHWAY: THIRD STEP IN GLYCOPEN BIOSYNTHESIS.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
-----
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DR EMBL; AF033856; AAD03472.1; -.
DR PFAM; PF00128; alpha-amylase; 1.
KW Glycogen biosynthesis; Transferase; Glycosyltransferase.
FT ACT_SITE 417 417 BY SIMILARITY.
FT ACT_SITE 470 470 BY SIMILARITY.
FT ACT_SITE 538 538 BY SIMILARITY.
SQ SEQUENCE 734 AA; 83623 MW; 70A3CD35A77F31B6 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 734;
Best Local Similarity 71.4%; Pred. No. 43;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSTSWP 7
Db 470 EESTSWP 476

RESULT 6
GLGB_SYNY3
ID GLGB_SYNY3 STANDARD; PRT; 770 AA.
AC P52981;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 1.4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYCOPEN BRANCHING
DE ENZYME).
GN GLGB OR SLL0158.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96127529.
RA Kaneko T., Tanaka A., Sato S., Kotani H., Sazuka T., Miyajima N.,
RA Sugliura M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. I. Sequence features in the 1 Mb
RT region from map positions 64% to 92% of the genome.";
RL DNA Res. 2:153-166(1995).
CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF
CC GLYCOPEN.
CC -1- PATHWAY: THIRD STEP IN GLYCOPEN BIOSYNTHESIS.
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
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-----
DR EMBL; D63999; BAA10073.1; -.
DR PFAM; PF00128; alpha-amylase; 1.
KW Glycogen biosynthesis; Transferase; Glycosyltransferase.
FT ACT_SITE 433 433 BY SIMILARITY.
FT ACT_SITE 486 486 BY SIMILARITY.
FT ACT_SITE 554 554 BY SIMILARITY.
SQ SEQUENCE 770 AA; 89527 MW; A435AFCA7703FABA CRC64;

Query Match 64.8%; Score 35; DB 1; Length 770;
Best Local Similarity 71.4%; Pred. No. 45;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSTSWP 7
Db 486 EESTSWP 492

RESULT 7
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GLGB_SNP7
ID GLGB_SNP7 STANDARD; PRT; 773 AA.
AC P16954;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE 1,4-ALPHA-GLUCAN BRANCHING ENZYME (EC 2.4.1.18) (GLYCOGEN BRANCHING
DE ENZYME).
GN GLGB.
OS Synechococcus sp. (strain PCC 7942) (Anacystis nidulans R2).
OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 90323609.
RA Kiel J.A.K.W., Boels J.M., Beldman G., Venema G.;
RT "Nucleotide sequence of the Synechococcus sp. PCC7942 branching
RT enzyme gene (glgB): expression in Bacillus subtilis.";
RL Gene 89:77-84(1990).
CC -1- CATALYTIC ACTIVITY: FORMATION OF 1,6-GLUCOSIDIC LINKAGES OF
CC GLYCOGEN.
CC -1- PATHWAY: THIRD STEP IN GLYCOGEN BIOSYNTHESIS.
CC -1- SUBUNIT: MONOMER.
CC -1- MISCELLANEOUS: THE TEMPERATURE FOR OPTIMAL ACTIVITY IS
CC APPROXIMATELY 35 DEGREES CELSIUS.
CC -1- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
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CC -----
DR EMBL; M31544; AAB39038.1; -.
DR PIR; JQ0550; JQ0550.
DR PFAM; PF00128; alpha-amylase; 1.
KW Glycogen biosynthesis; Transferase; Glycosyltransferase.
FT INIT_MET 0
FT ACT_SITE 439 439 BY SIMILARITY.
FT ACT_SITE 492 492 BY SIMILARITY.
FT ACT_SITE 560 560 BY SIMILARITY.
SQ SEQUENCE 773 AA; 89063 MW; 52BAAL7CA337BF57 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 773;
Best Local Similarity 71.4%; Pred. No. 46;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSTSWP 7
Db 492 BESTSWP 498

RESULT 8
CTC1_ACILW STANDARD; PRT; 96 AA.
AC O33947;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE MUONOLACTONE DELTA-ISOMERASE 1 (EC 5.3.3.4) (MIASE 1).
GN CATC1.
OS Acinetobacter lwoffii.
OC Bacteria; Proteobacteria; gamma subdivision; pseudomonas group;
OC Moraxellaceae; Acinetobacter.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-K24;
RA Kim S.T., Leem S.-H., Choi J.-S., Chung Y.H., Kim S., Park Y.-M.,
RA Park Y.K., Lee Y.N., Ha K.-S.;

"Cloning and characterization of two cata genes in Acinetobacter
lwoffii K24.";
J. Bacteriol. 179:5226-5231(1997).
[2]
RN SEQUENCE FROM N.A.
RX STRAIN-K24;
RX MEDLINE; 98139907.
RA Kim S.T., Leem S.-H., Choi J.-S., Ha K.-S.;
RT "Organization and transcriptional characterization of the catI gene
RT cluster in Acinetobacter lwoffii K24.";
RL Biochem. Biophys. Res. Commun. 243:289-294(1998).
CC -1- CATALYTIC ACTIVITY: 2,5-DIHYDRO-5-OXOFURAN-2-ACETATE -
CC 3,4-DIHYDRO-5-OXOFURAN-2-ACETATE.
CC -1- PATHWAY: THIRD STEP IN THE CATABOLISM OF CATECHOL TO SUCCINATE-
CC AND ACETYL-COA IN THE BETA-KETOADIPATE PATHWAY.
CC -1- SUBUNIT: HOMODECAMER (BY SIMILARITY).
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CC -----
DR EMBL; U77658; AAC46227.1; -.
KW Aromatic hydrocarbons catabolism; Isomerase.
SQ SEQUENCE 96 AA; 11048 MW; 6955AC14A5DDDEFA CRC64;

Query Match 63.0%; Score 34; DB 1; Length 96;
Best Local Similarity 62.5%; Pred. No. 8;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSTSWP 8
Db 35 QKSGKWP 42

RESULT 9
ATPQ_DROME STANDARD; PRT; 178 AA.
ID ATPQ_DROME STANDARD; PRT; 178 AA.
AC Q24251;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34).
GN ATPSYN-D.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 99168769.
RA Caggese C., Ragone G., Perrini B., Moschetti R., De Pinto V.,
RA Caizzi R., Barsanti P.;
RT "Identification of nuclear genes encoding mitochondrial proteins:
RT isolation of a collection of D. melanogaster cDNAs homologous to
RT sequences in the Human Gene Index database.";
RL Mol. Gen. Genet. 261:64-70(1999).
CC -1- FUNCTION: THIS IS ONE OF THE CHAINS OF THE NONENZYMATIC
CC COMPONENT (CF(0) SUBUNIT) OF THE MITOCHONDRIAL ATPASE COMPLEX.
CC IT HAS NO APPARENT BACTERIAL HOMOLOGY AND ITS EXACT FUNCTION IS
CC UNKNOWN.
CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(0) SEEMS TO
CC HAVE NINE SUBUNITS: A, B, C, D, E, F, G, F6 AND 8 (OR A6L).
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CC -----

DR EMBL; X99667; CAA67981.1; -;
DR FLYBASE; FBgn0016120; ATPsyn-d
KW Hydrogen ion transport; CF(0); Mitochondrion.
SQ SEQUENCE 178 AA; 20228 MW; 199843BEBA8E02B9 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 178;
Best Local Similarity 83.3%; Pred. No. 15;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 4 TSWPHT 9
| | | | |
DB 152 TFWPHT 157

RESULT 10
VG12_BPML5
ID VG12_BPML5 STANDARD; PRT; 254 AA.
AC Q05328;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE GENE 12 PROTEIN (GP12).
GN 12
OS Mycobacteriophage L5.
OC Viruses.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93211282.
RA Hatfull G.F., Sarkis G.J.;
RT "DNA sequence, structure and gene expression of mycobacteriophage L5:
RT a phage system for mycobacterial genetics.";
RL Mol. Microbiol. 7:395-405(1993).
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CC -----

DR EMBL; Z18946; CAA79388.1; -;
DR PIR; S30957; S30957.
SQ SEQUENCE 254 AA; 28847 MW; 8627B76D26E42360 CRC64;
Query Match 63.0%; Score 34; DB 1; Length 254;
Best Local Similarity 71.4%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 QSTSWPH 8
| | | | |
DB 234 QGFSWPH 240

RESULT 11
IE63_VZVD
ID IE63_VZVD STANDARD; PRT; 452 AA.
AC P09269;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE TRANSCRIPTIONAL REGULATOR IE63 HOMOLOG.
GN 4.
OS Varicella-zoster virus (strain Dumas) (VZV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE; 86306657.
RA Davison A.J., Scott J.E.;
RT "The complete DNA sequence of varicella-zoster virus.";
RL J. Gen. Virol. 67:1759-1816(1986).
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL54,
CC HSV-2 UL54, EBV-1 5, VZV 4, EBV BMLF1, HCMV UL69, AND HVS-1 57.
CC -----
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CC -----
DR EMBL; X04370; CAA27887.1; -;
DR PIR; D27212; WZBE4.
KW Transcription regulation.
SQ SEQUENCE 452 AA; 51543 MW; 42926E4A71E380B4 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 452;
Best Local Similarity 71.4%; Pred. No. 40;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 QOSTSWP 7
| | | | |
DB 242 KQNTSWP 248

RESULT 12
PRLR_MOUSE
ID PRLR_MOUSE STANDARD; PRT; 608 AA.
AC Q08501; Q62099; P15213; P15212;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE PROLACTIN RECEPTOR PRECURSOR (PRL-R).
GN PRLR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RX STRAIN=C3H; TISSUE=MAMMARY GLAND;
RX MEDLINE; 94085788.
RA Moore R.C., Oka T.;
RT "Cloning and sequencing of the cDNA encoding the murine mammary gland
RT long-form prolactin receptor.";
RL Gene 134:263-265(1993).
RN [2]
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RX STRAIN=SWISS WEBSTER; TISSUE=LIVER;
RX MEDLINE; 93307149.
RA Clarke D.L., Linzer D.I.H.;
RT "Changes in prolactin receptor expression during pregnancy in the
RT mouse ovary.";
RL Endocrinology 133:224-232(1993).
RN [3]
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RA Sasaki M.;
RL Submitted (JUL-1992) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A. (FORM PRL-R3).
RX STRAIN=BALB/C; TISSUE=MAMMARY GLAND;
RA Edery M., Pezet A., Nandi S., Kelly P.A.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A. (FORMS PRL-R2 AND PRL-R1).
RX STRAIN=SWISS WEBSTER; TISSUE=LIVER;
RX MEDLINE; 89261824.
RA Davis J.A., Linzer D.I.H.;

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RT "Expression of multiple forms of the prolactin receptor in mouse
RL liver."
CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN, AS WELL AS PLACENTAL LACTOGEN I AND II.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- ALTERNATIVE PRODUCTS: THREE FORMS, PRL-R1, PRL-R2 AND PRL-R3
CC (SHOWN HERE) ARE PRODUCED BY ALTERNATIVE SPLICING OF THE PRLR
CC GENE.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L13593; AAC37641.1; -
DR EMBL: L14811; AAA02686.1; -
DR EMBL: D10214; BAA01066.1; -
DR EMBL: X73372; CAA51789.1; -
DR EMBL: M22959; AAA39977.1; -
DR EMBL: M22958; AAA39976.1; -
DR PIR: JT0671; JT0671.
DR HSP: P16471; 1BP3.
DR MGD: MGI:97763; PRLR.
DR PROSITE: PS00241; RECEPTOR_CYTOKINES_1; 1.
DR PROSITE: PS00340; RECEPTOR_CYTOKINES_2; FALSE_NEG.
DR PRAM: PF00041; fn3; 2.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Alternative splicing.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 608 PROLACTIN RECEPTOR.
FT DOMAIN 20 229 EXTRACELLULAR (BY SIMILARITY).
FT TRANS 230 253 BY SIMILARITY.
FT DOMAIN 254 608 CYTOPLASMIC (BY SIMILARITY).
FT DOMAIN 20 117 FIBRONECTIN TYPE-III.
FT DOMAIN 119 222 FIBRONECTIN TYPE-III.
FT DISULFID 31 41 BY SIMILARITY.
FT DISULFID 70 81 BY SIMILARITY.
FT CARBOHYD 54 54 POTENTIAL.
FT CARBOHYD 99 99 POTENTIAL.
FT CARBOHYD 127 127 POTENTIAL.
FT VARSPLIC 281 292 KKKSEELLSALG -> VHNKQLENYVY (IN ISOFORM PRL-R2).
FT VARSPLIC 293 608 MISSING (IN ISOFORM PRL-R2).
FT VARSPLIC 281 303 KKKSEELLSALGCCDPPPTSCE -> LWCSTLQTLVLKI
FT VARSPLIC 304 608 PTTFELCDL (IN ISOFORM PRL-R1).
FT CONFLICT 558 558 MISSING (IN ISOFORM PRL-R1).
FT CONFLICT 558 558 L -> F (IN REF. 2).
FT SEQUENCE 608 AA; 68240 MW; B8CE202B2EFC9FC6 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 608;
Best Local Similarity 71.4%; Pred. No. 54;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSTSWP 7
Db 474 KONTSWP 480
:|||||
RESULT 13
BISZ_ECOLI STANDARD; PRT; 809 AA.
AC P46923; P76292; P97187;
DT 01-NOV-1995 (Rel. 32, Created)
DT *01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE BIOTIN SULFOXIDE REDUCTASE 2 (EC 1.-.-.-) (BDS REDUCTASE 2) (BSO

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DE REDUCTASE 2).
GN BISZ.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RC SEQUENCE FROM N.A.
RC STRAIN-K12 / ACC5;
RX MEDLINE; 97077292.
RA del Campillo-Campbell A., Campbell A.M.;
RT "Alternative gene for biotin sulfoxide reduction in Escherichia coli
RT K-12."
RL J. Mol. Evol. 42:85-90(1996).
RN [2]
RC SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE; 97426617.
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [3]
RC SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE; 97251358.
RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sampei G., Seki Y., Sivasubram S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map."
RL DNA Res. 3:379-392(1996).
CC -1- FUNCTION: THIS ENZYME MAY SERVE AS A SCAVENGER, ALLOWING THE CELL
CC TO UTILIZE BIOTIN SULFOXIDE AS A BIOTIN SOURCE (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: REDUCES A SPONTANEOUS OXIDATION PRODUCT OF
CC BIOTIN, D-BIOTIN D-SULFOXIDE (BSO OR BDS), BACK TO BIOTIN.
CC -1- COFACTOR: MOLYBDENUM (MOLYBDOPTERIN) (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PROKARYOTIC MOLYBDOPTERIN-CONTAINING
CC OXIDOREDUCTASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U38839; AAC44131.1; -
DR EMBL: AE000281; AAC74942.1; ALT_INIT.
DR EMBL: D90829; CAB21599.1; -
DR EMBL: D90830; CAB21618.1; -
DR HSP: Q57366; ICXT.
DR ECOGENE; EG13276; BISZ.
DR PROSITE; PS00551; MOLYBDOPTERIN_PROK_1; FALSE_NEG.
DR PROSITE; PS00490; MOLYBDOPTERIN_PROK_2; 1.
DR PROSITE; PS00932; MOLYBDOPTERIN_PROK_3; 1.
DR PFAM; PF00384; molybdopterin; 1.
DR PFAM; PF01568; molybdop_binding; 1.
KW Oxidoreductase; Molybdenum.
FT CONFLICT 76 76 A -> T (IN REF. 1).
FT CONFLICT 291 292 HD -> TI (IN REF. 1).
FT CONFLICT 299 304 YTTGYP -> TLTGIR (IN REF. 1).
FT CONFLICT 406 409 EMSA -> DFSGP (IN REF. 1).
FT CONFLICT 801 803 AFD -> GFG (IN REF. 1).
FT SEQUENCE 809 AA; 88964 MW; 44A84F6302531D09 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 809;

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FT DOMAIN 155 179 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 180 200 POTENTIAL.
FT DOMAIN 201 234 LUMENAL (POTENTIAL).
FT TRANSMEM 235 259 POTENTIAL.
FT DOMAIN 260 273 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 274 291 POTENTIAL.
FT DOMAIN 292 584 LUMENAL, CATALYTIC (POTENTIAL).
FT TRANSMEM 585 605 POTENTIAL.
FT DOMAIN 606 685 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 686 710 POTENTIAL.
FT DOMAIN 711 817 LUMENAL (POTENTIAL).
FT CARBOHYD 390 390 POTENTIAL.
FT CARBOHYD 513 513 POTENTIAL.
FT CARBOHYD 743 743 POTENTIAL.
SQ SEQUENCE 817 AA; 92675 MW; 6309BBA71BAD8D21 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 817;
Best Local Similarity 75.0%; Pred. No. 73;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPH 8
||||:|
DB 359 QOSTLYPH 366

RESULT 15
TORA_ECOLI STANDARD; PRT; 848 AA.
ID TORA_ECOLI
AC F33225; P78227;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TRIMETHYLAMINE-N-OXIDE REDUCTASE PRECURSOR (EC 1.6.6.9) (TMAO
REDUCTASE) (TRIMETHYLAMINE OXIDASE).
OS TORA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
SEQUENCE FROM N.A., AND SEQUENCE OF 40-46.
RC STRAIN-K12;
RX MEDLINE; 94293785.
RA Mejean V., Lobbi-Nivol C., Lepelletier M., Giordano G., Chippaux M.,
RA Pascal M.-C.;
RT "TMAO anaerobic respiration in Escherichia coli: involvement of the
RT tor operon.";
RL Mol. Microbiol. 11:1169-1179(1994).
RN [2]
SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE; 97426617.
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474 (1997).
RN [3]
SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE; 97061202.
RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
RA Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N.,
RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
RA Yano M., Horiuchi T.;
RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 12.7-28.0 min region on the linkage map.";
RL DNA Res. 3:137-155(1996).
RN [4]
SEQUENCE OF 767-848 FROM N.A.
PP

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RC STRAIN-K12;
RA MEDLINE; 94134696.
RA Deguchi C., Kakeda M., Yamada H., Mizuno T.;
RT "An analogue of the DnaJ molecular chaperone in Escherichia coli.";
RL Proc. Natl. Acad. Sci. U.S.A. 91:1054-1058(1994).
CC -1- FUNCTION: REDUCES TRIMETHYLAMINE-N-OXIDE (TMAO) INTO
CC TRIMETHYLAMINE; AN ANAEROBIC REACTION COUPLED TO ENERGY-YIELDING
CC REACTIONS.
CC -1- CATALYTIC ACTIVITY: NADH + TRIMETHYLAMINE-N-OXIDE = NAD(+) +
CC TRIMETHYLAMINE + H(2)O.
CC -1- SUBCELLULAR LOCATION: PERIPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE PROKARYOTIC MOLYBDOPTERIN-CONTAINING
CC OXIDOREDUCTASE FAMILY.
CC -----
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CC -----
DR EMBL; X73888; CAA52095.1; -.
DR EMBL; AE000201; AAC74082.1; -.
DR EMBL; D90736; BAA36139.1; -.
DR EMBL; D90737; BAA35764.1; -.
DR EMBL; D16500; -: NOT_ANNOTATED_CDS.
DR PIR; S34222; S34222.
DR HSP; Q57366; ICKT.
DR ECOGENE; EGI1814; TORA.
DR PROSITE; PS00551; MOLYBDOPTERIN_PROK_1; FALSE_NEG.
DR PROSITE; PS00490; MOLYBDOPTERIN_PROK_2; 1.
DR PROSITE; PS00932; MOLYBDOPTERIN_PROK_3; 1.
DR PFAM; PF00384; molybdopterin; 1.
DR PFAM; PF01568; Molybdp_binding; 1.
DR KX Oxidoreductase; NAD; Molybdenum; Periplasmic; Signal.
FT SIGNAL 1 39
FT CHAIN 40 848 TRIMETHYLAMINE-N-OXIDE REDUCTASE.
FT CONFLICT 173 173 L -> R (IN REF. 1).
FT CONFLICT 176 176 A -> R (IN REF. 1).
FT CONFLICT 256 256 A -> R (IN REF. 1).
FT CONFLICT 258 258 V -> S (IN REF. 1).
FT CONFLICT 281 281 R -> G (IN REF. 1).
FT CONFLICT 325 325 Q -> E (IN REF. 1).
FT CONFLICT 348 348 T -> S (IN REF. 1).
FT CONFLICT 503 504 KL -> NV (IN REF. 1).
FT CONFLICT 713 714 QQ -> HE (IN REF. 1).
FT CONFLICT 751 751 L -> M (IN REF. 1).
FT CONFLICT 781 781 P -> L (IN REF. 1 AND 3).
SQ SEQUENCE 848 AA; 94456 MW; 59DDACB00B1843E7 CRC64;
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Query Match 63.0%; Score 34; DB 1; Length 848;
Best Local Similarity 71.4%; Pred. No. 76;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQTSWP 7
:|
Db 210 EQQTSWP 216

Search completed: May 27, 2000, 20:07:21
Job time: 993 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:38:43 ; Search time 199.56 Seconds
(without alignments)
3.127 Million cell updates/sec

Title: US-09-016-061-88
Perfect score: 54
Sequence: 1 QQSTSWPHT

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

SPREMBL12:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	36	66.7	296	13 O93312	O93312 brachydanio
2	36	66.7	297	13 O73779	O73779 brachydanio
3	36	66.7	323	2 Q54490	Q54490 streptomyces
4	35	64.8	235	11 Q63471	Q63471 rattus norv
5	35	64.8	315	13 Q9YGU0	Q9YGU0 brachydanio
6	35	64.8	1109	10 Q9ZVX6	Q9ZVX6 arabidopsis
7	35	64.8	4845	11 O88738	O88738 mus musculu
8	34	63.0	94	2 Q9XCE0	Q9XCE0 mycobacteri
9	34	63.0	96	2 Q9Z9Y5	Q9Z9Y5 frateuria s
10	34	63.0	522	13 Q9YGX4	Q9YGX4 brachydanio
11	34	63.0	596	4 O00185	O00185 homo sapien
12	34	63.0	640	5 Q9XWZ6	Q9XWZ6 caenorhabdi
13	34	63.0	746	2 Q44289	Q44289 anabaena sp
14	34	63.0	1045	5 Q20047	Q20047 caenorhabdi
15	34	63.0	1919	6 Q29518	Q29518 oryctolagus
16	34	63.0	1920	6 Q29519	Q29519 oryctolagus
17	33.5	62.0	411	4 O75876	O75876 homo sapien
18	33	61.1	267	6 O02764	O02764 oryctolagus
19	33	61.1	387	5 Q39907	Q39907 gonyaulax p
20	33	61.1	491	5 O76269	O76269 leishmania

21	33	61.1	491	5	O76343	O76343 leishmania
22	33	61.1	523	12	P89903	P89903 chimpanzee
23	33	61.1	617	2	O68077	O68077 rhodobacter
24	33	61.1	780	5	Q94407	Q94407 caenorhabdi
25	33	61.1	810	11	O60583	O60583 mus musculu
26	33	61.1	810	11	O54690	O54690 mus musculu
27	33	61.1	946	12	O69139	O69139 human herpe
28	33	61.1	981	4	Q15042	Q15042 homo sapien
29	33	61.1	1186	12	O90061	O90061 human herpe
30	33	61.1	1290	11	O62827	O62827 rattus norv
31	33	61.1	1461	4	O43655	O43655 homo sapien
32	32	59.3	135	5	O44063	O44063 neospora sp
33	32	59.3	135	11	O62284	O62284 mus musculu
34	32	59.3	136	5	O61925	O61925 caenorhabdi
35	32	59.3	172	5	O15627	O15627 entamoeba h
36	32	59.3	174	10	O40733	O40733 oryza sativ
37	32	59.3	175	12	O83739	O83739 beet wester
38	32	59.3	278	5	Q25679	Q25679 podocoryne
39	32	59.3	285	12	O87013	O87013 subterranea
40	32	59.3	307	4	O14792	O14792 homo sapien
41	32	59.3	311	10	O9ZOG6	O9ZOG6 arabidopsis
42	32	59.3	318	2	Q9ZFB3	Q9ZFB3 bacillus an
43	32	59.3	348	8	O63918	O63918 myxine glut
44	32	59.3	374	11	O88768	O88768 rattus norv
45	32	59.3	374	12	Q9WH74	Q9WH74 african swi

ALIGNMENTS

RESULT 1
O93312 ID O93312 PRELIMINARY; PRT; 296 AA.
AC O93312;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE FORKHEAD-5.
GN FKH5.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Rasbora; Danio.
RN [1]
RP SEQUENCE FROM N.A.
RA GRINBLAT Y., GAMSE J., PATEL M., SIVE H.;
RT "Determination of the zebrafish forebrain: induction and patterning.";
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF052651; AAC25103.1; -.
DR HSSP; Q63245; 2HPH.
DR PFAM; PF00250; Fork_head; 1.
DR PRINTS; PR00053; FORKHEAD.
SQ SEQUENCE 296 AA; 33066 MW; A9517620 CRC32;

Query Match 66.7%; Score 36; DB 13; Length 296;
Best Local Similarity 62.5%; Pred. No. 26;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSTSWPH 8
| : : : :
Db 196 QLTAWPH 203

RESULT 2
O73779 ID O73779 PRELIMINARY; PRT; 297 AA.
AC O73779;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE FORK HEAD DOMAIN PROTEIN FKD3.
GN MAR OR FKD3.

```

OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprininae; Rasbora; Danio.
RN [1]
RP SEQUENCE FROM N.A.
RA ODENTHAL J., NUESSEIN-VOLHARD C.;
RL Dev. Genes Evol. 0:0-0(1998).
DR EMBL; AF052246; AAC06363.1; -.
DR HSP; Q63245; 2HPH.
DR ZFIN; ZDB-GENE-980526-563; mar.
DR PFAM; PF00250; Fork_head; 1.
DR PRINTS; PR00053; FORKHEAD.
SQ SEQUENCE 297 AA; 32945 MW; BB2942FD CRC32;

Query Match 66.7%; Score 36; DB 13; Length 297;
Best Local Similarity 62.5%; Pred. NO. 26;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPH 8
Db 191 QLTAWPH 198

RESULT 3
Q54490 PRELIMINARY; PRT; 323 AA.
AC Q54490;
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-NOV-1998 (TREMREL. 08, Last sequence update)
DT 01-NOV-1998 (TREMREL. 08, Last annotation update)
DE SNOE (AROMATASE).
GN SNOE.
OS Streptomyces nogalater.
OC Actinobacteria; Actinobacteriales; Streptomyces.
OC Actinomycetales; Streptomyces; Streptomyces.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 27451;
RA YLHONKO K.P.J.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 27451;
RX MEDLINE; 96242142.
RA YLHONKO K., TUUKKANEN J., JUSSILA S., CONG L., MANTSALA P.;
RT "A gene cluster involved in nogalamycin biosynthesis from Streptomyces
RT nogalater: sequence analysis and complementation of early-block
RT mutations in the anthracycline pathway."
RL Mol. Gen. Genet. 251:113-120(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 27451;
RX MEDLINE; 96349102.
RA YLHONKO K., HAKALA J., KUNNARI T., MANTSALA P.;
RT "Production of hybrid anthracycline antibiotics by heterologous
RT expression of Streptomyces nogalater nogalamycin biosynthesis genes."
RL Microbiology 142:1965-1972(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 27451;
RX MEDLINE; 98007868.
RA TORKKELL S., YLHONKO K., HAKALA J., SKURNIK M., MANTSALA P.;
RT "Characterization of Streptomyces nogalater genes encoding enzymes
RT involved in glycosylation steps in nogalamycin biosynthesis."
RL Mol. Gen. Genet. 256:203-209(1997).
DR EMBL; AJ224512; CAAL2012.1; -.
SQ SEQUENCE 323 AA; 35864 MW; B71D76BA CRC32;

Query Match 66.7%; Score 36; DB 2; Length 323;
Best Local Similarity 83.3%; Pred. NO. 28;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TSWPHT 9
Db 34 TSWPHT 39

RESULT 4
Q63471 PRELIMINARY; PRT; 235 AA.
AC Q63471;
DT 01-NOV-1996 (TREMREL. 01, Created)
DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
DT 01-NOV-1998 (TREMREL. 08, Last annotation update)
DE PAROTID SECRETORY PROTEIN PRECURSOR.
GN PSP.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92129360.
RA MIRELS L., BALL W.D.;
RT "Neonatal rat submandibular gland protein SMG-A and parotid secretory
RT protein are alternatively regulated members of a salivary protein
RT multigene family."
RL J. Biol. Chem. 267:2679-2687(1992).
DR EMBL; M83209; AAC06334.1; -.
KW Signal.
FT SIGNAL. 1 20 POTENTIAL.
FT CHAIN 21 235 PAROTID SECRETORY PROTEIN.
SQ SEQUENCE 235 AA; 24529 MW; 3DD571BA CRC32;

Query Match 64.8%; Score 35; DB 11; Length 235;
Best Local Similarity 71.4%; Pred. NO. 31;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 QOSTSWP 7
Db 54 QOATTWP 60

RESULT 5
Q9YGU0 PRELIMINARY; PRT; 315 AA.
AC Q9YGU0;
DT 01-MAY-1999 (TREMREL. 10, Created)
DT 01-MAY-1999 (TREMREL. 10, Last sequence update)
DT 01-NOV-1999 (TREMREL. 12, Last annotation update)
DE HOMEOBOX PROTEIN.
GN HOXA11.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprininae; Rasbora; Danio.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 99051425.
RA AMORES A., FORCE A., YAN Y.-L., WANG Y.-L., FRITZ A., PRINCE V.,
RA HO R., AMEMIYA C., LANGELAND J., WESTERFELD M., EKKER M.,
RA POSTLETHWAIT J.;
RT "Zebrafish hox clusters and vertebrate genome evolution."
RL Science 282:1711-1714(1998).
DR EMBL; AF071240; AAD15934.1; -.
DR HSP; P02833; 9ANT.
KW Homeobox; DNA-binding; Nuclear protein.
SQ SEQUENCE 315 AA; 36239 MW; 6CE73EC1 CRC32;

Query Match 64.8%; Score 35; DB 13; Length 315;
Best Local Similarity 83.3%; Pred. NO. 41;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 3 STSWPH 8
 || |||
 Db 71 STRKPH 76

RESULT 6
 Q9ZVX6 PRELIMINARY; PRT; 1109 AA.
 AC Q9ZVX6;

DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE PUTATIVE TWV RESISTANCE PROTEIN.

GN F12A24.5.

OS Arabidopsis thaliana (Mouse-ear cross).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 OC Arabidopsis.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-CV, COLUMBIA;

RA ROUNSLEY S.D., LIN X., KAUL S., SHEA T.P., FUJII C.Y., MASON T.M.,

RA SHEN M., RONNING C.M., FRASER C.M., SOMERVILLE C.R., VENTER J.C.;

RT "Arabidopsis thaliana chromosome II BAC F12A24 genomic sequence.";

RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AC005167; AAC64218.1; -

SQ SEQUENCE 1109 AA; 125680 MW; E4B43E12 CRC32;

Query Match 64.8%; Score 35; DB 10; Length 1109;
 Best Local Similarity 66.7%; Pred. No. 1.4e+02;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 QOQTSWPH 9
 || |||
 Db 900 QOQHSWEHT 908

RESULT 7

O88738

ID O88738 PRELIMINARY; PRT; 4845 AA.

AC O88738;

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)

DE UBIQUITIN-CONJUGATING ENZYME.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 98292517.

RA HAUSER H.P., BARDOFF M., PYRONOLAKIS G., JENTSCH S.;

RT "A giant ubiquitin-conjugating enzyme related to IAP apoptosis

inhibitors.";

RL J. Cell Biol. 141:1415-1422(1998).

DR EMBL; Y17267; CAA76720.1; -

DR HSSP; P25865; 2AAK.

DR PFAM; PF00853; BIR.1.

DR PFAM; PF00179; UQ_con; 1.

SQ SEQUENCE 4845 AA; 528411 MW; 1ECD3A23 CRC32;

Query Match 64.8%; Score 35; DB 11; Length 4845;
 Best Local Similarity 100.0%; Pred. No. 5.6e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TSWPH 8

|||||

Db 269 TSWPH 273

RESULT 8

Q9XCE0

ID Q9XCE0 PRELIMINARY; PRT; 94 AA.

AC Q9XCE0;

DT 01-NOV-1999 (TREMBlrel. 12, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)

DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)

DE MUCONOLACTONE ISOMERASE.

GN CATC.

OS Mycobacterium smegmatis.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-MC2-155;

RX MEDLINE; 99328972.

RA FERNANDES N.D., WU Q.-L., KONG D., PUYANG X., GARG S., HUSSON R.N.;

RT "A mycobacterial extracytoplasmic sigma factor involved in survival

following heat shock and oxidative stress.";

RL J. Bacteriol. 181:4266-4274(1999).

DR EMBL; AF144091; AAD41808.1; -

KW Isomerase.

SQ SEQUENCE 94 AA; 10966 MW; 119E4C3E CRC32;

Query Match 63.0%; Score 34; DB 2; Length 94;
 Best Local Similarity 62.5%; Pred. No. 20;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQTSWPH 8

|| |||

Db 35 QRSWKPH 42

RESULT 9

Q9Z9Y5

ID Q9Z9Y5 PRELIMINARY; PRT; 96 AA.

AC Q9Z9Y5;

DT 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)

DE MUCONOLACTONE ISOMERASE (EC 5.3.3.4).

GN CATCI.

OS Frateuria sp. ANA-18.

OC Bacteria; Proteobacteria; gamma subphylum; Frateuria.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 99132292.

RA MURAKAMI S., TAKASHIMA A., TAKEMOTO J., TAKENAKA S., SHINKE R.;

RA AOKI K.;

RT "Cloning and sequence analysis of two catechol-degrading gene clusters

from the aniline-assimilating bacterium Frateuria species ANA-18.";

RL Gene 226:189-198(1999).

DR EMBL; AB009343; BAA75206.1; -

KW Isomerase.

SQ SEQUENCE 96 AA; 11034 MW; D742C03F CRC32;

Query Match 63.0%; Score 34; DB 2; Length 96;
 Best Local Similarity 62.5%; Pred. No. 20;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQTSWPH 8

|| |||

Db 35 QKSGKPH 42

RESULT 10

Q9YGX4

ID Q9YGX4 PRELIMINARY; PRT; 522 AA.

AC Q9YGX4;

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DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
DE ZOR-2.
GN ZOR-2.
OS Brachydanio rerio (Zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Rasbora; Danio.
RN [1]
RP SEQUENCE FROM N.A.
RA SUZUKI H., MEGAWA S., MURAKAWA M., HOSHIIJIMA K., SHIMURA Y.,
RA YASUDA K., INOUE K.;
RT "Identification of zebrafish maternal RNA-binding proteins, ZOR-1 and
RT -2."
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB011681; BAA75638.1; -. 1CB4E09D CRC32;
SQ SEQUENCE 522 AA; 58259 MW; 1CB4E09D CRC32;

Query Match 63.0%; Score 34; DB 13; Length 522;
Best Local Similarity 55.6%; Pred. No. 1e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
DB 31 KQHTNWKHT 39

RESULT 11
ID 000185 PRELIMINARY; PRT; 596 AA.
AC 000185;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE HTCF-4 PROTEIN.
GN HTCF-4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97218301.
RA KORINEK V., BARKER N., MORIN P.J., VAN WICHEN D., DE WEGER R.,
RA KINZLER K.W., VOGELSTEIN B., CLEVERS H.;
RT "Constitutive transcriptional activation by a beta-catenin-Tcf complex
RT in APC-/- colon carcinoma."
RL Science 275:1784-1787(1997).
RN [2]
RP REVISIONS.
RA BARKER N.;
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; Y11306; CAA72166.2; -.
DR HSSP; P27782; 2LEF.
DR PFAM; PF00505; HMG_box; 1.
SQ SEQUENCE 596 AA; 65357 MW; A813E620 CRC32;

Query Match 63.0%; Score 34; DB 4; Length 596;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
DB 568 QPSTSWLHS 576

RESULT 12
ID 09XW26 PRELIMINARY; PRT; 640 AA.
AC 09XW26;
DT 01-NOV-1999 (TREMBlrel. 12, Created)

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DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE Y42A5A.2 PROTEIN.
GN Y42A5A.2.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA STEWARD C.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., COULSON A.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., FULTON L.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
DR EMBL; AL032618; CAA21485.1; -.
SQ SEQUENCE 640 AA; 73874 MW; 169DFE70 CRC32;

Query Match 63.0%; Score 34; DB 5; Length 640;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 STSWPHT 9
DB 426 SGAWPHT 432

RESULT 13
Q44289 PRELIMINARY; PRT; 746 AA.
ID Q44289
AC Q44289;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE (STRAIN PCC 7120).
GN NARB.
OS Anabaena sp.
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=PCC 7120;
RX MEDLINE; 97136629.
RA CAI Y., WOLK C.P.;
RT "Nitrogen deprivation of Anabaena sp. strain PCC 7120 elicits rapid
RT activation of a gene cluster that is essential for uptake and
RT utilization of nitrate."
RL J. Bacteriol. 179:258-266(1997).
DR EMBL; L49163; AAB40292.1; -.
DR HSSP; P07658; 1AA6.
DR PFAM; PF00384; molybdopterin; 1.
DR PFAM; PF01568; molybdop_binding; 1.
SQ SEQUENCE 746 AA; 83012 MW; C32AFDDF CRC32;

Query Match 63.0%; Score 34; DB 2; Length 746;
Best Local Similarity 55.6%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY 1 QOQTSWPT 9
| | | | |
Db 542 QGPTOWPHS 550

RESULT 14

Q20047 PRELIMINARY; PRT; 1045 AA.
AC Q20047;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE SIMILAR TO S. CEREVISIAE HAP4 TRANSCRIPTIONAL ACTIVATOR.
GN F35D2.5.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAYTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.;
RL Nature 368:32-38(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX CONNELL M.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL; U28741; AAA68329.1; -.
DR PFAM; PF00595; PDZ; 1.
DR PFAM; PF00620; RhoGAP; 1.
SQ SEQUENCE 1045 AA; 116115 MW; 4E6A1E4A CRC32;

Query Match 63.0%; Score 34; DB 5; Length 1045;
Best Local Similarity 55.6%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQTSWPT 9
| | | | |
Db 565 QRATRWST 573

RESULT 15

Q29518 PRELIMINARY; PRT; 1919 AA.
AC Q29518;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
DE LACTASE-PHLORIZIN HYDROLASE PRECURSOR (EC 3.2.1.23)
DE (BETA-GALACTOSIDASE) (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]

RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=INTESTINAL EPITHELIAL LINING;
RX MEDLINE; 94085594.
RA VILLA M., BRUNSCHWILER D., GAECHTER T., BOLL W., SEMENZA G.,
RA MANTEI N.;
RT "Region-specific expression of multiple lactase-phlorizin hydrolase
genes in intestine of rabbit.";
RL FEBS Lett. 336:70-74(1993).
CC -I- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING BETA-D-
CC GALACTOSE RESIDUES IN BETA-D-GALACTOSIDES.
DR EMBL; Z27166; CAAB1690.1; -.
DR HSSP; P26205; ICBG.
DR PROSITE; PS00572; GLYCOSYL_HYDROL_F1_1; 2.
DR PROSITE; PS00653; GLYCOSYL_HYDROL_F1_2; 3.
DR PFAM; PF00232; Glyco_hydro_1; 4.
KW Signal; Hydrolase; Glycosidase.
FT NON_TER 1
FT SIGNAL <1 13 POTENTIAL.
FT CHAIN 861 1919 LACTASE-PHLORIZIN HYDROLASE, GLYCOSYL
FT CERAMIDASE (AA 848 TO 1906).
SQ SEQUENCE 1919 AA; 217088 MW; B35CE342 CRC32;

Query Match 63.0%; Score 34; DB 6; Length 1919;
Best Local Similarity 55.6%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQTSWPT 9
| | | | |
Db 1227 EEDTSWPTT 1235

Search completed: May 27, 2000, 19:38:45
Job time: 2378 sec

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49870.
 PR Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 9 AA;

Query Match 90.7%; Score 49; DB 1; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.5e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QOSTSWPHT 9
 ||| |||||
 DB 1 QOSTSWPHT 9

RESULT 3
 R25729
 ID R25729 standard; Protein; 107 AA.
 AC R25729;
 DT 13-JAN-1993 (first entry)
 DE Humanised VL region of the mouse CMV5 antibody.
 KW Murine; immunoglobulin; CDR; non immunogenic; cytomegalovirus;
 KW gH; light chain; variable region; framework; human; Wol.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT region 24..34
 FT /note= "CDR"
 FT region 50..56
 FT /note= "CDR"
 FT region 89..97
 FT /note= "CDR"
 FT misc_difference 49
 FT /note= "mutated residue"
 PN WO9211018-A.
 PD 09-JUL-1992.
 PF 19-DEC-1991; U09711.
 PR 19-DEC-1990; US-634278.
 PA (PROT-) PROTEIN DESIGN LABS INC.
 PI Co MS, Coeligh KL, Landolfi NF, Queen CL, Schneider WP;
 DR WPI; 92-249842/30.
 PR New immunoglobulin(s) having murine CDRs in human framework
 PT regions - have lower antigenicity; useful for treating e.g. HSV,
 PT CMV, T-cell disorders, myeloid disorders and auto-immune
 PT conditions
 PS Claim 40; Fig 27A; 141pp; English.

CC The sequence shows the humanised mature light chain variable
 CC region of the mouse CMV5 antibody. Murine CDRs were used
 CC in a human Wol framework to produce a pure humanised immunoglobulin
 CC (Ig) which is capable of binding to the gH glycoprotein of
 CC cytomegalovirus. The Ig is non immunogenic, due to the human
 CC framework, and has a strong affinity for its predetermined
 CC antigen. They can be produced in large quantities via recombinant
 CC DNA and monoclonal antibody technology. The humanised Igs may be
 CC used alone or in combination with chemotherapeutic agents such as
 CC non-steroidal anti-inflammatory drugs or immunosuppressants.
 CC See also R25721-32.
 SQ Sequence 107 AA;

Query Match 90.7%; Score 49; DB 1; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.048;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 QOSTSWPHT 9
 ||| |||||
 DB 89 QOSTSWPHT 97

RESULT 4
 R54093
 ID R54093 standard; Protein; 127 AA.
 AC R54093;
 DT 29-DEC-1994 (first entry)
 DE Sequence of mouse V-kappa showing the sequences of recombinant
 DE anti-FHV-1 antibody CDRs 1, 2 and 3.
 DE Feline herpes virus; FHV-1; monoclonal antibody; CDR;
 KW complementarity determining region.
 OS Mus musculus.
 FH Key Location/Qualifiers
 FT peptide 1..20
 FT /label= leader
 FT region 21..43
 FT /label= FR1
 FT region 44..54
 FT /label= CDR1
 FT region 55..70
 FT /label= FR2
 FT region 71..76
 FT /label= CDR2
 FT region 77..108
 FT /label= FR3
 FT region 109..117
 FT /label= CDR3
 FT region 118..127
 FT /label= FR4
 PN WO9412661-A.
 PD 09-JUN-1994.
 PF 25-NOV-1993; J01724.
 PR 28-NOV-1992; JP-341255.
 PA (KAGA) CHEMA SERO THERAPEUTIC RES INST.
 PI Kimachi K, Maeda H, Nishiyama K, Tokiyoshi S;
 DR WPI; 94-200288/24.
 DR N-PSDB; Q64167.
 PT Feline monoclonal antibody and recombinant antibodies specific
 PT for FHV-1 - for detection, treatment and prevention of FHV-1
 PT infection.
 PS Disclosure; Page 18-19; 53pp; Japanese.
 CC The inventors claim a monoclonal antibody against feline herpes
 CC virus (FHV-1). They also claim a recombinant antibody against FHV-1
 CC and fragments of VH and VL CDR1, CDR2 and CDR3. The antibodies are
 CC used in the detection, treatment and prevention of FHV-1. The
 CC sequences of the CDRs in the VH of the recombinant anti-FHV-1
 CC antibody are given in R54092. The sequences of the CDRs in the VL of
 CC the recombinant anti-FHV-1 antibody are given in R54093. These CDR
 CC sequences are claimed.
 SQ Sequence 127 AA;

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Query Match      90.7%; Score 49; DB 1; Length 127;
Best Local Similarity 88.9%; Pred. No. 0.057;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
Db 109 QQSGSWPHT 117

RESULT 5
W76013
ID W76013 standard; Protein; 9 AA.
AC W76013;
DE 02-NOV-1998 (first entry)
DT LM609 grafted antibody V-L region CDR3 protein fragment #1.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-L region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
N-PSDB; V49850.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Disclosure; Page 40; 129pp; English.
CC LM609 heavy and light chain fragments of the grafted monoclonal antibody
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 9 AA;

Query Match      87.0%; Score 47; DB 1; Length 9;
Best Local Similarity 88.9%; Pred. No. 1.5e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
Db 1 QQSGSWPHT 9

RESULT 6
W76006
ID W76006 standard; Protein; 107 AA.
AC W76006;
DE 02-NOV-1998 (first entry)
DT LM609 grafted antibody light chain variable region protein fragment.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
N-PSDB; V49821.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 1; Fig 1b; 129pp; English.
CC This sequence represents the vitaxin antibody variable light chain
CC region. Vitaxin and the antibody LM609 bind selectively to integrin
CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a
CC ligand and thus block integrin-mediated signal transduction. This is
CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
CC disease, specifically angiogenesis and restenosis (but also e.g.
CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
CC osteoporosis etc.). The antibodies contain non-murine framework regions
CC so are suitable for use in humans. Enhanced types of LM609 have affinity
CC more than 90 times greater than that of parent the parent antibody.

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FT W09833919-A2.
PN 06-AUG-1998.
PD 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49843.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 19; Fig 7; 129pp; English.
CC This sequence represents a LM609 grafted antibody variable light chain
CC region. LM609 and the antibody vitaxin bind selectively to integrin
CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand
CC and thus block integrin-mediated signal transduction. This is useful in
CC the treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
SQ Sequence 107 AA;

Query Match      87.0%; Score 47; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
Db 89 QQSGSWPHT 97

RESULT 7
W76002
ID W76002 standard; Protein; 107 AA.
AC W76002;
DT 02-NOV-1998 (first entry)
DE Vitaxin antibody light chain variable region protein fragment.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49821.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 1; Fig 1b; 129pp; English.
CC This sequence represents the vitaxin antibody variable light chain
CC region. Vitaxin and the antibody LM609 bind selectively to integrin
CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a
CC ligand and thus block integrin-mediated signal transduction. This is
CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
CC disease, specifically angiogenesis and restenosis (but also e.g.
CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
CC osteoporosis etc.). The antibodies contain non-murine framework regions
CC so are suitable for use in humans. Enhanced types of LM609 have affinity
CC more than 90 times greater than that of parent the parent antibody.

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SQ Sequence 107 AA;
Query Match 87.0%; Score 47; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSTSWPHT 9
   ||| |||||
Db 89 QQSGSWPHT 97

RESULT 8
W76004
ID W76004 standard; Protein; 107 AA.
AC 02-AUG-1998
DT 02-NOV-1998 (first entry)
DE LM609 antibody light chain variable region protein fragment.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSY INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; W76004.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related nucleic acid, used to treat, prevent or diagnose
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 46; Fig 2b; 129pp; English.
CC This sequence represents the LM609 antibody variable light chain region.
CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC block integrin-mediated signal transduction. This is useful in the
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
CC Sequence 107 AA;

Query Match 87.0%; Score 47; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSTSWPHT 9
   ||| |||||
Db 89 QQSGSWPHT 97

RESULT 9
R38601
ID R38601 standard; peptide; 107 AA.
AC R38601;
DT 28-OCT-1993 (first entry)
DE HVH light chain.
KW Antibody; variable domain; light; L; heavy; H; consensus;
KW affinity; antigen; immunogenicity; humanisation; framework.
OS Homo sapiens.
PN WO9311794-A.
PD 24-JUN-1993.
PF 13-DEC-1992; U10906.
PR 13-DEC-1991; US-808464.

Query Match 79.6%; Score 43; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 0.55;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSTSWPHT 9
   ||| |||||
Db 89 QQSGSWPHT 97

RESULT 10
W58482
ID W58482 standard; protein; 107 AA.
AC W58482;
DT 18-AUG-1998 (first entry)
DE Murine HVH antibody light chain variable domain.
KW Humanised; human; mouse; CD5; anti-CD5 antibody; immunoglobulin;
KW depletion; cytotoxic; immunoconjugate; fusion protein; psoriasis;
KW autoimmune disease; rheumatoid arthritis; type I diabetes.
OS Mus sp.
PN US5770196-A.
PD 23-JUN-1998.
PF 07-JUN-1995; 472788.
PR 23-JUN-1993; US-082842.
PR 13-DEC-1991; US-808464.
PR 14-DEC-1992; WO-U10906.
PR 07-JUN-1995; US-472788.
PA (XOMA ) XOMA CORP.
PI Studnicka GM;
DR WPI; 98-376744/32.
DE Depletion of CD5-positive cells in vivo - using anti-CD5 antibodies
PT with humanised variable regions
PS Disclosure: Column 43-44; 77pp; English.
CC A method has been developed of depleting CD5+ cells in an animal. The
CC method comprises administering a cytotoxic protein containing a modified
CC immunoglobulin (Ig) variable domain, where the protein is an anti-CD5 Ig
CC molecule or an immunoconjugate or fusion protein containing an anti-CD5
CC Ig molecule, and where the modified Ig variable domain comprises at
CC least one of (a) a modified light chain variable region (see W58478 or
CC W58480), and (b) a modified heavy chain variable region (see W58479 or
CC W58481), where W58478 and W58479 are humanised forms of the H65 light
CC and heavy chain variable domains with low risk amino acid substitutions
CC [i.e. low risk of reducing antigen-binding specificity.] and W58480 and
CC W58481 are humanised forms of the H65 light and heavy chain variable
CC domains with moderate risk amino acid substitutions and are present in
CC humanised H65 antibody he3 (ATCC HB 11206). The method is useful for
CC treating autoimmune diseases, especially systemic lupus erythematosus,
CC rheumatoid arthritis, psoriasis or type I diabetes. The present sequence
CC represents the murine HVH antibody light chain variable domain.
CC Sequence 107 AA;

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Query Match      79.6%; Score 43; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 0.55;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 QOSTSWPHT 9
   ||| |||:|
Db 89 QQSNSWPYT 97

RESULT 11
R15438
ID R15438 standard; Protein; 108 AA.
AC R15438;
DT 25-FEB-1992 (first entry)
DE Light chain variable region of MAb 1A6.
KW HRV; ICAM-1; antigen-binding fragment; inflammation;
KW auto-immune disease.
OS Homo sapiens.
PN EP-459577-A.
PD 04-DEC-1991.
PF 25-MAY-1991; 201243.
PR 01-JUN-1990; US-532001.
PA (MERI ) MERCK & CO INC..
PI Colonna RJ, Condra JH, Tomassini JE, Sardana VV;
DR WPI; 91-355850/49.
PT Microbially expressed portions of monoclonal antibody - can block
PT attachment of rhinovirus ligands to inter-cellular adhesion
PT molecule (ICAM-1)
PS Claim 1; Page 19; 28pp; English.
CC This is one of six antibody fragments from MAb's specific for domain
CC 1 of ICAM-1. MAb 1A6 also specifically blocks the major group of
CC human rhinovirus from binding to and infecting HeLa cells. The
CC peptide fragments can be used to treat or prevent rhinovirus
CC infection. See R15437-R15443.
SQ Sequence 108 AA;

Query Match      79.6%; Score 43; DB 1; Length 108;
Best Local Similarity 77.8%; Pred. No. 0.56;
Matches 7; Conservative 1; Mismatches 0; Gaps 0;

QY 1 QOSTSWPHT 9
   ||| |||:|
Db 89 QQSNSWPYT 97

RESULT 12
R52033
ID R52033 standard; Protein; 109 AA.
AC R2033;
DT 26-SEP-1996 (first entry)
DE Light chain variable region of murine antibody 3HfM.
KW antibody; humanised; murine; human; heavy chain; light; variable;
KW framework region; complementarity determining region; reshaping;
KW modelling; surface residue; modify.
OS Mus sp.
PN Key
DR Key
FT region 1. .23
   /label= framework_region_1
   /note= "FR 1"
FT region 24. .34
   /label= complementarity_determining_region_1
   /note= "CDR 1"
FT region 35. .49
   /label= FR_2
FT region 50. .56
   /label= CDR_2
FT region 57. .88
   /label= FR_3
FT region 89. .97
   /label= CDR_3
FT region 98. .109

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FT EP-592106-A1.
PN 13-APR-1994.
PD 07-SEP-1993; 307051.
PR 09-SEP-1992; US-942245.
PA (PEDE/) PEDERSEN J T.
PA (IMMU-) IMMUNOGEN INC.
PI Guild BC, Pedersen JT, Rees AR, Roguska MA, Searle SMJ;
DR WPI; 94-120230/15.
PT Method of resurfacing of rodent antibodies to produce humanised
PT antibody forms - for producing non-human antibodies with improved
PT therapeutic efficiency by presenting human surface on V-region
PS Example 1; Fig 3A; 230pp; English.
CC The present sequence is that of the light chain variable (LC VR) region
CC of murine antibody 3HfM. This sequence was aligned with 11 other known
CC antibody LC VRs and a set of framework positions of surface exposed amino
CC acid residues was determined. This information can be used in a method to
CC determine how to modify a rodent antibody or fragment by resurfacing in
CC order to produce a humanised rodent antibody. Residues (determined from
CC alignment) at positions 1, 3, 5, 9, 15, 18, 46, 47, 51, 63, 66, 73, 86,
CC 87, 111, 115, 116 and 117 are accessible residues. None of the entire
CC combinations of surface residues in the murine sequences were found in
CC the human sequences and vice versa. However the residues in individual
CC positions appear to be conserved.
SQ Sequence 109 AA;

Query Match      79.6%; Score 43; DB 1; Length 109;
Best Local Similarity 77.8%; Pred. No. 0.56;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOSTSWPHT 9
   ||| |||:|
Db 89 QQSNSWPYT 97

RESULT 13
W19580
ID W19580 standard; Protein; 143 AA.
AC W19580;
DT 30-JUL-1997 (first entry)
DE Mouse anti-idiotypic antibody 5A6 light chain variable region.
KW Anti-idiotypic; anti-EGFR; epidermal growth factor receptor; tumour;
KW cancer; neoplasia; glioma; melanoma; carcinoma; drug manufacture; ss.
OS Mus musculus.
PN Key
DR Key
FT peptide 1. .20
   /label= sig_peptide
FT region 21. .43
   /label= FR1
   /note= "framework region 1"
FT region 44. .54
   /label= CDR1
   /note= "complementarity determining region 1"
FT region 55. .69
   /label= FR2
   /note= "framework region 2"
FT region 70. .76
   /label= CDR2
   /note= "complementarity determining region 2"
FT region 77. .108
   /label= FR3
   /note= "framework region 3"
FT region 109. .117
   /label= CDR3
   /note= "complementarity determining region 3"
FT region 118. .128
   /label= FR4
   /note= "framework region 4"
FT region 129. .143
   /note= "mouse constant kappa region"
PN EP-745612-A1.
PD 04-DEC-1996.

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PF 14-MAY-1996; 107651.
PR 26-MAY-1995; EP-107967.
PA (MERE ) MERCK PATENT GMBH.
PI Adan J, Carceller A, Gomez A, Piulats J, Rosell E;
DR WPI: 97-013659/02.
DR N-PSDB; T70811.
PT Monoclonal anti-idiotypic antibodies mimicking epidermal growth
PT factor receptor - useful for tumour therapy
PS Claim 6; Fig 5F; 28pp; English.
CC Murine monoclonal anti-idiotypic antibodies, 15H8, 3B6 and 5A6 are
CC new. They induce an immune response against epidermal growth factor
CC receptor (EGFR). The sequences of the heavy and light chain variable
CC regions of these antibodies are given in the specification. The
CC antibodies are used for the manufacture of drugs directed against
CC tumours that express EGFR on their surface, including melanomas,
CC gliomas and carcinomas.
SQ Sequence 143 AA;

Query Match 79.6%; Score 43; DB 1; Length 143;
Best Local Similarity 77.8%; Pred. No. 0.75;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9
Db 109 QQNSWPYT 117
||| |||:|

RESULT 14
R15443
ID R15443 standard; Protein; 240 AA.
AC R15443;
DE 25-FEB-1992 (first entry)
DE Single chain Fv from pSCV1 for blocking HRV binding to ICAM-1.
KW antigen-binding fragment; inflammation; auto-immune disease.
OS Homo sapiens.
PN EP-459577-A.
PD 04-DEC-1991.
PP 25-MAY-1991; 201243.
PR 01-JUN-1990; US-532001.
PA (MERI ) MERCK & CO INC.
PI Colonna RJ, Condra JH, Tomassini JE, Sardana VV;
DR WPI: 91-355850/49.
PT Microbially expressed portions of monoclonal antibody - can block
PT attachment of rhinovirus ligands to inter-cellular adhesion
PT molecule (ICAM-1)
PS Claim 5; Page 21; 28pp; English.
CC The Fv fragment encoded by pSCV1 was able to protect cells against
CC infection by HRV-14. It was less active than modified Fv fragments
CC which included a Gly-Gly-Gly-Ser flexible linker between the L
CC and H chains as either a monomer or a dimer.
CC See also R15437-R15442.
SQ Sequence 240 AA;

Query Match 79.6%; Score 43; DB 1; Length 240;
Best Local Similarity 77.8%; Pred. No. 1.3;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSTSWPHT 9
Db 89 QQNSWPYT 97
||| |||:|

RESULT 15
W87456
ID W87456 standard; Protein; 105 AA.
AC W87456;
DE 15-MAR-1999 (first entry)
DE JK gene product.
KW Humanised antibody; monoclonal antibody; MAb; antibody engineering;
KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;

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KW angiogenesis; diabetic retinopathy; inflammation;
KW macular degeneration; osteoporosis; Paget's disease;
KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
KW D12H2REI; JK protein.
OS Mus sp.
PN W09840488-A1.
PD 17-SEP-1998.
PF 12-MAR-1998; U04987.
PR 12-MAR-1997; US-039609.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PI Johanson KO, Jonak ZL, Taylor AH;
DR WPI: 99-034590/03.
DR N-PSDB; V71803.
PT New anti alpha_v beta_3 vitronectin receptor antibodies - used for
PT immunotherapeutic treatment of e.g. diabetic retinopathy,
PT inflammatory disorders, atherosclerosis, restenosis, cancers or
PT osteoporosis
PS Example 14; Page 66; 97pp; English.
CC This polypeptide is encoded by a JK synthetic gene segment (see
CC V71803). It was utilising in novel D12H2REI humanised light chain
CC variable region (see W87458), which comprises a human REI framework
CC and complementarity determining regions from the anti-human alpha-v
CC beta-3 vitronectin receptor monoclonal antibody D12. Humanised D12
CC antibodies can be used for passive immunotherapy of disorders
CC mediated by the alpha-v beta-3 vitronectin receptor, e.g. restenosis
CC and angiogenic associated diseases.
SQ Sequence 105 AA;

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Query Match 74.1%; Score 40; DB 1; Length 105;
Best Local Similarity 77.8%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 QOSTSWPHT 9
Db 89 QQNSWPYT 97
||| |||:|

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Search completed: May 27, 2000, 19:21:39
Job time: 1593 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:26:47 ; Search time 163.56 Seconds
(without alignments)
3.226 Million cell updates/sec

Title: US-09-016-061-90
Perfect score: 51
Sequence: 1 QQSGSWPLT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_63:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	45	88.2	104	2 B43413	Ig kappa chain V r
2	45	88.2	138	2 A26471	Ig kappa chain pre
3	40	78.4	106	2 PL0267	Ig kappa chain V r
4	40	78.4	106	2 PC4282	Ig kappa chain (an
5	40	78.4	107	2 C45722	anti-glycoprotein
6	39	76.5	67	2 PH1081	Ig light chain V r
7	39	76.5	69	2 PH1080	Ig light chain V r
8	39	76.5	553	2 T15220	hypothetical prote
9	38	74.5	107	2 A45722	anti-glycoprotein
10	38	74.5	123	2 S35479	Ig kappa chain pre
11	37	72.5	102	2 S26346	Ig kappa chain V r
12	37	72.5	128	2 PN0445	Ig kappa chain pre
13	37	72.5	144	2 PL0106	Ig kappa chain pre
14	37	72.5	154	2 T17816	hypothetical prote
15	37	72.5	642	2 H69466	conserved hypothet
16	36	70.6	87	2 PH1082	Ig light chain V r
17	36	70.6	91	2 S37525	Ig kappa chain V r
18	36	70.6	108	2 C30502	Ig kappa chain V r
19	36	70.6	115	1 KVM5L7	Ig kappa chain pre
20	36	70.6	117	2 S40362	Ig kappa chain - h
21	36	70.6	169	2 D65126	probable general s
22	36	70.6	204	2 T32062	hypothetical prote
23	36	70.6	275	2 D70737	hypothetical prote
24	36	70.6	543	2 T06523	cytochrome P450 mo
25	35	68.6	107	2 B45722	anti-glycoprotein
26	35	68.6	235	1 SQMS	parotid secretory
27	35	68.6	365	1 SAVLWE	large surface anti
28	35	68.6	366	1 SAVLBD	large surface anti
29	35	68.6	366	1 SAVLWD	large surface anti
30	35	68.6	499	2 A27198	cellulase (EC 3.2.

ALIGNMENTS

RESULT 1

B43413

Ig kappa chain V region - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-May-1999

C;Accession: B43413

R;Tomiyama, Y.; Brojer, F.; Ruggeri, Z.M.; Shattil, S.J.; Smiltneck, J.; Gorski, J.;

J. Biol. Chem. 267, 18085-18092, 1992

A;Title: A molecular model of RGD ligands. Antibody D gene segments that direct speci

A;Reference number: A43413; MUID:92388177

A;Accession: B43413

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-104 <TOM>

A;Note: sequence extracted from NCBI backbone (NCBIP:112818)

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 88.2%; Score 45; DB 2; Length 104;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9

DB 86 QQNSWPLT 94

RESULT 2

A26471

Ig kappa chain precursor V region (MAK33) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 23-Jul-1999

C;Accession: A26471

R;Buckel, P.; Hubner-Parajsz, C.; Mattes, R.; Lenz, H.; Haug, H.; Beaucamp, K.

Gene 51, 13-19, 1987

A;Title: Cloning and nucleotide sequence of heavy- and light-chain cDNAs from a creat

A;Reference number: A91572; MUID:87248058

A;Accession: A26471

A;Molecule type: mRNA

A;Residues: 1-138 <BUC>

A;Cross-references: GB:M16162; NID:g196893; PIDN:AAA38823.1; PID:g196894

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-138/Product: Ig kappa chain V region #status predicted <WAT>

Query Match

Best Local Similarity 88.2%; Score 45; DB 2; Length 138;

Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9

Db 109 QQSNWPLT 117
||| |||||

RESULT 3

PL0267 Ig kappa chain V region (anti-DNA, DP12VK) - mouse (fragment)

C:Species: Mus musculus (house mouse)
C:Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 16-Aug-1996

C:Accession: PL0267

R:Shlomchik, M.; Mascellli, M.; Shan, H.; Radic, M.Z.; Pisetsky, D.; Marshak-Rothstein, A

J. Exp. Med. 171, 265-297, 1990

A:Title: Anti-DNA antibodies from autoimmune mice arise by clonal expansion and somatic

A:Reference number: PL0231; MUID:90111618

A:Accession: PL0267

A:Molecule type: mRNA

A:Residues: 1-106 <SHL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-23/Region: framework 1

F:24-34/Region: complementarity-determining 1

F:35-49/Region: framework 2

F:50-56/Region: complementarity-determining 2

F:57-88/Region: framework 3

F:89-97/Region: complementarity-determining 3

F:98-106/Region: framework 4

Query Match 78.4%; Score 40; DB 2; Length 106;

Best Local Similarity 77.8%; Pred. No. 2.6;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9

||| |||||

Db 89 QQSNWPLYT 97

RESULT 4

PC4282 Ig kappa chain (anti-SS-A/Ro 60K peptide) (E-42 and E-56) - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 07-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 07-May-1999

C:Accession: PC4282; PC4284

R:Suzuki, H.; Takemura, H.; Suzuki, M.; Sekine, Y.; Kashiwagi, H.

Biochem. Biophys. Res. Commun. 232, 101-106, 1997

A:Title: Molecular cloning of anti-ss-A/Ro 60-kDa peptide fab fragments from infiltratin

A:Reference number: PC4279; MUID:97236289

A:Accession: PC4282

A:Molecule type: protein

A:Residues: 1-106 <SU2>

A:Note: E-42

A:Accession: PC4284

A:Molecule type: protein

A:Residues: 1-106 <SU2>

A:Note: E-56

C:Comment: This antibody is commonly found in systemic autoimmune diseases such as Sjogren

C:Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match

Best Local Similarity 78.4%; Score 40; DB 2; Length 106;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9

||| |||||

Db 87 QQRASWPLT 95

RESULT 5

C45722 anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 115) - mouse (f

C:Species: Mus musculus (house mouse)

C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997

C:Accession: C45722

R:Simpson, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Va

J. Virol. 67, 489-496, 1993

A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on

A:Reference number: A45722; MUID:93100833

A:Accession: C45722

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-107 <SIM>

A:Note: sequence extracted from NCBI backbone (NCBIP:120591)

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: glycoprotein

Query Match

Best Local Similarity 78.4%; Score 40; DB 2; Length 107;

Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9

||| |||||

Db 89 QQSHNWPLT 97

RESULT 6

PH1081

Ig light chain V region (clone 165.6) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996

C:Accession: PH1081

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444

A:Accession: PH1081

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-67 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

Query Match

Best Local Similarity 76.5%; Score 39; DB 2; Length 67;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9

||| |||||

Db 58 QQSNWPLT 66

RESULT 7

PH1080

Ig light chain V region (clone 165.60) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 15-Jun-1996

C:Accession: PH1080

R:Tillman, D.M.; Jou, N.T.; Hill, R.J.; Marion, T.N.

J. Exp. Med. 176, 761-779, 1992

A:Title: Both IgM and IgG anti-DNA antibodies are the products of clonally selective

A:Reference number: PH0971; MUID:92381444

A:Accession: PH1080

A>Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-69 <TIL>

A:Experimental source: B cell, strain [NZB x NZW]F1

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: immunoglobulin

Query Match

Best Local Similarity 76.5%; Score 39; DB 2; Length 69;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
||| ||| |
Db 60 QOQSNWPQT 68

RESULT 8
T15220
hypothetical protein F57C9.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T15220
R:Geisel, C.; Kramer, J.; Gibson, A.
submitted to the EMBL Data Library, May 1997
A:Description: The sequence of C. elegans cosmid F57C9.
A:Reference number: Z18309
A:Accession: T15220
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-553 <GEI>
A:Cross-references: EMBL:AF003142; NID:g2088743; PID:AA54191.1; GSPDB:GN
A:Experimental source: strain Bristol N2; clone F57C9
C:Genetics:
A:Gene: CESP:F57C9.8
A:Map position: 1
A:Introns: 184/1; 233/3; 286/3; 496/1

Query Match 76.5%; Score 39; DB 2; Length 553;
Best Local Similarity 66.7%; Pred. No. 21;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
|:||||| :
Db 373 QOQSGSWPFS 381

RESULT 9
A45722
anti-glycoprotein H monoclonal antibody light-chain variable domain (Mab 5) - mouse (fra
C:Species: Mus musculus (house mouse)
C:Date: 03-Mar-1994 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C:Accession: A45722
R:Simpton, J.A.; Chow, J.C.; Baker, J.; Avdalovic, N.; Yuan, S.; Au, D.; Co, M.S.; Vasqu
J. Virol. 67, 489-496, 1993
A:Title: Neutralizing monoclonal antibodies that distinguish three antigenic sites on hu
A:Reference number: A45722; MUID:93100833
A:Accession: A45722
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-107 <SIM>
A:Note: sequence extracted from NCBI backbone (NCBIP:120589)
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: glycoprotein

Query Match 74.5%; Score 38; DB 2; Length 107;
Best Local Similarity 77.8%; Pred. No. 5.9;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
||| ||| |
Db 89 QOQSNWPHT 97

RESULT 10
S35479
Ig kappa chain precursor V region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 19-Mar-1997 #sequence_revision 05-Dec-1998 #text_change 23-Jul-1999
C:Accession: S35479
R:Takeda, Y.; Wise, K.S.; Hoffman, R.W.
Nucleic Acids Res. 20, 4099, 1992

A:Title: Nucleotide sequences of immunoglobulin heavy and light chain V-regions from
A:Reference number: S35479; MUID:92375706
A:Accession: S35479
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-123 <TAK>
A:Cross-references: EMBL:M93959; NID:g197572; PIDN:AAA39079.1; PID:g554148
C:Genetics:
A:Map position: 6
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;1-12/Domain: signal sequence (fragment) #status predicted <SIG>
F;13-123/Product: Ig kappa chain V region (fragment) #status predicted <MAV>

Query Match 74.5%; Score 38; DB 2; Length 123;
Best Local Similarity 77.8%; Pred. No. 6.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
||| ||| |
Db 101 QOQSNWPHT 109

RESULT 11
S26346
Ig kappa chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26346
R:Stark, S.E.; Caton, A.J.
J. Exp. Med. 174, 613-624, 1991
A:Title: Antibodies that are specific for a single amino acid interchange in a protei
A:Reference number: S26309; MUID:91341421
A:Accession: S26346
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-102 <STA>
A:Cross-references: EMBL:X59211; NID:g52338; PIDN:CAA41921.1; PID:e36191; PID:g133407
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 72.5%; Score 37; DB 2; Length 102;
Best Local Similarity 66.7%; Pred. No. 8.3;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
||| :||| |
Db 87 QOQSNWPYT 95

RESULT 12
PN0445
Ig kappa chain precursor V-I region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 17-Mar-1999
C:Accession: PN0445
R:Kaluz, B.; Betzl, G.; Shao, H.; Diamantsein, T.; Weidle, U.H.
Gene 122, 321-328, 1992
A:Title: A general method for chimerization of monoclonal antibodies by inverse polym
A:Reference number: PN0444; MUID:93138402
A:Accession: PN0445
A:Molecule type: mRNA
A:Residues: 1-128 <KAL>
A:Cross-references: GB:L02347
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F;1-10/Domain: signal sequence #status predicted <SIG>
F;11-128/Product: Ig light chain kappa-1 V region #status predicted <MAV>

Query Match 72.5%; Score 37; DB 2; Length 128;

```
Best Local Similarity 66.7%; Pred. NO. 10;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
Db 99 QQTNSWPT 107

RESULT 13
PL0106
Ig kappa chain precursor V-J-C region (LSI) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Aug-1996
C:Accession: PL0106
R:Silberstein, L.E.; Litwin, S.; Carmack, C.E.
J. Exp. Med. 169, 1631-1643, 1989
A:Title: Relationship of variable region genes expressed by a human B cell lymphoma secret
A:Reference number: PL0106; MUID:89235583
A:Accession: PL0106
A:Molecule type: mRNA
A:Residues: 1-144 <SI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-115/Domain: V region <VRE>
F:44-54/Region: complementarity-determining 1
F:70-76/Region: complementarity-determining 2
F:109-115/Region: complementarity-determining 3
F:116-127/Domain: J region <JRG>
F:128-144/Domain: C region (fragment) <CRE>

Query Match 72.5%; Score 37; DB 2; Length 144;
Best Local Similarity 66.7%; Pred. NO. 12;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 QOQSGSWPLT 9
Db 109 QQRNSWPLT 117

RESULT 14
TI7816
hypothetical protein a317L - Chlorella virus PBCV-1
C:Species: Chlorella virus PBCV-1
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: TI7816
R:Graves, M.V.; Van Etten, J.L.
submitted to the EMBL Data Library, May 1999
A:Reference number: Z18806
A:Accession: TI7816
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-154 <GRA>
A:Cross-references: EMBL:U42580; NID:94028896; PIDN:AAC96685.1
A:Experimental source: specific host Chlorella strain NC64A
C:Genetics:
A:Note: a317L

Query Match 72.5%; Score 37; DB 2; Length 154;
Best Local Similarity 75.0%; Pred. NO. 13;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWPL 8
Db 33 QTSQSWPV 40

RESULT 15
H69466
conserved hypothetical protein AF1737 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
```

```
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
C:Accession: H69466
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
.: Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A:Reference number: A69250; MUID:98049343
A:Accession: H69466
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-642 <KLE>
A:Cross-references: GB:AE000983; GB:AE000782; NID:g2689306; PIDN:AAB89512.1; PID:g264
C:Superfamily: conserved hypothetical protein yyaL
```

```
Query Match 72.5%; Score 37; DB 2; Length 642;
Best Local Similarity 85.7%; Pred. NO. 54;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 3 SSGSWPLT 9
Db 101 SSGWPLT 107
```

Search completed: May 27, 2000, 19:26:48
Job time: 1771 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 20:07:21 ; Search time 69.28 seconds
(without alignments)
3.956 Million cell updates/sec

Title: US-09-016-061-90
Perfect score: 51
Sequence: 1 QSGSWPLT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	78.4	745	1 CUL2_HUMAN	Q13617 homo sapien
2	36	70.6	115	1 KSV1_MOUSE	P01642 mus musculus
3	36	70.6	169	1 GSPH_ECOLI	P41443 escherichia
4	36	70.6	543	1 C821_PEA	Q43068 pisum sativ
5	35	68.6	235	1 PSP_MOUSE	P07743 mus musculus
6	35	68.6	365	1 VMSA_HBEDC	F30029 duck hepato
7	35	68.6	366	1 VMSA_HBEDB	P17194 duck hepato
8	35	68.6	366	1 VMSA_HBEDB	P17195 duck hepato
9	35	68.6	499	1 GUN1_BACSU	P07983 bacillus su
10	35	68.6	939	1 SYV_CHLTR	O84304 chlamydia t
11	35	68.6	940	1 SYV_CHLPN	Q92987 chlamydia p
12	34	66.7	92	1 CATC_RHOOP	P95609 rhodococcus
13	34	66.7	96	1 CTC1_ACILW	O33947 acinetobact
14	34	66.7	146	1 YFDK_ECOLI	P77656 escherichia
15	34	66.7	470	1 IE63_HSVB	P28939 equine herp
16	34	66.7	470	1 IE63_HSVK	Q05906 equine herp
17	34	66.7	540	1 NUSA_MYCPN	P75591 mycoplasma
18	34	66.7	777	1 BISC_ECOLI	P20099 escherichia
19	34	66.7	1456	1 RRPO_PVX	P09395 potato viru
20	34	66.7	1456	1 RRPO_PVXCP	P22591 potato viru
21	34	66.7	1456	1 RRPO_PVXHB	Q07630 potato viru
22	34	66.7	1456	1 RRPO_PVX3	P17779 potato viru
23	34	66.7	2329	1 YS89_CAEEL	Q09624 caenorhabdi
24	33	64.7	226	1 NUKM_NEUCR	O47950 neurospora
25	33	64.7	251	1 BIOC_ECOLI	P12999 escherichia
26	33	64.7	300	1 GP40_HUMAN	O14842 homo sapien
27	33	64.7	468	1 NIFE_KLEPN	P10380 klebsiella
28	33	64.7	516	1 Y4NM_RHISN	P55585 rhizobium s
29	33	64.7	796	1 PTPA_RAT	Q03348 rattus norv
30	33	64.7	802	1 PTPA_HUMAN	P18433 homo sapien
31	33	64.7	829	1 PTPA_MOUSE	P18052 mus musculus
32	33	64.7	3329	1 BR2C_MOUSE	P97929 mus musculus
33	33	64.7	3418	1 BR2C_HUMAN	P51587 homo sapien
34	32	62.7	302	1 CYSD_ECOLI	P21156 escherichia

ALIGNMENTS

RESULT 1

ID	CUL2_HUMAN	STANDARD:	PRT:	745 AA.
AC	Q13617; O00200;			
DT	01-NOV-1997 (Rel. 35, Created)			
DT	01-NOV-1997 (Rel. 35, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	CULLIN HOMOLOG 2 (CUL-2).			
GN	CUL2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Homnidae; Homo.			
[1]				
RP	SEQUENCE FROM N.A.			
RP	TISSUE-KIDNEY.			
RC	MEDLINE; 97225922.			
RA	Pause A., Lee S., Worrel R., Chen D.Y.T., Burgess W.H.,			
RA	Linehan W.M., Klausner R.D.;			
RT	"The von Hippel-Lindau tumor-suppressor gene product forms a stable			
RT	complex with human CUL-2, a member of the Cdc53 family of proteins.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 94:2156-2161(1997).			
[2]				
RP	SEQUENCE OF 95-745 FROM N.A.			
RP	MEDLINE; 96279828.			
RA	Kipreos E.T., Lander L.E., Wing J.P., He W.W., Hedgecock E.M.;			
RT	"cul-1 is required for cell cycle exit in C. elegans and identifies a			
RT	novel gene family.";			
RL	Cell 85:829-839(1996).			
CC	-1- FUNCTION: FORMS A STABLE COMPLEX WITH THE VHL TUMOR SUPPRESSOR.			
CC	-1- SIMILARITY: BELONGS TO THE CULLIN FAMILY.			
CC				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC				
DR	EMBL; U83410; AAC51190.1; -.			
DR	EMBL; U58088; AAC50545.1; -.			
DR	MIN; 603135; -.			
DR	PROSITE; PS01256; CULLIN_1; 1.			
DR	PROSITE; PS50069; CULLIN_2; 1.			
DR	PFAM; PF00888; Cullin; 1.			
DR	CONFLICT 95 98			
FT	SKGA -> IRHE (IN REF. 2).			
FT	S -> N (IN REF. 2).			
FT	CONFLICT 109 109			
FT	O -> H (IN REF. 2).			
FT	CONFLICT 681 681			
SQ	SEQUENCE 745 AA; 86956 MW; A39475AE379C9005 CRC64;			

Query Match 78.4%; Score 40; DB 1; Length 745;
Best Local Similarity 75.0%; Pred. No. 7.7;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSGSWPLT 9
|:|:|:|

```

Db 513 QAGAWPLT 520

RESULT 2
KV51_MOUSE
ID KV51_MOUSE STANDARD; PRT; 115 AA.
AC P01642;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG KAPPA CHAIN V-V REGION L7 PRECURSOR (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 81220975.
RA Pech M., Hochli J., Schnell H., Zachau H.G.;
RT "Differences between germ-line and rearranged immunoglobulin V kappa
RT coding sequences suggest a localized mutation mechanism.";
RL Nature 291:668-670(1981).
CC -1- MISCELLANEOUS: THERE APPEAR TO BE TWO POSSIBLE SPLICE JUNCTIONS AT
CC THE 3' END OF THE INTRON. THE ALTERNATE WOULD CODE FOR A PROTEIN
CC LACKING RESIDUES 17-19.
DR PTR; A01925; KVM5L7.
DR PFAM; PF00047; Ig; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL
FT SIGNAL 1 20
FT CHAIN 21 >115 IG KAPPA CHAIN V-V REGION L7.
FT DOMAIN 21 43 FRAMEWORK 1.
FT DOMAIN 21 43 COMPLEMENTARITY-DETERMINING 1.
FT DOMAIN 44 54 FRAMEWORK 2.
FT DOMAIN 55 69 FRAMEWORK 2.
FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING 2.
FT DOMAIN 77 108 FRAMEWORK 3.
FT DOMAIN 109 >115 COMPLEMENTARITY-DETERMINING 3.
FT DISULFID 43 108 BY SIMILARITY.
FT NON_TER 115 115
SQ SEQUENCE 115 AA; 12615 MW; C17BEC758C577E00 CRC64;

Query Match 70.6%; Score 36; DB 1; Length 115;
Best Local Similarity 85.7%; Pred. No. 6.4;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSGSWP 7
III III
Db 109 QOQSNWSP 115

RESULT 3
GSPH_ECOLI
ID GSPH_ECOLI STANDARD; PRT; 169 AA.
AC P41443;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE PUTATIVE GENERAL SECRETION PATHWAY PROTEIN H PRECURSOR (PROTEIN
DE TRANSPORT PROTEIN HOFH).
DE HOFH OR HOFH.
GN HOFH OR HOFH.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE; 97426617.
RA Blattner F.R., Plunkett G., Blosch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]

SEQUENCE OF 1-30 FROM N.A.
RP STRAIN=K12;
RX MEDLINE; 95204361.
RA Stojiljkovic I., Schoenherr R., Kusters J.G.;
RT "Identification of the hopG gene, a component of Escherichia coli
RT K-12 type II export system, and its conservation among different
RT pathogenic Escherichia coli and Shigella isolates.";
RL J. Bacteriol. 177:1892-1895(1995).
CC -1- FUNCTION: INVOLVED IN A GENERAL SECRETION PATHWAY (GSP) FOR THE
CC EXPORT OF PROTEINS (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE PULH/OUTH/XPSH/EXEH/XCPU FAMILY.
CC
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CC
DR EMBL; U18997; AAA58126.1; -
DR EMBL; AF000409; AAC76354.1; -
DR EMBL; U20786; AAA69032.1; -
DR ECOGENE; EGI2887; HOPH.
DR PRINTS; PR00885; BCTERIALGSPH.
DR PROSITE; PS00409; PROKAR_NTER_METHYL; 1.
KW Transport; Methylation.
FT PROPEP 1 6 BY SIMILARITY.
FT CHAIN 7 169 PUTATIVE GENERAL SECRETION PATHWAY
FT PROTEIN H.
FT MOD_RES 7 7 METHYLATION (BY SIMILARITY).
SQ SEQUENCE 169 AA; 18565 MW; D42B1127FBB81A09 CRC64;

Query Match 70.6%; Score 36; DB 1; Length 169;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGSWPL 8
IIIIII
Db 154 SGSWPL 159

RESULT 4
C821_PEA
ID C821_PEA STANDARD; PRT; 543 AA.
AC Q43068;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE CYTOCHROME P450 82A1 (EC 1.14.-.-) (CYPLXXXII) (FRAGMENT).
GN CYP82A1 OR CYP82.
OS Pisum sativum (Garden pea).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
OC Pisum.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 96417083.
RA Frank M.R., Deyneka J.M., Schuler M.A.;
RT "Cloning of wound-induced cytochrome P450 monooxygenases expressed in
RT pea.";
RL Plant Physiol. 110:1035-1046(1996).
CC -1- INDUCTION: BY WOUND.
CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
CC
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DR EMBL; M32990; AAA45755.1; ALT_INIT.

DR PIR; D33746; SAVLWD.

DR PFAM; PF00695; VMSA; 1.

FT Antigen.

FT PROPEP 1 199

FT CHAIN 200 366 MAJOR SURFACE ANTIGEN.

FT CARBOHYD 170 170 POTENTIAL.

FT CARBOHYD 298 298 POTENTIAL.

FT SEQUENCE 366 AA; 40897 MW; 5B72879A182EFF38 CRC64;

Query Match 68.6%; Score 35; DB 1; Length 366;

Best Local Similarity 71.4%; Pred. No. 29;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOQGSWP 7

Db 96 QOQGAWP 102

RESULT 8

ID VMSA_HPBWD STANDARD; PRT; 366 AA.

AC P17195;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-MAY-1991 (Rel. 18, Last sequence update)

DT 01-MAY-1991 (Rel. 18, Last annotation update)

DE MAJOR SURFACE ANTIGEN PRECURSOR.

GN S.

OS Duck hepatitis B virus (white Shanghai duck isolate S31) (DHBV).

OC Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 90085807.

RA Uchida M., Esumi M., Shikata T.;

RT "Molecular cloning and sequence analysis of duck hepatitis B virus

genomes of a new variant isolated from Shanghai ducks.";

RL Virology 173:600-606(1989).

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DR EMBL; M32991; AAA45752.1; ALT_INIT.

DR PIR; D33746; SAVLWD.

DR PFAM; PF00695; VMSA; 1.

KW Antigen.

FT PROPEP 1 199

FT CHAIN 200 366 MAJOR SURFACE ANTIGEN.

FT CARBOHYD 170 170 POTENTIAL.

FT CARBOHYD 298 298 POTENTIAL.

FT SEQUENCE 366 AA; 40858 MW; CF60E78B7B2FCD52 CRC64;

Query Match 68.6%; Score 35; DB 1; Length 366;

Best Local Similarity 71.4%; Pred. No. 29;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOQGSWP 7

Db 96 QOQGAWP 102

RESULT 9

GUNL_BACSU

ID GUNL_BACSU STANDARD; PRT; 499 AA.

AC P07983;

DT 01-AUG-1988 (Rel. 08, Created)

DT 01-NOV-1991 (Rel. 20, Last sequence update)

DT 01-OCT-1994 (Rel. 30, Last annotation update)

DE ENDOGLUCANASE PRECURSOR (EC 3.2.1.4) (ENDO-1,4-BETA-GLUCANASE)

DE (CELLULOSE).

GN BGLC OR GLD.

OS Bacillus subtilis.

OC Bacteria; Firmicutes; Bacillus/Clostridium group;

OC Bacillus/Staphylococcus group; Bacillus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-DLG;

RX MEDLINE; 87194581.

RA Robson L.M., Chambliss G.H.;

RT "Endo-beta-1,4-glucanase gene of Bacillus subtilis DLG.";

RL J. Bacteriol. 169:2017-2025(1987).

CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-GLUCOSIDIC

CC LINKAGES IN CELLULOSE.

CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY A (FAMILY 5 OF GLYCOSYL

CC HYDROLASES).

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DR EMBL; M16185; AAA22496.1; ALT_INIT.

DR PIR; A26874; A26874.

DR HSSP; Q06851; INBC.

DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; 1.

DR PFAM; PF00150; cellulase; 1.

DR PFAM; PF00342; CBD_3; 1.

KW Cellulose degradation; Hydrolase; Glycosidase; Signal.

FT SIGNAL 1 29

FT CHAIN 30 499 ENDOGLUCANASE.

FT ACT_SITE 169 169 PROTON DONOR (BY SIMILARITY).

FT ACT_SITE 257 257 NUCLEOPHILE (BY SIMILARITY).

FT DOMAIN 350 499 CELLULOSE-BINDING (BY SIMILARITY).

FT SEQUENCE 499 AA; 55187 MW; 339D04EE95A63EE1 CRC64;

Query Match 68.6%; Score 35; DB 1; Length 499;

Best Local Similarity 62.5%; Pred. No. 39;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QOQGSWPLT 9

Db 309 KTGGSWPLT 316

RESULT 10

SVV_CHLTR

ID SVV_CHLTR STANDARD; PRT; 939 AA.

AC O84304;

DT 15-FEB-2000 (Rel. 39, Created)

DT 15-FEB-2000 (Rel. 39, Last sequence update)

DT 15-FEB-2000 (Rel. 39, Last annotation update)

DE VALYL-TRNA SYNTHETASE (EC 6.1.1.9) (VALINE--TRNA LIGASE) (VALRS).

GN VALS OR CT302

OS Chlamydia trachomatis.

OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-D/UW-3/CX;

RX MEDLINE; 99000809.

RA Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,

RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.;
RT "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis";
RL Science 282:754-759(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-VALINE + TRNA(VAL) -> AMP +
CC PYROPHOSPHATE + L-VALYL-TRNA(VAL).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL: AB001302; AAC67895.1; -.
DR PRINTS: PRO0986; TRNASYNTHVAL.
DR PROSITE: PS00178; AA_TRNA_LIGASE_I; 1.
DR PFAM: PF00133; trna-synt_1; 1.
KW Aminoacyl-tRNA synthetase; "HIGH" REGION.
FT SIMILAR 47 57 "KMSKS" REGION.
FT BINDING 563 567 ATP (BY SIMILARITY).
FT BINDING 566 566 ATP (BY SIMILARITY).
SQ SEQUENCE 939 AA; 107036 MW; CEB8449DC7BB9066 CRC64;

Query Match 68.6%; Score 35; DB 1; Length 939;
Best Local Similarity 85.7%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SGSWPLT 9
Db 459 SGLWPLT 465

RESULT 11
ID SVV_CHLNP STANDARD; PRT; 940 AA.
AC Q92987;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE VALYL-TRNA SYNTHETASE (EC 6.1.1.9) (VALINE--TRNA LIGASE) (VALRS).
GN VALS OR CPN0094.
OS Chlamydia pneumoniae (Chlamydia pneumoniae).
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia. [1]
RN SEQUENCE FROM N.A.
RP STRAIN=CWL029;
RX MEDLINE: 99206606.
RA Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL Nat. Genet. 21:385-389(1999).
CC -1- CATALYTIC ACTIVITY: ATP + L-VALINE + TRNA(VAL) -> AMP +
CC PYROPHOSPHATE + L-VALYL-TRNA(VAL).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL: AB001595; AAD18247.1; -.

DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 47 57 "HIGH" REGION.
FT BINDING 564 568 "KMSKS" REGION.
FT BINDING 567 567 ATP (BY SIMILARITY).
SQ SEQUENCE 940 AA; 107111 MW; 28054683FB9D0404 CRC64;

Query Match 68.6%; Score 35; DB 1; Length 940;
Best Local Similarity 85.7%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SGSWPLT 9
Db 460 SGLWPLT 466

RESULT 12
ID CATC_RHOOP STANDARD; PRT; 92 AA.
AC P95609;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE MUCONOLACTONE DELTA-ISOMERASE (EC 5.3.3.4) (MIASE).
GN CATC.
OS Rhodococcus opacus.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus. [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.
RP STRAIN=1CP;
RX MEDLINE: 97144521.
RA Eulberg D., Golovleva L.A., Schloemann M.;
RT "Characterization of catechol catabolic genes from Rhodococcus
RT erythropolis 1CP.";
RL J. Bacteriol. 179:370-381(1997).
CC -1- CATALYTIC ACTIVITY: 2,5-DIHYDRO-5-OXOFURAN-2-ACETATE ->
CC 3,4-DIHYDRO-5-OXOFURAN-2-ACETATE.
CC -1- PATHWAY: THIRD STEP IN THE CATABOLISM OF CATECHOL TO SUCCINATE-
CC AND ACETYL-COA IN THE BETA-KETOADIPATE PATHWAY.
CC -1- SUBUNIT: HOMODECAMER (BY SIMILARITY).
CC -----
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CC -----
DR EMBL: X99622; CAA67935.1; -.
KW Aromatic hydrocarbons catabolism; Isomerase.
FT INIT_MET 0
SQ SEQUENCE 92 AA; 10780 MW; 9CC5A17DED4B153 CRC64;

Query Match 66.7%; Score 34; DB 1; Length 92;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOSGSWP 7
Db 35 QRSWKWP 41

RESULT 13
ID CTCL_ACILW STANDARD; PRT; 96 AA.
AC O33947;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)


```

DE MUCONOLACTONE DELTA-ISOMERASE 1 (EC 5.3.3.4) (MIASE 1).
GN ACYCL.
OS Acinetobacter lwoffii.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonas group;
OC Moraxellaceae; Acinetobacter.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K24;
RX MEDLINE; 97405925.
RA Kim S.I., Lee S.-H., Choi J.-S., Chung Y.H., Kim S., Park Y.-M.,
RA Park Y.K., Lee Y.N., Ha K.-S.;
RT Cloning and characterization of two catA genes in Acinetobacter
RT lwoffii K24.;
RN J. Bacteriol. 179:5226-5231(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K24;
RX MEDLINE; 98139907.
RA Kim S.I., Lee S.-H., Choi J.-S., Ha K.-S.;
RT "Organization and transcriptional characterization of the catI gene
RT cluster in Acinetobacter lwoffii K24.";
RL Biochem. Biophys. Res. Commun. 243:289-294(1998).
CC -1- CATALYTIC ACTIVITY: 2,5-DIHYDRO-5-OXOFURAN-2-ACETATE -
CC 3,4-DIHYDRO-5-OXOFURAN-2-ACETATE.
CC -1- PATHWAY: THIRD STEP IN THE CATABOLISM OF CATECHOL TO SUCCINATE-
CC AND ACETYL-COA IN THE BETA-KETOADIPATE PATHWAY.
CC -1- SUBUNIT: HOMODECAMER (BY SIMILARITY).
CC -----
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CC -----
DR EMBL; U77658; AAC46227.1; -.
KW Aromatic hydrocarbons catabolism; Isomerase.
SQ SEQUENCE 96 AA; 11048 MW; 6955AC14A5DDDEFA CRC64;

Query Match 66.7%; Score 34; DB 1; Length 96;
Best Local Similarity 71.4%; Pred. No. 12;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QSGSWP 7
Db 35 QKSGKW 41

RESULT 14
YFDK_ECOLI
ID YFDK_ECOLI STANDARD; PRT; 146 AA.
AC P77656;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HYPOTHETICAL 16.4 KD PROTEIN IN INTC-DSDC INTERGENIC REGION.
GN YFDK.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE; 97426617.
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]

SEQUENCE FROM N.A.
RA Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T.,
RA Ikemoto K., Inada T., Isono K., Isono S., Itoh T., Kanai K., Kasai H.,
RA Kasimoto K., Kim S., Kimura S., Kitagawa M., Kitakawa M., Makino K.,
RA Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y.,
RA Nashimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,
RA Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: STRONG, TO E.COLI YMFS.
CC -----
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CC -----
DR EMBL; AB000324; AAC75413.1; -.
DR EMBL; D90866; CAB22145.1; -.
DR EMBL; D90865; CAB22143.1; -.
DR EMBL; EGI4135; YFDK.
KW Hypothetical protein.
SQ SEQUENCE 146 AA; 16408 MW; 28F3CA711C5E9C79 CRC64;

Query Match 66.7%; Score 34; DB 1; Length 146;
Best Local Similarity 83.3%; Pred. No. 18;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QSGSWP 7
Db 23 QAGSWP 28

RESULT 15
IE63_HSVB
ID IE63_HSVB STANDARD; PRT; 470 AA.
AC P28939;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-APR-1993 (Rel. 25, Last annotation update)
DE TRANSCRIPTIONAL REGULATOR IE63 HOMOLOG.
GN 5.
OS Equine herpesvirus type 1 (strain Ab4p) (EHV-1).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicellovirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92295566.
RA Telford E.A.R., Watson M.S., McBride K., Davison A.J.;
RT "The DNA sequence of equine herpesvirus-1.";
RL Virology 189:304-316(1992).
CC -1- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL54,
CC HSV-2 UL54, EHV-1 5, VZV 4, EBV BMLF1, HCMV UL69, AND HVS-1 57.
CC -----
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CC -----
DR EMBL; M86664; AAB02440.1; -.
DR PIR; F36795; WZBEA4.
KW Transcription regulation.
SQ SEQUENCE 470 AA; 51320 MW; 99AC5258EFB74B0E CRC64;

Query Match 66.7%; Score 34; DB 1; Length 470;
Best Local Similarity 71.4%; Pred. No. 56;

```

Matches	5;	Conservative	1;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	1	QSGSWP	7						
			:						
Db	127	QSGSWP	133						

Search completed: May 27, 2000, 20:07:22
Job time: 994 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:38:45 ; Search time 199.56 Seconds
(without alignments)
3.127 Million cell updates/sec

Title: US-09-016-061-90
Perfect score: 51
Sequence: 1 QSGSWPLT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SPTREMBL_12:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_prodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	41	80.4	153	13	Q9YH52	Q9YH52 gallus gall
2	39	76.5	553	5	O01825	O01825 caenorhabdi
3	38	74.5	459	4	Q9Y638	Q9Y638 homo sapien
4	37	72.5	154	12	Q84631	Q84631 paramecium
5	37	72.5	642	1	O28537	O28537 archaeglob
6	36	70.6	204	5	O16703	O16703 caenorhabdi
7	36	70.6	275	2	Q50711	Q50711 mycobacteri
8	35	68.6	327	12	O67852	O67852 duck hepati
9	35	68.6	330	12	O72885	O72885 duck hepati
10	35	68.6	330	12	O66405	O66405 duck hepati
11	35	68.6	366	12	O66404	O66404 duck hepati
12	35	68.6	415	2	Q92HJ1	Q92HJ1 serpulina i
13	35	68.6	416	2	Q92HJ3	Q92HJ3 brachyspira
14	35	68.6	418	2	Q92HJ6	Q92HJ6 brachyspira
15	35	68.6	420	2	Q92HJ7	Q92HJ7 serpulina s
16	35	68.6	421	2	Q92HJ8	Q92HJ8 serpulina a
17	35	68.6	423	2	Q92HJ0	Q92HJ0 serpulina i
18	35	68.6	423	2	Q92HJ2	Q92HJ2 brachyspira
19	35	68.6	424	2	Q92HJ9	Q92HJ9 serpulina m
20	35	68.6	452	2	Q59917	Q59917 treponema h

21	35	68.6	499	2	Q45532	Q45532 bacillus su
22	35	68.6	501	2	O83012	O83012 bacillus sp
23	35	68.6	1367	11	O35206	O35206 mus musculu
24	34	66.7	94	2	Q9XCE0	Q9XCE0 mycobacteri
25	34	66.7	96	2	O929Y5	O929Y5 frateuria s
26	34	66.7	345	1	O26847	O26847 methanobact
27	34	66.7	692	2	O67902	O67902 aquifex aeo
28	34	66.7	701	13	Q03853	Q03853 gallus gall
29	34	66.7	763	11	Q92299	Q92299 mus musculu
30	34	66.7	789	10	O42451	O42451 triticum ae
31	34	66.7	1456	12	O85198	O85198 potato viru
32	34	66.7	1456	12	O85245	O85245 potato viru
33	33	64.7	107	12	O91281	O91281 chimpanzee
34	33	64.7	107	12	O91282	O91282 chimpanzee
35	33	64.7	107	12	O91283	O91283 chimpanzee
36	33	64.7	107	12	O9Y670	O9Y670 chimpanzee
37	33	64.7	107	12	O9Y669	O9Y669 chimpanzee
38	33	64.7	107	12	O9YIM5	O9YIM5 chimpanzee
39	33	64.7	131	12	O91105	O91105 human immun
40	33	64.7	145	2	O53312	O53312 mycobacteri
41	33	64.7	174	4	O9Y3T7	O9Y3T7 homo sapien
42	33	64.7	195	12	O9YUH5	O9YUH5 rhesus cyto
43	33	64.7	226	8	O47950	O47950 neurospora
44	33	64.7	268	5	O62353	O62353 caenorhabdi
45	33	64.7	292	10	O22561	O22561 arabidopsis

ALIGNMENTS

RESULT 1

Q9YH52
ID Q9YH52 PRELIMINARY; PRT; 153 AA.
AC Q9YH52;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE HYPOTHETICAL 17.4 KD PROTEIN.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-H B19.
RX MEDLINE; 90077532.
RA KAUFMAN J., SALOMONSEN J., SKJODT K.;
RT "B-G cDNA clones have multiple small repeats and hybridize to both
RT chicken MHC regions.";
RL Immunogenetics 30:440-451(1989).
DR EMBL; M27666; AAA69840.1; -.
KW Hypothetical protein.
SQ SEQUENCE 153 AA; 17404 MW; E037D120 CRC32;

Query Match 80.4%; Score 41; DB 13; Length 153;
Best Local Similarity 87.5%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSGSWPLT 9

Db 65 QSGHWPLT 72

RESULT 2

O01825
ID O01825 PRELIMINARY; PRT; 553 AA.
AC O01825;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE SIMILAR TO BETA-CHIMAERIN.
GN F57C9.8.
OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabdittia; Rhabdittia; Rhabdittia;
 OC Rhabdittia; Rhabdittidae; Rhabdittidae; Pelodermidae; Caenorhabdittis.
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE: 94150718;
 RA WILSON R., AINSWORTH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIEKEN A., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIRRY-MTEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.,
 RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA GEISEL C., KRAMER J., GIBSON A.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA WATERSTON R.;
 RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF003142; AAB54191.1; -;
 DR HSSP: P27986; 1PBW.
 DR PFAM: PF00620; RBOGAP: 1.
 SQ SEQUENCE 553 AA; 60849 MW; 5AA150B3 CRC32;

Query Match 76.5%; Score 39; DB 5; Length 553;
 Best Local Similarity 66.7%; Pred. No. 19;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSGSWPLT 9
 I:|||||:
 Db 373 QSGSWPFS 381

RESULT 3
 QY638 PRELIMINARY; PRT; 459 AA.
 AC QY638;
 DT 01-NOV-1999 (TREMREL. 12, Created)
 DT 01-NOV-1999 (TREMREL. 12, Last sequence update)
 DT 01-NOV-1999 (TREMREL. 12, Last annotation update)
 DE P2X2A RECEPTOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RA MCMAHON R.A., EGAN T.M., HURLEY P.T., NELSON A., ROGERS M., MARTIN F.;
 RT "Cloning of the human P2X2 receptor cDNA and multiple splice
 RT variants.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBUNIT: HOMO- OR HETEROOLYMERS (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE P2X RECEPTOR FAMILY.
 DR EMBL: AF109387; AAD42947.1; -;
 DR PROSITE: PS01212; P2X-RECEPTOR; 1.
 KW Receptor; Ionic channel; Transmembrane; Ion transport.
 SQ SEQUENCE 459 AA; 50655 MW; 2F0B3CAD CRC32;

Query Match 74.5%; Score 38; DB 4; Length 459;
 Best Local Similarity 85.7%; Pred. No. 24;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 SSGSWPLT 9
 I:|||||:
 Db 376 SSGSWPVT 382

RESULT 4
 QY638 PRELIMINARY; PRT; 154 AA.
 AC QY638;
 DT 01-NOV-1996 (TREMREL. 01, Created)
 DT 01-NOV-1996 (TREMREL. 01, Last sequence update)
 DT 01-NOV-1998 (TREMREL. 08, Last annotation update)
 DE GENOME, PARTIAL SEQUENCE.
 GN A317L.
 OS Paramyxium bursaria chlorella virus 1 (PBCV-1).
 OC Viruses; dsDNA viruses, no RNA stage; Phycodnaviridae; Phycodnavirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 95133167.
 RA LU Z., LI Y., ZHANG Y., KUTISH G.F., ROCK D.L., VAN ETTEN J.L.;
 RT "Analysis of 45 kb of DNA located at the left end of the chlorella
 RT virus PBCV-1 genome.";
 RL Virology 206:339-352(1995).
 DR EMBL: U42580; AAC96685.1; -;
 SQ SEQUENCE 154 AA; 18564 MW; 8E31B6C7 CRC32;

Query Match 72.5%; Score 37; DB 12; Length 154;
 Best Local Similarity 75.0%; Pred. No. 13;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QSGSWPL 8
 I:|||||:
 Db 33 QSGSWPV 40

RESULT 5
 QY637 PRELIMINARY; PRT; 642 AA.
 AC QY637;
 DT 01-JAN-1998 (TREMREL. 05, Created)
 DT 01-JAN-1998 (TREMREL. 05, Last sequence update)
 DT 01-AUG-1998 (TREMREL. 07, Last annotation update)
 DE CONSERVED HYPOTHETICAL PROTEIN.
 GN AF1737.
 OS Archaeoglobus fulgidus.
 OC Archaea; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
 OC Archaeoglobus.
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;
 RX MEDLINE: 98049343.
 RA KLENK H.-P., CLAYTON R.A., TOMB J.-F., WHITE O., NELSON K.E.,
 RA KETCHUM K.A., DODSON R.J., GWINN M., HICKEY E.K., PETERSON J.D.,
 RA RICHARDSON D.L., KERLAVAGE A.R., GRAHAM D.E., KYRPIDES N.C.,
 RA FLEISSCHMANN R.D., QUACKENBUSH J., LEE N.H., SUTTON G.G., GILL S.,
 RA KIRKNESS E.F., DOUGHERTY B.A., MCKENNEY K., ADAMS M.D., LOFTUS B.,
 RA PETERSON S., REICH C.I., MCNEIL L.K., BADGER J.H., GLODEK A., ZHOU L.,
 RA OVERBECK R., GOCAYNE J.D., WEIDMAN J.F., MCDONALD L., UTTERBACK T.,
 RA COTTON M.D., SPRIGGS T., ARTIACH P., KATNE B.P., SYKES S.M.,
 RA SADOW P.W., D'ANDREA K.P., BOWMAN C., FUJII C., GARLAND S.A.,
 RA MASON T.M., OLSEN G.J., FRASER C.M., SMITH H.O., WOESE C.R.,
 RA VENTER J.C.;
 RT "The complete genome sequence of the hyperthermophilic, sulphate-
 RT reducing archaeon Archaeoglobus fulgidus.";
 RL Nature 390:364-370(1997).
 DR EMBL: AF000983; AAB89512.1; -;
 DR TIGR: AF1737; -;
 KW Hypothetical protein.
 SQ SEQUENCE 642 AA; 74057 MW; CD15A363 CRC32;

Query Match 72.5%; Score 37; DB 1; Length 642;
 Best Local Similarity 85.7%; Pred. No. 50;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 QSGSWPLT 9
 || |||||
 DB 101 SGGWPLT 107

RESULT 6
 ID O16703 PRELIMINARY; PRT; 204 AA.
 AC O16703;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE D2062.1 PROTEIN.
 GN D2062.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
 OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE; 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT *2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans*;
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA GRAVES T., WOHLDMANN P., CLARKE K.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA WATERSTON R.;
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF016681; AAB66166.1; -.
 SQ SEQUENCE 204 AA; 22758 MW; B8A27C17 CRC32;

Query Match 70.6%; Score 36; DB 5; Length 204;
 Best Local Similarity 85.7%; Pred. No. 25;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSGSWPL 8
 ||| ||||
 DB 107 QSGCWPL 113

RESULT 7
 ID Q50711 PRELIMINARY; PRT; 275 AA.
 AC Q50711;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-FEB-1997 (TREMBlrel. 02, Last annotation update)
 DE HYPOTHETICAL 28.7 KD PROTEIN CY78.14.
 GN MTCY78.14.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RA OLIVER K., HARRIS D., BARRELL B.G., RAJANDREAM M.A., WALSH S.V.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: STRONG, TO M.LEPRAE B229_C1_175 AND B1620_C3_232.
 DR EMBL; Z77165; CAB01008.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 275 AA; 28659 MW; 7150A3B6 CRC32;

Query Match 70.6%; Score 36; DB 2; Length 275;
 Best Local Similarity 85.7%; Pred. No. 33;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 QSGSWPL 8
 || |||||
 DB 22 QPGSWPL 28

RESULT 8
 ID Q67852 PRELIMINARY; PRT; 327 AA.
 AC Q67852;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE SURFACE PROTEIN.
 GN PRES.
 OS Duck hepatitis B virus (DHBV).
 OC Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SHI H., CULLEN J.M., NEWBOLD J.E.;
 RL Submitted (DEC-1992) to the EMBL/GenBank/DBJ databases.
 DR EMBL; M95589; AAA45749.1; -.
 DR PFAM; PF00695; vNSA; 1.
 SQ SEQUENCE 327 AA; 36356 MW; 9C461203 CRC32;

Query Match 68.6%; Score 35; DB 12; Length 327;
 Best Local Similarity 71.4%; Pred. No. 59;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWP 7
 || | |||
 DB 60 QQQGAWP 66

RESULT 9
 ID O72885 PRELIMINARY; PRT; 330 AA.
 AC O72885;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE SURFACE PROTEIN.
 OS Duck hepatitis B virus (DHBV).
 OC Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AUSTRALIAN DHBV;
 RA TRIVATNI M., QIAO M., EV P., BURRELL C., JILBERT A.R.;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ006350; CAA06988.1; -.
 DR PFAM; PF00695; vNSA; 1.
 SQ SEQUENCE 330 AA; 36789 MW; 95C123D4 CRC32;

Query Match 68.6%; Score 35; DB 12; Length 330;
 Best Local Similarity 71.4%; Pred. No. 59;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSWP 7
 || |:
 Db 60 QOQAWP 66

RESULT 10
 Q66405 PRELIMINARY; PRT; 330 AA.

AC Q66405;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
 DE PRE-S PROTEIN.

OS Duck hepatitis B virus (DHBV).

OC Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=DHBVQCA34;

RA SCHNEIDER R.;

RL Submitted (JUN-1991) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=DHBVQCA34;

RA TONG S., MATTES F., BLUM H.E., FERNHOLZ D., SCHNEIDER R., WILL H.;

RL Nucleic Acids Res. 0:0-0(0).

DR EMBL; X60213; CAA42771.1; -

DR PFAM; PF00695; VMSA; 1.

SQ SEQUENCE 330 AA; 36959 MW; AC388D8F CRC32;

Query Match 68.6%; Score 35; DB 12; Length 330;

Best Local Similarity 71.4%; Pred. No. 59;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSWP 7
 || |:
 Db 60 QOQAWP 66

RESULT 11
 Q66404 PRELIMINARY; PRT; 366 AA.

AC Q66404;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)

DE PRE-S/S.

OS Duck hepatitis B virus (DHBV).

OC Viruses; Retroid viruses; Hepadnaviridae; Avihepadnavirus.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=DHBVQCA34;

RA SCHNEIDER R.;

RL Submitted (JUN-1991) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=DHBVQCA34;

RA TONG S., MATTES F., BLUM H.E., FERNHOLZ D., SCHNEIDER R., WILL H.;

RL Nucleic Acids Res. 0:0-0(0).

DR EMBL; X60213; CAA42770.1; -

DR PFAM; PF00695; VMSA; 1.

SQ SEQUENCE 366 AA; 41057 MW; 3EE7C0D6 CRC32;

Query Match

Best Local Similarity 68.6%; Score 35; DB 12; Length 366;

Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QOQSWP 7
 || |:
 Db 96 QOQAWP 102

RESULT 12
 Q92HJ1 PRELIMINARY; PRT; 415 AA.

AC Q92HJ1;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)

DE NADH OXIDASE (FRAGMENT).

OS Serpulina intermedia.

OC Bacteria; Spirochaetales; Spirochaetaceae; Serpulina.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=2818.5;

RA ATYEO R.F., JENSEN N.S., STANTON T.B., HAMPSON D.J.;

RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF060810; AAC78819.1; -

DR HSSP; P37062; IJOA.

FT NON_TER 1

FT NON_TER 1

SQ SEQUENCE 415 AA; 45825 MW; 5119500D CRC32;

Query Match 68.6%; Score 35; DB 2; Length 415;

Best Local Similarity 71.4%; Pred. No. 74;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGSWPLT 9

Db 101 TGSWPVT 107

RESULT 13
 Q92HJ3 PRELIMINARY; PRT; 416 AA.

AC Q92HJ3;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)

DE NADH OXIDASE (FRAGMENT).

OS Brachyspira innocens.

OC Bacteria; Spirochaetales; Spirochaetaceae; Brachyspira.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=4/71;

RA ATYEO R.F., JENSEN N.S., STANTON T.B., HAMPSON D.J.;

RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF060805; AAC78814.1; -

DR HSSP; P37062; IJOA.

FT NON_TER 1

FT NON_TER 1

SQ SEQUENCE 416 AA; 46107 MW; F47307A8 CRC32;

Query Match 68.6%; Score 35; DB 2; Length 416;

Best Local Similarity 71.4%; Pred. No. 74;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGSWPLT 9

Db 102 TGSWPVT 108

RESULT 14
 Q92H16 PRELIMINARY; PRT; 418 AA.

AC Q92H16;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)

DE NADH OXIDASE (FRAGMENT).

OS Brachyspira aalborgi.

OC Bacteria; Spirochaetales; Spirochaetaceae; Brachyspira.

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC43994;
 RA ATYEO R.F., JENSEN N.S., STANTON T.B., HAMPSON D.J.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF060816; AAC78825.1; -
 DR HSP; P37062; IJOA.
 FT NON_TER 1
 FT NON_TER 418
 SQ SEQUENCE 418 AA; 46305 MW; B29F20BF CRC32;

Query Match 68.6%; Score 35; DB 2; Length 418;
 Best Local Similarity 71.4%; Pred. No. 74;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGSWPLT 9
 Db 103 TGSWPVT 109

RESULT 15
 Q92HI7
 ID Q92HI7 PRELIMINARY; PRT; 420 AA.
 AC Q92HI7;
 DT 01-MAY-1999 (TReMBLrel. 10, Created)
 DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
 DT 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
 DE NADH OXIDASE (FRAGMENT).
 OS Serpulina sp. P280/1.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Serpulina.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-P280/1;
 RA ATYEO R.F., JENSEN N.S., STANTON T.B., HAMPSON D.J.;
 RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF060815; AAC78824.1; -
 DR HSP; P37062; IJOA.
 FT NON_TER 1
 FT NON_TER 420
 SQ SEQUENCE 420 AA; 46594 MW; BCE88D66 CRC32;

Query Match 68.6%; Score 35; DB 2; Length 420;
 Best Local Similarity 71.4%; Pred. No. 75;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 SGSWPLT 9
 Db 98 TGSWPVT 104

Search completed: May 27, 2000, 19:38:46
 Job time: 2379 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:21:39 ; Search time 148.45 Seconds
(without alignments)
1.436 Million cell updates/sec

Title: US-09-016-061-90
Perfect score: 51
Sequence: 1 QQSGSWPLT 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	9	W76035	LM609 grafted anti
2	45	88.2	9	R37604	hIL2R Ab L chain V
3	45	88.2	9	W76036	LM609 grafted anti
4	45	88.2	107	R37612	hIL2R Ab L chain V
5	45	88.2	107	R37610	B-B10 MAb L chain
6	44	86.3	9	W76013	LM609 grafted anti
7	44	86.3	107	W76006	LM609 grafted anti
8	44	86.3	107	W76002	Vitaxin antibody 1
9	44	86.3	107	W76004	LM609 antibody lig
10	41	80.4	105	W87456	Jk gene product. N
11	41	80.4	105	W87458	Humanised anti-alp
12	41	80.4	107	W84098	Humanised anti-alp
13	41	80.4	108	W84094	Murine vitronectin
14	41	80.4	112	W84100	Vitronectin alpha-
15	40	78.4	107	R38601	HYH light chain. A
16	40	78.4	107	W58482	Murine HYH antibody
17	40	78.4	108	R15438	Light chain variab
18	40	78.4	109	R52033	Light chain variab
19	40	78.4	143	R19580	Mouse anti-idiotyp
20	40	78.4	240	R15443	Single chain Fv fr
21	39	76.5	9	W44180	Monoclonal antibody
22	39	76.5	106	W71241	Light chain variab
23	39	76.5	107	R50190	Light chain variab
24	39	76.5	107	W28531	Humanised cA2 ligh
25	39	76.5	107	W40820	Light chain variab
26	39	76.5	127	R50187	Light chain variab
27	39	76.5	127	R50191	Light chain variab
28	39	76.5	127	R50192	Light chain variab
29	39	76.5	127	W44176	Monoclonal antibod
30	39	76.5	240	W71243	scFv comprising he
31	38	74.5	9	W76033	LM609 grafted anti
32	38	74.5	107	R25729	Humanised VL regio
33	38	74.5	127	R54093	Sequence of mouse
34	37	72.5	10	W89161	Anti-p53 monoclonal

ALIGNMENTS

RESULT 1

W76035
ID W76035 standard; Protein; 9 AA.
AC W76035;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-L region CDR3 protein fragment #4.
KW Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-L region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IASY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB: V49872.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62: Page 44; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation, cancer,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 9 AA;

Query Match 100.0%; Score 51; DB 1; Length 9;

Best Local Similarity 100.0%; Pred. No. 1.5e+05;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9

Db 1 QQSGSWPLT 9

RESULT 2

R37604

ID R37604 standard; peptide; 9 AA.

AC R37604;

DT 13-OCT-1993 (first entry)

DE hIL2R Ab L chain V region CDR3.

KW Complementarity-determining region; CDR; humanised; antibody; hIL2R;

KW human; interleukin; IL-2; receptor; murine; anti-human; Ab; T-cell;
 KW monoclonal antibody; B-B10; mixed lymphocyte reaction; variable; V;
 KW region; PCR; framework; plasmid.
 OS Mus musculus.
 PN W09311238-A.
 PD 10-JUN-1993.
 PF 03-DEC-1992; J01583.
 PR 06-DEC-1991; JP-323319.
 PA (BIOT) BIOTEST PHARMA GMBH.
 PA (INNO-) INNOTHERAPIE LAB.
 PA (SUMU) SUMITOMO PHARM CO LTD.
 PI Gomi H, Nakatani T, Noguchi H, Wijdenes J;
 DR WPI; 93-197057/24.
 PT Humanised antibody comprising - CDR region of mouse MAB B-B10
 PT specific for IL-2 receptor useful for treating carcinoma
 PT expressing IL-2 receptor
 PS Claim 1; Page 43; 62pp; English.
 CC The sequences given in R37599-604 represent the complementarity-
 CC determining regions (CDRs) of a humanised antibody (Ab) which binds
 CC specifically to human interleukin (IL)-2 receptor (hIL2R). These
 CC CDRs were derived from the murine anti-human IL-2 receptor monoclonal
 CC Ab (Mab) B-B10 (see also Q43242-43). This Mab is antagonistic to the
 CC binding of IL-2 to the IL-2 receptor on human T-cells. It also
 CC inhibits the human mixed lymphocyte reaction. The cDNA encoding the
 CC variable (V) region of the B-B10 Ab was cloned by PCR and sequenced
 CC (see also Q43226-32 and Q43233-36). A human Ab with high levels of
 CC amino acid sequence homology to the murine sequence was selected and
 CC the framework of this Ab was bound with the B-B10 V region CDR and a
 CC part of the framework to design several kinds of the humanised B-B10 V
 CC region (see also Q43244-45). The DNA sequence coding this humanised
 CC B-B10 was synthesised and a plasmid expressing humanised B-B10 was
 CC constructed.
 SQ Sequence 9 AA;

Query Match 88.2%; Score 45; DB 1; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.5e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
 ||| |||||
 Db 1 QQSSSWPLT 9

RESULT 3

ID W76036 standard; Protein; 9 AA.
 AC W76036;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-L region CDR3 protein fragment #5.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-L region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49873.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 44; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to

CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 9 AA;

Query Match 88.2%; Score 45; DB 1; Length 9;
 Best Local Similarity 88.9%; Pred. No. 1.5e+05;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
 ||||| |||
 Db 1 QQSGSWPQT 9

RESULT 4

ID R37612 standard; Protein; 107 AA.
 AC R37612;
 DT 13-OCT-1993 (first entry)
 DE hIL2R Ab L chain V region.
 KW Complementarity-determining region; CDR; humanised; antibody; hIL2R;
 KW human; interleukin; IL-2; receptor; murine; anti-human; Ab; T-cell;
 KW monoclonal antibody; B-B10; mixed lymphocyte reaction; variable; V;
 KW region; PCR; framework; plasmid; heavy; H; light; L.
 OS Mus musculus/Homo sapiens.
 PN W09311238-A.
 PD 10-JUN-1993.
 PF 03-DEC-1992; J01583.
 PR 06-DEC-1991; JP-323319.
 PA (BIOT) BIOTEST PHARMA GMBH.
 PA (INNO-) INNOTHERAPIE LAB.
 PA (SUMU) SUMITOMO PHARM CO LTD.
 PI Gomi H, Nakatani T, Noguchi H, Wijdenes J;
 DR WPI; 93-197057/24.
 DR N-PSDB; Q43245.
 PT Humanised antibody comprising - CDR region of mouse MAB B-B10
 PT specific for IL-2 receptor useful for treating carcinoma
 PT expressing IL-2 receptor
 PS Claim 2; Fig 5; 62pp; English.
 CC The sequences given in R37611-12 represent the heavy (H) and light (L)
 CC chain variable (V) regions of a humanised antibody (Ab) which binds
 CC specifically to human interleukin (IL)-2 receptor (hIL2R). The
 CC complementarity-determining regions (CDRs) of these V regions were
 CC derived from the murine anti-human IL-2 receptor monoclonal Ab (Mab)
 CC B-B10 (see also R37599-04). This Mab is antagonistic to the binding
 CC of IL-2 to the IL-2 receptor on human T-cells. It also inhibits
 CC the human mixed lymphocyte reaction. The cDNA encoding the variable
 CC (V) region of the B-B10 Ab was cloned by PCR and sequenced (see also
 CC Q43226-32 and Q43233-36). A human Ab with high levels of amino acid
 CC sequence homology to the murine sequence was selected and the
 CC framework of this Ab was bound with the B-B10 V region CDR and a
 CC part of the framework to design several kinds of the humanised B-B10
 CC V region. The DNA sequence coding this humanised B-B10 was
 CC synthesised and a plasmid expressing humanised B-B10 was constructed.
 SQ Sequence 107 AA;

Query Match 88.2%; Score 45; DB 1; Length 107;
 Best Local Similarity 88.9%; Pred. No. 0.33;
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QQSGSWPLT 9
 ||| |||||
 Db 89 QQSSSWPLT 97

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RESULT 5
R37610
ID R37610 standard; Protein; 107 AA.
AC R37610;
DT 13-OCT-1993 (first entry)
DE B-B10 MAb L chain V region.
KW Complementarity-determining region; CDR; humanised; antibody; hIL2R;
KW human; interleukin; IL-2; receptor; murine; anti-human; Ab; T-cell;
KW monoclonal antibody; B-B10; mixed lymphocyte reaction; variable; V;
KW region; PCR; framework; plasmid; heavy; H; light; L.
OS Mus musculus.
PN W09311238-A.
PD 10-JUN-1993.
PF 03-DEC-1992; J01583.
PR 06-DEC-1991; JP-323319.
PA (BIOT ) BIOTEST PHARMA GMBH.
PA (INNO-) INNOTHERAPIE LAB.
PA (SUMU) SUMITOMO PHARM CO LTD.
PI Gomi H, Nakatani T, Noguchi H, Wijdenes J;
DR WPI; 93-197057/24.
DR N-PSDB; Q43243.
PT Humanised antibody comprising - CDR region of mouse MAB B-B10
PT specific for IL-2 receptor useful for treating carcinoma
PT expressing IL-2 receptor
PS Disclosure; Fig 2; 62pp; English.
CC The sequences given in R37609-10 represent the heavy (H) and light (L)
CC chain variable (V) regions of the murine anti-human IL-2 receptor
CC monoclonal antibody (MAB) B-B10, respectively. This MAB was used in
CC the construction of a humanised antibody (Ab) which binds specifically
CC to human interleukin (IL)-2 receptor (hIL2R). The complementarity-
CC determining regions (CDRs) for the hIL2R MAB were derived from B-B10
CC (see also R37599-04). The hIL2R MAB is antagonistic to the binding
CC of IL-2 to the IL-2 receptor on human T-cells. It also inhibits
CC the human mixed lymphocyte reaction. The cDNA encoding the variable
CC (V) region of the B-B10 Ab was cloned by PCR and sequenced (see also
CC Q43226-32 and Q43233-36). A human Ab with high levels of amino acid
CC sequence homology to the murine sequence was selected and the
CC framework of this Ab was bound with the B-B10 V region CDR and a
CC part of the framework to design several kinds of the humanised B-B10
CC V region. The DNA sequence coding this humanised B-B10 was
CC synthesised and a plasmid expressing humanised B-B10 was constructed.
SQ Sequence 107 AA;

Query Match 88.2%; Score 45; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 0.33;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
Db 89 QQSSSWPLT 97

RESULT 6
W76013
ID W76013 standard; Protein; 9 AA.
AC W76013;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-L region CDR3 protein fragment #1.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-L region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PR 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49843.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 19; Fig 7; 129pp; English.
CC This sequence represents a LM609 grafted antibody variable light chain
CC region. LM609 and the antibody vitaxin bind selectively to integrin
CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand
CC and thus block integrin-mediated signal transduction. This is useful in
CC the treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
SQ Sequence 107 AA;

Query Match 86.3%; Score 44; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 1.5e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
Db 1 QQSGSWPHT 9

RESULT 7
W76006
ID W76006 standard; Protein; 107 AA.
AC W76006;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody light chain variable region protein fragment.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PR 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49843.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 19; Fig 7; 129pp; English.
CC This sequence represents a LM609 grafted antibody variable light chain
CC region. LM609 and the antibody vitaxin bind selectively to integrin
CC alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand
CC and thus block integrin-mediated signal transduction. This is useful in
CC the treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
SQ Sequence 107 AA;

Query Match 86.3%; Score 44; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. No. 1.5e+05;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QQSGSWPLT 9
Db 1 QQSGSWPHT 9

N-PSDB; V49850.
DR Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
DR integrin - and related grafted antibodies based on murine monoclonal
DR LM609, also related nucleic acid, used to treat, prevent or diagnose
DR angiogenesis or restenosis
PS Disclosure; Page 40; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 9 AA;

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Best Local Similarity 88.9%; Pred. NO. 0.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOQSGSWPLT 9
Db 89 QOQSGSWPHT 97

RESULT 8
W76002
ID W76002 standard; Protein; 107 AA.
AC W76002;
DE Vitaxin antibody light chain variable region protein fragment.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB; V49821.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 1; Fig 1b; 129pp; English.
CC This sequence represents the vitaxin antibody variable light chain region.
CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
CC block integrin-mediated signal transduction. This is useful in the
CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
CC etc.). The antibodies contain non-murine framework regions so are
CC suitable for use in humans. Enhanced types of LM609 have affinity more
CC than 90 times greater than that of parent the parent antibody.
SQ Sequence 107 AA;

Query Match 86.3%; Score 44; DB 1; Length 107;
Best Local Similarity 88.9%; Pred. NO. 0.5;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QOQSGSWPLT 9
Db 89 QOQSGSWPHT 97

RESULT 10
W87456
ID W87456 standard; Protein; 105 AA.
AC W87456;
DE 15-MAR-1999 (first entry)
DE Jk gene product.
KW Humanised antibody; monoclonal antibody; MAB; antibody engineering;
KW mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
KW cancer; metastasis; rheumatoid arthritis; atherosclerosis;
KW angiogenesis; diabetic retinopathy; inflammation;
KW macular degeneration; osteoporosis; Paget's disease;
KW hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
KW D12H2RET; Jk protein.
OS Mus sp.
PN WO9840488-A1.
PD 17-SEP-1998.
PF 12-MAR-1998; U04987.
PR 12-MAR-1997; US-039609.
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PI Johanson KO, Jonak ZL, Taylor AH;
DR WPI: 99-034590/03.
DR N-PSDB; V71803.
PT New anti alpha.v beta.3 vitronectin receptor antibodies - used for
PT immunotherapeutic treatment of e.g. diabetic retinopathy,
PT inflammatory disorders, atherosclerosis, restenosis, cancers or
PT osteoporosis
PS Example 14; Page 66; 97pp; English.
CC This polypeptide is encoded by a Jk synthetic gene segment (see
CC V71803). It was utilising in novel D12H2REI humanised light chain
CC variable region (see W87456), which comprises a human REI framework
CC and complementarily determining regions from the anti-human alpha-v
CC beta-3 vitronectin receptor monoclonal antibody D12. Humanised D12
CC antibodies can be used for passive immunotherapy of disorders
CC mediated by the alpha-v beta-3 vitronectin receptor, e.g. restenosis
CC and angiogenic associated diseases.
SQ Sequence 105 AA;

Query Match 80.4%; Score 41; DB 1; Length 105;
Best Local Similarity 77.8%; Pred. NO. 1.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QOQSGSWPLT 9
Db 89 QOQSGSWPHT 97

RESULT 9
W76004
ID W76004 standard; Protein; 107 AA.
AC W76004;
DE LM609 antibody light chain variable region protein fragment.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.

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QY      1 QQSGSWPLT 9
      ||| ||| |
Db      89 QQSNSWPFT 97

RESULT 11
W87458
ID      W87458 standard; Protein; 105 AA.
AC      W87458;
DT      15-MAR-1999 (first entry)
DE      Humanised anti-alpha-v beta-3 Mab D12H2LCREI VL.
KW      Humanised antibody; monoclonal antibody; MAb; antibody engineering;
KW      mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
KW      cancer; metastasis; rheumatoid arthritis; atherosclerosis;
KW      angiogenesis; diabetic retinopathy; inflammation;
KW      macular degeneration; osteoporosis; Paget's disease;
KW      hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
KW      D12H2LCREI.
OS      Homo sapiens.
PN      W09840488-A1.
PD      17-SEP-1998.
PF      12-MAR-1998; U04987.
PR      12-MAR-1997; US-039609.
PA      (SMIK ) SMITHKLINE BEECHAM CORP.
PI      Johanson KO, Jonak ZL, Taylor AH;
DR      WPI: 99-034590/03.
DR      N-PSDB; V71805.
PT      New anti alpha-v beta_3 vitronectin receptor antibodies - used for
PT      immunotherapeutic treatment of e.g. diabetic retinopathy,
PT      inflammatory disorders, atherosclerosis, restenosis, cancers or
PT      osteoporosis
PS      Example 14; Page 68-69; 97pp; English.
CC      This is the amino acid sequence of the light chain variable region
CC      (VL) of humanised anti-alpha-v beta-3 vitronectin receptor
CC      monoclonal antibody D12H2LCREI. It is based on a synthetic
CC      humanised kappa chain based on a modified human REI kappa
CC      framework and complementarity determining regions from the murine
CC      anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody
CC      D12 (see W84094). Humanised antibodies of the invention can be used
CC      for passive immunotherapy of a disorder mediated by the alpha-v
CC      beta-3 receptor, e.g. cardiovascular disorders or angiogenic-
CC      related disorders, such as angiogenesis associated with diabetic
CC      retinopathy, atherosclerosis and restenosis, chronic inflammatory
CC      disorders, macular degeneration, rheumatoid arthritis and cancer,
CC      e.g. solid tumour metastasis, and diseases where bone resorption is
CC      associated with pathology such as osteoporosis, hyperparathyroidism,
CC      Paget's disease, hypercalcaemia of malignancy, osteolytic lesions
CC      produced by bone metastasis, bone loss due to immobilisation or sex
CC      hormone deficiency. They can also be used for targeted drug
CC      therapy, and for detection and diagnosis.
SQ      Sequence 105 AA;

Query Match      80.4%; Score 41; DB 1; Length 105;
Best Local Similarity 77.8%; Pred. No. 1.6;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 QQSGSWPLT 9
      ||| ||| |
Db      89 QQSNSWPFT 97

RESULT 12
W84098
ID      W84098 standard; Protein; 107 AA.
AC      W84098;
DT      15-MAR-1999 (first entry)
DE      Humanised anti-alpha-v beta-3 Mab D12H2HC 1-0 VL.
KW      Humanised antibody; monoclonal antibody; MAb; antibody engineering;
KW      mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
KW      cancer; metastasis; rheumatoid arthritis; atherosclerosis;
KW      angiogenesis; diabetic retinopathy; inflammation;

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KW      macular degeneration; osteoporosis; Paget's disease;
KW      hyperparathyroidism; hypercalcaemia; therapy; immunotherapy;
KW      D12H2HC-10.
OS      Homo sapiens.
FH      Synthetic.
FH      Key      Location/Qualifiers
FT      Region      24..34
FT      /label= CDR1
FT      Region      50..56
FT      /label= CDR2
FT      Region      89..97
FT      /label= CDR3
PN      W09840488-A1.
PD      17-SEP-1998.
PF      12-MAR-1998; U04987.
PR      12-MAR-1997; US-039609.
PA      (SMIK ) SMITHKLINE BEECHAM CORP.
PI      Johanson KO, Jonak ZL, Taylor AH;
DR      WPI: 99-034590/03.
DR      N-PSDB; V71800.
PT      New anti alpha-v beta_3 vitronectin receptor antibodies - used for
PT      immunotherapeutic treatment of e.g. diabetic retinopathy,
PT      inflammatory disorders, atherosclerosis, restenosis, cancers or
PT      osteoporosis
PS      Claim 2; Page 61-62; 97pp; English.
CC      This is the amino acid sequence of the light chain variable region
CC      (VL) of humanised anti-alpha-v beta-3 vitronectin receptor
CC      monoclonal antibody D12H2HC 1-0. It is based on the VL sequence
CC      (see W84096) of human Kabat subgroup III kappa chain, with
CC      complementarity determining regions (CDRs) from the murine
CC      anti-human alpha-v beta-3 vitronectin receptor monoclonal antibody
CC      D12 (see W84093). 3 Murine framework residues (1, 49 and 60)
CC      are retained. The humanised light chain can be expressed in host
CC      cells using nucleic acid molecules (see V71800) of the invention.
CC      Humanised D12 VH is also provided (see W84097). The humanised
CC      antibodies can be used for passive immunotherapy of disorders
CC      mediated by the alpha-v beta-3 receptor, e.g. cardiovascular or
CC      angiogenic-related disorders, such as angiogenesis associated
CC      with diabetic retinopathy, atherosclerosis and restenosis, chronic
CC      inflammatory disorders, macular degeneration, rheumatoid arthritis
CC      and cancer, e.g. solid tumour metastasis, and diseases where bone
CC      resorption is associated with pathology such as osteoporosis,
CC      hyperparathyroidism, Paget's disease, hypercalcaemia of malignancy,
CC      osteolytic lesions produced by bone metastasis, bone loss due to
CC      immobilisation or sex hormone deficiency. They can also be used for
CC      targeted drug therapy, and for detection and diagnosis.
SQ      Sequence 107 AA;

Query Match      80.4%; Score 41; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 QQSGSWPLT 9
      ||| ||| |
Db      89 QQSNSWPFT 97

RESULT 13
W84094
ID      W84094 standard; Protein; 108 AA.
AC      W84094;
DT      15-MAR-1999 (first entry)
DE      Murine vitronectin alpha-v beta-3 receptor MAB VL region.
KW      Humanised antibody; monoclonal antibody; MAb; antibody engineering;
KW      mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
KW      cancer; metastasis; rheumatoid arthritis; atherosclerosis;
KW      angiogenesis; diabetic retinopathy; inflammation;
KW      macular degeneration; osteoporosis; Paget's disease;
KW      hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.
OS      Mus sp.
FH      Key      Location/Qualifiers
FT      Region      24..34

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FT      Region      /label= CDR1
FT      50..56
FT      /label= CDR2
FT      89..97
FT      /label= CDR3
PN      WO9840488-A1.
PD      17-SEP-1998.
PF      12-MAR-1998; US-039609.
PR      12-MAR-1997; US-039609.
PA      (SMIK ) SMITHKLINE BEECHAM CORP.
PI      Johanson KO, Jonak ZL, Taylor AH;
DR      WPI; 99-034590/03.
DR      N-PSDB; V71798.
PT      New anti alpha_v beta_3 vitronectin receptor antibodies - used for
PT      immunotherapeutic treatment of e.g. diabetic retinopathy,
PT      inflammatory disorders, atherosclerosis, restenosis, cancers or
PT      osteoporosis
PS      Example 13; Page 59-60; 97pp; English.
CC      This is the amino acid sequence of the light chain variable region
CC      (VL) of the anti-human alpha-v beta-3 vitronectin receptor murine
CC      monoclonal antibody D12, as deduced from isolated cDNA (see
CC      V71798). D12 VH (see W84093) and VL show sequence similarity to
CC      Kabat VH subgroup I (see W84095) and Kabat VK subgroup III (see
CC      W84096), respectively. Humanised VH (see W84097) and VL (see
CC      W84098) were constructed by combining the framework regions of the
CC      human v region consensus sequences with complementarity determining
CC      regions of D12 (keeping some preferred murine framework residues).
CC      The humanised antibodies are specifically reactive with the human
CC      alpha-v beta-3 protein receptor and capable of neutralising the
CC      receptor. They can be used for passive immunotherapy of a disorder
CC      mediated by the alpha-v beta-3 receptor, e.g. cardiovascular
CC      disorders or angiogenic-related disorders, such as angiogenesis
CC      associated with diabetic retinopathy, atherosclerosis and
CC      restenosis, chronic inflammatory disorders, macular degeneration,
CC      rheumatoid arthritis and cancer, e.g. solid tumour metastasis, and
CC      diseases where bone resorption is associated with pathology such as
CC      osteoporosis, hyperparathyroidism, Paget's disease, hypercalcaemia
CC      of malignancy, osteolytic lesions produced by bone metastasis, bone
CC      loss due to immobilisation or sex hormone deficiency. They can also
CC      be used for targeted drug therapy, and for detection and diagnosis.
SQ      Sequence 108 AA;

Query Match      80.4%; Score 41; DB 1; Length 108;
Best Local Similarity 77.8%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 QQSGSWPLT 9
      ||| ||| |
Db      89 QQSNSWPFT 97

RESULT 14
W84100
ID      W84100 standard; Protein; 112 AA.
AC      W84100;
DT      15-MAR-1999 (first entry)
DE      Vitronectin alpha-v beta-3 MAB VL.
KW      Humanised antibody; monoclonal antibody; MAB; antibody engineering;
KW      mouse; human; vitronectin; alpha-v beta-3; receptor; restenosis;
KW      cancer; metastasis; rheumatoid arthritis; atherosclerosis;
KW      angiogenesis; diabetic retinopathy; inflammation;
KW      macular degeneration; osteoporosis; Paget's disease;
KW      hyperparathyroidism; hypercalcaemia; therapy; immunotherapy.
OS      Mus sp.
PN      WO9840488-A1.
PD      17-SEP-1998.
PF      12-MAR-1998; U04987.
PR      12-MAR-1997; US-039609.
PA      (SMIK ) SMITHKLINE BEECHAM CORP.
PI      Johanson KO, Jonak ZL, Taylor AH;
DR      WPI; 99-034590/03.
DR      N-PSDB; V71802.

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PT      New anti alpha_v beta_3 vitronectin receptor antibodies - used for
PT      immunotherapeutic treatment of e.g. diabetic retinopathy,
PT      inflammatory disorders, atherosclerosis, restenosis, cancers or
PT      osteoporosis
PS      Example 13; Page 64; 97pp; English.
CC      This is the amino acid sequence of the region of the murine
CC      monoclonal antibody (MAB) D12 light chain variable region (VL)
CC      that is altered in humanised D12 VL (see also W84098). A
CC      synthetic gene (see W81902) encoding the protein was prepared
CC      from synthetic oligonucleotides and used to prepare an expression
CC      vector for humanised D12 VL. D12 is an anti-human alpha-v beta-3
CC      vitronectin receptor MAB. Humanised D12 MABs can be used for
CC      passive immunotherapy of disorders mediated by the alpha-v beta-3
CC      vitronectin receptor, e.g. restenosis and angiogenic associated
CC      diseases.
SQ      Sequence 112 AA;

Query Match      80.4%; Score 41; DB 1; Length 112;
Best Local Similarity 77.8%; Pred. No. 1.8;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 QQSGSWPLT 9
      ||| ||| |
Db      89 QQSNSWPFT 97

RESULT 15
R38601
ID      R38601 standard; peptide; 107 AA.
AC      R38601;
DT      28-OCT-1993 (first entry)
DE      HVH light chain.
KW      Antibody; variable domain; light; L; heavy; H; consensus;
KW      affinity; antigen; immunogenicity; humanisation; framework.
OS      Homo sapiens.
PN      WO9311794-A.
PD      24-JUN-1993.
PF      14-DEC-1992; U10906.
PR      13-DEC-1991; US-808464.
PA      (XOMA ) XOMA CORP.
PI      Fishwild DM, Kohn FR, Little RG, Studnicka GM;
DR      WPI; 93-213827/26.
PT      Antibodies prep. used for treatment of auto-immune diseases - by
PT      replacement of critical residues to reduce immunogenicity but
PT      retain binding affinity, etc.
PS      Disclosure; Page 84; 160pp; English.
CC      The amino acid sequences of the light and heavy chains of the
CC      variable domains from antibodies HVH [HYHEL-10 Fab-lysosyme complex]
CC      (R38601 and R38608, respectively), MCPC [IgA Fab MCP603-phosphocholine
CC      complex] (R38602-03 and R38609-10, respectively), NEWM [Ig Fab' NEW]
CC      (R38604-05 and R38611, respectively) and KOL [IgG1 KOL] (R38606-07 and
CC      R38612, respectively) may be used to determine an alignment from which
CC      appropriate changes may be made.
CC      Unlike other methods of humanisation, which advocate the
CC      replacement of entire antibody framework regions with those of human
CC      antibodies, this method involves only the introduction of human
CC      residues into those positions not critical for antigen binding.
CC      This ensures that the binding properties of the modified antibody
CC      are not diminished.
SQ      Sequence 107 AA;

Query Match      78.4%; Score 40; DB 1; Length 107;
Best Local Similarity 77.8%; Pred. No. 2.5;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 QQSGSWPLT 9
      ||| ||| |
Db      89 QQSNSWPFT 97

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Search completed: May 27, 2000, 19:21:39
Job time: 1593 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:26:57 ; Search time 29.7 Seconds
(without alignments)
19.741 Million cell updates/sec

Title: US-09-016-061-94
Perfect score: 55
Sequence: 1 ARNHGGSFAS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_63:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	38	69.1	195	2	H64968	acetyl CoA acetyl
2	38	69.1	219	1	Q0ECS5	hypothetical 23.4k
3	37	67.3	731	1	JC2464	probable copper-tr
4	36	65.5	322	1	A29928	membrane-associate
5	36	65.5	360	2	S48566	hypothetical prote
6	36	65.5	470	2	H71667	glutamate--tRNA li
7	36	65.5	473	2	D70405	glutamate--tRNA li
8	35	63.6	272	2	S27819	vitelline B1 precu
9	35	63.6	272	2	S27820	vitelline B2 precu
10	35	63.6	446	2	T19625	hypothetical prote
11	35	63.6	448	1	A60003	nucleocapsid prote
12	35	63.6	538	2	T28874	hypothetical prote
13	35	63.6	628	1	A56707	protein-tyrosine k
14	35	63.6	1291	2	S64492	hypothetical prote
15	35	63.6	1291	2	T13389	hypothetical prote
16	34	61.8	89	2	S38688	MHC class II histo
17	34	61.8	89	2	S38683	MHC class II histo
18	34	61.8	89	2	S38684	MHC class II histo
19	34	61.8	127	2	D54759	terminal oxidase (
20	34	61.8	170	2	D75554	hypothetical prote
21	34	61.8	225	2	I47095	MHC class II OVAR-
22	34	61.8	236	2	S16389	sporamin - sweet p
23	34	61.8	284	2	S62931	probable membrane
24	34	61.8	284	2	S62955	probable membrane
25	34	61.8	379	1	F64633	site-specific DNA-
26	34	61.8	381	2	A71882	type II DNA modifi
27	34	61.8	1446	1	A45344	immediate-early pr
28	34	61.8	1460	1	EDBE1F	immediate-early pr
29	33	60.0	259	2	D72425	conserved hypothet
30	33	60.0	275	2	T04480	acyl-CoA oxidase h

31	33	60.0	339	2	F69776	conserved hypothet
32	33	60.0	369	2	D72238	peptide chain rele
33	33	60.0	480	2	B64059	glutamate--tRNA li
34	33	60.0	542	2	S42089	Rot(57) protein -
35	33	60.0	858	2	S54119	phosphoprotein - f
36	33	60.0	907	2	A57087	cell division cont
37	33	60.0	927	2	T38127	phosphoprotein - f
38	33	60.0	1403	2	T11583	probable translati
39	33	60.0	2109	1	ZLVN	genome polyprotein
40	32	58.2	54	2	S28711	hypothetical prote
41	32	58.2	62	2	S73032	hypothetical prote
42	32	58.2	129	2	H70727	hypothetical prote
43	32	58.2	154	2	E72126	ct296 hypothetical
44	32	58.2	175	2	PH0261	hypothetical 17.8k
45	32	58.2	190	2	D64087	probable peptidylp

ALIGNMENTS

RESULT 1
H64968
acetyl CoA acetyltransferase - Escherichia coli
C:Species: Escherichia coli
C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 18-Jun-1999
C:Accession: H64968; I69646; I69656
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: H64968
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-196 <BLAT>
A:Cross-references: GB:AE000294; GB:U00096; NID:gi1788338; PIDN:AAC75094.1; PID:gi17883
A:Experimental source: strain K-12, substrain MG1655
R:Yao, Z.; Valvano, M.A.
J. Bacteriol. 176, 4133-4143, 1994
A:Title: Genetic analysis of the O-specific lipopolysaccharide biosynthesis region (r
erotypes Y and 4a.
A:Reference number: I55053; MUID:94292434
A:Accession: I69646
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-167, 'LFRRYCHC', 177-186, 'IMR', 190-196 <RES>
A:Cross-references: EMBL:U03041; NID:g501028; PIDN:AAC31635.1; PID:g510256
R:Stevenson, G.; Neal, B.; Liu, D.; Hobbs, M.; Packer, N.H.; Batley, M.; Redmond, J.W
J. Bacteriol. 176, 4144-4156, 1994
A:Title: Structure of the O antigen of Escherichia coli K-12 and the sequence of its
A:Reference number: I55054; MUID:94292435
A:Accession: I69656
A:Molecule type: DNA
A>Status: translated from GB/EMBL/DBJ
A:Residues: 1-167, 'LFRRYCHC', 177-186, 'IMR', 190-196 <RE2>
A:Cross-references: EMBL:U09876; NID:g508236; PID:g508245
C:Genetics:
A:Gene: yefH
A:Map position: 45 min
C:Superfamily: galactoside acetyltransferase

Query Match 69.1%; Score 38; DB 2; Length 196;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNHGSF 8

Db 105 HNHGSF 110

RESULT 2
Q0ECS5

hypothetical 23.4K protein (ansa 3' region) - Escherichia coli
 C:Species: Escherichia coli
 C>Date: 31-Dec-1990 #sequence_revision 17-Oct-1997 #text_change 26-Aug-1999
 C:Accession: H64936; J00048
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cohen, A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617
 A:Accession: H64936
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-219 <BLAT>
 A:Cross-references: GB:AE000271; GB:U00096; NID:gl788058; PIDN:AACT4838.1; PID:gl788066;
 A:Experimental source: strain K-12, substrain MG1655
 R:Jerlstrom, P.G.; Bejak, D.A.; Jennings, M.P.; Beacham, I.R.
 Gene 78, 37-46, 1989
 A:Title: Structure and expression in Escherichia coli K-12 of the L-asparaginase I-encoding gene
 A:Reference number: J00047; MUID:89357501
 A:Accession: J00048
 A:Molecule type: DNA
 A:Residues: 7-219 <JER>
 A:Cross-references: GB:M26934; NID:gl45278; PIDN:AAA23447.1; PID:gl45280
 C:Genetics:
 A:Gene: ynfB
 A:Map position: 39 min
 C:Superfamily: Escherichia coli hypothetical 23.4K protein (ansa 3' region)
 Query Match 69.1%; Score 38; DB 1; Length 219;
 Best Local Similarity 100.0%; Pred. No. 6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 NHGSPAS 10
 Db 63 NHGSPAS 69
 RESULT 3
 JC2464
 Probable copper-transporting ATPase (EC 3.6.1.1) HRA-1 - Enterobacteriaceae spp.
 C:Species: Enterobacteriaceae spp.
 C>Date: 16-Oct-1998 #sequence_revision 16-Oct-1998 #text_change 18-Jun-1999
 C:Accession: JC2464
 R:Trenor III, C.; Lin, W.; Andrews, N.C.
 Biochem. Biophys. Res. Commun. 205, 1644-1650, 1994
 A:Title: Novel bacterial P-type ATPases with histidine-rich heavy-metal-associated sequence
 A:Reference number: JC2464; MUID:95110304
 A:Accession: JC2464
 A:Molecule type: mRNA
 A:Residues: 1-731 <TRE>
 A:Cross-references: GB:U16658; NID:g643612; PIDN:AAA62113.1; PID:g643613
 A:Experimental source: human small intestine cDNA library
 A:Note: the source species is uncertain; the cloned sequence did not hybridize with human cDNA
 C:Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding domain
 C:Keywords: ATP; copper transport; hydrolase; ion transport; phosphoprotein; transmembrane
 F:7-92/Region: His-rich
 F:135-477/Domain: ATPase transduction domain homology <ATP>
 F:544-685/Domain: ATPase nucleotide-binding domain homology <ATN>
 F:287/Active site: Glu #status predicted
 F:431/Active site: Asp (aspartylphosphate intermediate) #status predicted
 Query Match 67.3%; Score 37; DB 1; Length 731;
 Best Local Similarity 75.0%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ARNHGSP 8
 Db 88 AHHHGSP 95
 RESULT 4
 JC2464
 Membrane-associated 40K protein precursor - Vibrio anguillarum
 C:Species: Vibrio anguillarum
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
 C:Accession: A29928; C41671
 R:Actis, L.A.; Tolmasky, M.E.; Farrell, D.H.; Croa, J.H.
 J. Biol. Chem. 263, 2853-2860, 1988
 A:Title: Genetic and molecular characterization of essential components of the Vibrio
 A:Reference number: A92707; MUID:88139336
 A:Accession: A29928
 A:Molecule type: DNA
 A:Residues: 1-322 <ACT>
 R:Koeester, W.L.; Actis, L.A.; Waldbeser, L.S.; Tolmasky, M.E.; Croa, J.H.
 J. Biol. Chem. 266, 23829-23833, 1991
 A:Title: Molecular characterization of the iron transport system mediated by the pum1
 A:Reference number: A41671; MUID:92084677
 A:Accession: C41671
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-154 <KOE>
 A:Cross-references: GB:M74068
 C:Superfamily: Iron(III) dicitrate transport protein
 C:Keywords: membrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-322/Product: membrane-associated 40K protein #status predicted <MAT>
 Query Match 65.5%; Score 36; DB 1; Length 322;
 Best Local Similarity 75.0%; Pred. No. 21;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HNHGSPAS 10
 Db 203 HNHGSPAS 210
 RESULT 5
 S48566
 Hypothetical protein YLR215c - yeast (Saccharomyces cerevisiae)
 N:Alternate names: hypothetical protein L8167.23
 C:Species: Saccharomyces cerevisiae
 C>Date: 02-Dec-1994 #sequence_revision 02-Dec-1994 #text_change 24-Nov-1999
 C:Accession: S48566
 R:Pauley, A.
 submitted to the EMBL Data Library, September 1994
 A:Description: The sequence of S. cerevisiae cosmid 8167.
 A:Reference number: S48545
 A:Accession: S48566
 A:Molecule type: DNA
 A:Residues: 1-360 <PAU>
 A:Cross-references: EMBL:U14913; NID:g544497; PIDN:AAB67444.1; PID:g544519; GSPDB:GNO
 C:Genetics:
 A:Gene: MIPS:YLR215C
 A:Map position: 12R
 C:Superfamily: Saccharomyces cerevisiae hypothetical protein YLR215c
 Query Match 65.5%; Score 36; DB 2; Length 360;
 Best Local Similarity 77.8%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 RHNHGSPAS 10
 Db 304 RHNHGSPAS 312
 RESULT 6
 H71667
 glutamate--tRNA ligase (EC 6.1.1.17) (gltx2) RP623 - Rickettsia prowazekii
 C:Species: Rickettsia prowazekii
 C>Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 08-Oct-1999
 C:Accession: H71667
 R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sichteritz-Ponten, T.; Alsmark

Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499
A:Accession: H71667
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-470 <AND>
A:Cross-references: GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAA15066.1; PID:el34291
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: gltX2; RP623
C:Superfamily: glutamate--trNA ligase; glutamine--trNA ligase homology
C:Keywords: aminoacyl-trNA synthetase; ligase; protein biosynthesis

Query Match 65.5%; Score 36; DB 2; Length 470;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARNHGGSF 8
|||||
Db 31 ARHNGKF 38

RESULT 7
D70405
glutamate--trNA ligase (EC 6.1.1.17) - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999
C:Accession: D70405
R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.

Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666
A:Accession: D70405
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-473 <AQF>
A:Cross-references: GB:AE000729; NID:g2983659; PIDN:AAC07230.1; PID:g2983664; GB:AE00065
A:Experimental source: strain VF5
C:Genetics:
A:Gene: gltX
C:Superfamily: glutamate--trNA ligase; glutamine--trNA ligase homology
C:Keywords: aminoacyl-trNA synthetase; ligase; protein biosynthesis

Query Match 65.5%; Score 36; DB 2; Length 473;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARNHGGSF 8
|||||
Db 31 ARHNGGF 38

RESULT 8
S27819
vitelline B1 precursor - liver fluke
N:Alternate names: eggshell protein B1
C:Species: Fasciola hepatica (liver fluke)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Oct-1999
C:Accession: A48436; S27819
R:Rice-Ficht, A.C.; Dusek, K.A.; Kochevar, G.J.; Waite, J.H.
Mol. Biochem. Parasitol. 54, 129-141, 1992
A:Title: Eggshell precursor proteins of Fasciola hepatica, I. Structure and expression of
A:Reference number: A48436; MUID:93063029
A:Accession: A48436
A:Molecule type: mRNA; protein
A:Residues: 1-272 <RI2>
A:Cross-references: EMBL:M93024; NID:q159065; PID:g159066
A:Note: sequence extracted from NCBI backbone (NCBIN:117208, NCBIP:117210)
C:Keywords: egg shell

F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-272/Product: vitelline B1 #status predicted <MAT>

Query Match 63.6%; Score 35; DB 2; Length 272;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARNHGGSF 8
|||||
Db 19 ARHPHGKF 26

RESULT 9

S27820
vitelline B2 precursor - liver fluke
N:Alternate names: eggshell protein B2
C:Species: Fasciola hepatica (liver fluke)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Oct-1999
C:Accession: S27820
R:Rice-Ficht, A.C.; Dusek, K.A.; Kochevar, G.J.; Waite, J.H.

submitted to the EMBL Data Library, May 1992
A:Description: Eggshell precursor proteins of Fasciola hepatica: I. structure and exp
A:Reference number: S27819
A:Accession: S27820
A:Molecule type: mRNA
A:Residues: 1-272 <RIC>
A:Cross-references: EMBL:M93025; NID:g159067; PID:g159068
C:Keywords: egg shell

F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-272/Product: vitelline B2 #status predicted <MAT>

Query Match 63.6%; Score 35; DB 2; Length 272;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARNHGGSF 8
|||||
Db 19 ARHPHGKF 26

RESULT 10

T19625
hypothetical protein C31H5.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19625
R:Kershaw, J.

submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19625
A>Status: preliminary; translated from GB/EMBL/DDBI

A:Molecule type: DNA
A:Residues: 1-446 <N1L>
A:Cross-references: EMBL:293778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6
A:Experimental source: clone C31H5
C:Genetics:

A:Gene: CESP:C31H5.6
A:Map position: 1
A:Introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3

Query Match 63.6%; Score 35; DB 2; Length 446;
Best Local Similarity 66.7%; Pred. No. 44;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNHGSFAS 10
|||||
Db 51 RHNHGSFAS 59

RESULT 11

A60003
nucleocapsid protein - human coronavirus (strain OC43)
C:Species: human coronavirus
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Feb-1999
C:Accession: A60003
R:Kamashora, T.; Soe, L.H.; Lai, M.M.C.
Virus Res. 12, 1-9, 1989
A:Title: Sequence analysis of nucleocapsid gene and leader RNA of human coronavirus OC43
A:Reference number: A60003; MUID:89243809
A:Accession: A60003
A:Molecule type: genomic RNA
A:Residues: 1-448 <RAM>
C:Genetics:
A:Gene: N
C:Superfamily: coronavirus nucleocapsid protein
C:Keywords: glycoprotein; nucleocapsid
F:17,221,336,388,408,421/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:17,221,336,388,408,421/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 63.6%; Score 35; DB 1; Length 448;
Best Local Similarity 85.7%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNHGSF 8
DB 103 RHNRGSF 109

RESULT 12
T28874
hypothetical protein R04E5.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T28874
R:Miller, N.
submitted to the EMBL Data Library, December 1995
A:Description: The sequence of C. elegans cosmid R04E5.
A:Reference number: Z20535
A:Accession: T28874
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-538 <MIL>
A:Cross-references: EMBL:U41538; PIDN:AAC48179.1; GSPDB:GN00028; CESP:R04E5.2
A:Experimental source: strain Bristol N2; clone R04E5
C:Genetics:
A:Gene: CESP:R04E5.2
A:Map position: 10
A:Introns: 28/2; 52/3; 91/2; 133/3; 169/1; 199/3; 240/2; 269/3; 302/3; 329/3; 368/3; 450/3

Query Match 63.6%; Score 35; DB 2; Length 538;
Best Local Similarity 62.5%; Pred. No. 53;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNHGSFA 9
DB 434 KHHGRFA 441

RESULT 13
A56707
protein-tyrosine kinase (EC 2.7.1.112) syk, splice form B - rat
N:Contains: protein-tyrosine kinase Syk, splice form A
C:Species: Rattus norvegicus (Norway rat)
C>Date: 19-Oct-1995 #sequence_revision 23-May-1997 #text_change 10-Sep-1999
C:Accession: A56707; B56707; A48875
R:Rowley, R.B.; Bolen, J.B.; Fargnoli, J.
J. Biol. Chem. 270, 12659-12664, 1995
A:Title: Molecular cloning of rodent p72(Syk). Evidence of alternative mRNA splicing.
A:Reference number: A56707; MUID:95279402
A:Accession: A56707
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA

A:Residues: 1-628 <ROW>
A:Cross-references: GB:U21684
A:Accession: B56707
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-275,299-628 <RO2>
A:Cross-references: GB:U21683
R:Benhamou, M.; Ryba, N.J.P.; Nishikata, H.; Kihara, H.; Siraganian, R.P.
J. Biol. Chem. 268, 23318-23324, 1993
A:Title: Protein tyrosine kinase p72syk in high affinity IgE receptor signaling: Idem

A:Reference number: A48875; MUID:94043123
A:Accession: A48875
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 15-22, 'E', 23-263, 'M', 265-269, 'S', 271-444, 'EL', 447-628 <RES>
A:Cross-references: GB:T20838; NID:9416152; PIDN:AAA42308.1; PID:9416153
C:Superfamily: protein-tyrosine kinase ZAP-70; protein kinase homology; SH2 homology
C:Keywords: alternative splicing; ATP; autophosphorylation; phosphoprotein; phosphotyrosine; phosphotyrosine kinase; splice form B #status predicted <PRB>
F:1-275,299-628/Product: protein-tyrosine kinase syk, splice form B #status predicted <PRB>
F:14-105/Domain: SH2 homology <SH2A>
F:166-257/Domain: SH2 homology <SH2B>
F:362-626/Domain: protein kinase homology <KIN>
F:370-378/Region: protein kinase ATP-binding motif

Query Match 63.6%; Score 35; DB 1; Length 628;
Best Local Similarity 77.8%; Pred. No. 62;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSFA 9
DB 194 ARDNNGSFA 202

RESULT 14
S64492
hypothetical protein YGR178c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein G7139
C:Species: Saccharomyces cerevisiae
C>Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 29-Oct-1999
C:Accession: S64492
R:Habbing, U.; Hofmann, B.; Delius, H.
submitted to the Protein Sequence Database, May 1996
A:Reference number: S64003
A:Accession: S64492
A:Molecule type: DNA
A:Residues: 1-722 <HEB>
A:Cross-references: EMBL:Z72963; NID:q1323314; PIDN:CAA97204.1; PID:e243559; PID:g132
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SGD:PBPI
A:Cross-references: SGD:S0003410; MIPS:YGR178c
A:Map position: 7R

Query Match 63.6%; Score 35; DB 2; Length 722;
Best Local Similarity 85.7%; Pred. No. 71;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNHGSF 8
DB 474 RHNHGSF 480

RESULT 15
T13389
hypothetical protein EG:ll5c2.10 - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999
C:Accession: T13389
R:Salles, C.; Valenti, P.; Darlamitsou, A.; Henderson, N.; Campbell, L.; Glover, D.

submitted to the EMBL Data Library, May 1999
A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A:Reference number: Z17665
A:Accession: T13389
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-1291 <CAT>
A:Cross-references: EMBL:AL031581; NID:e1320978; PID:e1426292; PIDN:CAA20894.2
C:Genetics:
A:Map position: X
A:Introns: 238/3: 1225/1
A:Note: EG:115C2.10

Query Match 63.6%; Score 35; DB 2; Length 1291;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 3 HNHGSFAS 10
||| ||
Db 554 HNHGQHAS 561

Search completed: May 27, 2000, 19:52:02
Job time: 1505 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 20:07:26 ; Search time 48.34 Seconds
(without alignments)
6.300 Million cell updates/sec

Title: US-09-016-061-94
Perfect score: 55
Sequence: 1 ARNHGSPAS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	69.1	196	1 WBBJ_ECOLI	P37750 escherichia
2	38	69.1	213	1 PNCA_ECOLI	P21369 escherichia
3	36	65.5	218	1 Y4VH_RHISN	Q53216 rhizobium s
4	36	65.5	322	1 PATB_VIBAN	P11460 vibrio angu
5	36	65.5	470	1 SYE2_RICPR	O92ct8 rickettsia
6	36	65.5	473	1 SYE_AQUAE	O67271 aquifex aeo
7	35	63.6	197	1 EGG5_FASHE	P07915 fasciola he
8	35	63.6	448	1 NCAP_CVHOC	P33469 human coron
9	35	63.6	567	1 CC45_XENLA	Q9yh26 xenopus lae
10	35	63.6	629	1 KSYK_RAT	Q64725 rattus norv
11	35	63.6	722	1 PBPL_YEAST	P53297 saccharomyc
12	34	61.8	284	1 YNB9_YEAST	P53975 saccharomyc
13	34	61.8	284	1 YND3_YEAST	P53964 saccharomyc
14	34	61.8	1446	1 IE18_PRYKA	P33479 pseudorabic
15	34	61.8	1461	1 IE18_PRVIF	P11675 pseudorabic
16	33	60.0	480	1 SYE_HAEIN	P43818 haemophilus
17	33	60.0	927	1 CC15_SCHPO	Q09822 schizosacch
18	33	60.0	966	1 MI72_HUMAN	Q14596 homo sapien
19	33	60.0	1403	1 YDF3_SCHPO	Q10475 schizosacch
20	33	60.0	2109	1 RRPL_VSVSJ	P03523 vesicular s
21	32	58.2	129	1 YP56_MYCTU	Q50742 mycobacteri
22	32	58.2	190	1 SLVD_HAEIN	P44830 haemophilus
23	32	58.2	231	1 ARAD_ECOLI	P08203 escherichia
24	32	58.2	231	1 ARAD_SALTY	P06190 salmonella
25	32	58.2	231	1 SGBE_ECOLI	P37680 escherichia
26	32	58.2	231	1 SGBE_HAEIN	P44989 haemophilus
27	32	58.2	376	1 HPPD_RAT	P32755 rattus norv
28	32	58.2	392	1 HPPD_HUMAN	P32754 homo sapien
29	32	58.2	392	1 HPPD_MOUSE	P49429 mus musculu
30	32	58.2	434	1 TA47_TREPA	P29723 treponema p
31	32	58.2	473	1 SYTM_SCHPO	O13969 schizosacch
32	32	58.2	593	1 ARSD_HUMAN	P51689 homo sapien
33	32	58.2	635	1 KSYK_HUMAN	P43405 homo sapien
34	32	58.2	676	1 HS7C_TRYBB	P20030 trypanosoma

35 32 58.2 1178 1 RPOB_MYCTU P47766 mycobacteri
36 32 58.2 1179 1 RPOB_MYCLE P30760 mycobacteri
37 31 56.4 65 1 CCSA_PEA P31172 pisum sativ
38 31 56.4 69 1 GLUC_CANFA P29794 canis famil
39 31 56.4 141 1 HBAL_IGUIG P18974 iguana igua
40 31 56.4 151 1 GLUC_CHICK P01277 gallus gall
41 31 56.4 158 1 GLUC_PIG P01274 sus scrofa
42 31 56.4 161 1 PTB1_XENLA P48532 xenopus lae
43 31 56.4 180 1 GLUC_BOVIN P01272 bos taurus
44 31 56.4 180 1 GLUC_CAVPO P05110 cavia porce
45 31 56.4 180 1 GLUC_HUMAN P01275 homo sapien

ALIGNMENTS

RESULT 1
WBBJ_ECOLI
ID WBBJ_ECOLI STANDARD; PRT; 196 AA.
AC P37750; P76375;
DT 01-OCT-1994 (Rel. 30, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE PUTATIVE LIPOPOLYSACCHARIDE BIOSYNTHESIS O-ACETYL TRANSFERASE WBBJ
(EC 2.3.1.-).
GN WBBJ.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / W3110;
RX MEDLINE; 94292434.
RA Yao Z., Valvano M.A.;
RT "Genetic analysis of the O-specific lipopolysaccharide biosynthesis
region (rfb) of Escherichia coli K-12 W3110: identification of genes
that confer group 6 specificity to Shigella flexneri serotypes Y and
RT 4a";
RL J. Bacteriol. 176:4133-4143(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / WGI;
RX MEDLINE; 94292435.
RA Stevenson G., Neal B., Liu D., Hobbs M., Packer N.H., Batley M.,
Redmond J.W., Lindquist L., Reeves P.R.;
RT "Structure of the O antigen of Escherichia coli K-12 and the sequence
of its rfb gene cluster";
RL J. Bacteriol. 176:4144-4156(1994).
RN [3]
RP REVISIONS TO 168-176 AND 187-189.
RC STRAIN-K12 / WGI;
RA Stevenson G.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / WGI655;
RX MEDLINE; 97426617.
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE; 97251358.
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T.,
Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
Saito N., Sampei G., Seki Y., Sivasubram S., Tagami H.,
Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;

RT "A 460-kb DNA sequence of the *Escherichia coli* K-12 genome
 RL corresponding to the 40.1-50.0 min region on the linkage map.";
 CC DNA Res. 3:379-392(1996).
 CC 1- FUNCTION: PUTATIVE O-ACETYLTRANSFERASE THAT TRANSFERS AN O-ACETYL
 CC ON THE O ANTIGEN.
 CC 1- PATHWAY: LIPOLYSACCHARIDE BIOSYNTHESIS.
 CC 1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NODL FAMILY OF
 CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
 CC -----
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 CC EMBL: U03041; AAC31635.1; -;
 CC EMBL: U09876; AAB88406.1; -;
 CC EMBL: AE000294; AAC75094.1; -;
 CC EMBL: D90841; CAB21803.1; -;
 CC EMBL: D90842; CAB21811.1; -;
 CC ECOGENE: EGI1984; WBBU.
 CC PROSITE: PS00101; HEXAPEP_TRANSFERASES; FALSE_NEG.
 CC PFAM: PF00132; hexapep; 1.
 CC KW Lipopolysaccharide biosynthesis; Transferase; Acyltransferase; Repeat.
 CC FT CONFLICT 168 176 SPENTVIA -> LFRKYCHC (IN REF. 1).
 CC FT CONFLICT 187 189 NHE -> IMR (IN REF. 1).
 CC SEQUENCE 196 AA; 21675 MW; DIC2FA7D3B29A1B1 CRC64;

Query Match 69.1%; Score 38; DB 1; Length 196;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HHGFSF 8
 Db 105 HHGFSF 110
 |||||

RESULT 2
 PNCA_ECOLI STANDARD; PRT; 213 AA.
 AC P21369; P76229; P76910;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PYRAZINAMIDASE/NICOTINAMIDASE [INCLUDES: PYRAZINAMIDASE (EC 3.5.1.-)
 DE (PZASE); NICOTINAMIDASE (EC 3.5.1.19) (NICOTINE DEAMIDASE)].
 GN PNCA OR NAM.
 OS *Escherichia coli*.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC *Escherichia*.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE; 89357501.
 RA Jerlstrom P.G., Bezjak D.A., Jennings M.P., Beacham I.R.;
 RT "Structure and expression in *Escherichia coli* K-12 of the
 RT L-asparaginase I-encoding *ansA* gene and its flanking regions.";
 RL Gene 78:37-46(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96338362.
 RA Frothingham R., Meeker-O'Connell W.A., Talbot E.A., George J.W.,
 RA Kreuzer K.N.;
 RT "Identification, cloning, and expression of the *Escherichia coli*
 RT pyrazinamidase and nicotinamidase gene, *pnca*.";
 RL Antimicrob. Agents Chemother. 40:1426-1431(1996).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE; 97426617.

RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1453-1474(1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RA Alba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T.,
 RA Ikemoto K., Inada T., Isono K., Isono S., Itoh T., Kanai K.,
 RA Kasai H., Kashimoto K., Kim S., Kimura S., Kitagawa M.,
 RA Kitakawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H.,
 RA Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
 RA Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C.,
 RA Yamamoto Y., Yano M.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 CC 1- CATALYTIC ACTIVITY: NICOTINAMIDE + H(2)O = NICOTINATE + NH(3).
 CC 1- PATHWAY: PYRIDINE NUCLEOTIDE CYCLE.
 CC 1- SIMILARITY: TO YEAST YGL037C.
 CC -----
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 CC -----
 CC EMBL: M26934; AAA23447.1; -;
 CC EMBL: AE000271; AAC74838.1; ALT_INIT.
 CC EMBL: D90820; CAB21476.1; -;
 CC EMBL: D90821; CAB21489.1; -;
 CC PIR: JU0048; QQECAS.
 CC ECOGENE: EGI1135; PNCA.
 CC PFAM: PF00857; Isochorismatase; 1.
 CC KW Hydrolase.
 CC SEQUENCE 213 AA; 23362 MW; B9F8D946FAL8433F CRC64;

Query Match 69.1%; Score 38; DB 1; Length 213;
 Best Local Similarity 100.0%; Pred. No. 2.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NHGSFAS 10
 Db 57 NHGSFAS 63
 |||||

RESULT 3
 Y4VH_RHISN STANDARD; PRT; 218 AA.
 ID Y4VH_RHISN
 AC Q53216;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHETICAL 24.6 KD PROTEIN Y4VH.
 GN Y4VH.
 OS *Rhizobium* sp. (strain NGR234).
 OG Plasmid sym pNGR234a.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97305956.
 RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
 RA Perret X.;
 RT "Molecular basis of symbiosis between *Rhizobium* and legumes.";
 RL Nature 387:394-401(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96389014.
 RA Freiberg C., Perret X., Broughton W.J., Rosenthal A.;

RT "Sequencing the 500-kb GC-rich symbiotic replicon of *Rhizobium* sp.
RT NGR234 using dye terminators and a thermostable 'sequenase': a
RL Genome Res. 6:590-600(1996).
CC -1- SIMILARITY: NONE OBVIOUS.
CC -----
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CC -----
DR EMBL; Z68203; CAA92423.1; -.
DR EMBL; AE00101; AAB91896.1; -.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 218 AA; 24594 MW; 501C6CB38A09A2E5 CRC64;

Query Match 65.5%; Score 36; DB 1; Length 218;
Best Local Similarity 66.7%; Pred. No. 5.1;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSPA 9
|||
Db 68 ARDNHGSYS 76
|||

RESULT 4
FATB_VIBAN STANDARD; PRT; 322 AA.
AC P11460;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-1994 (Rel. 30, Last annotation update)
DE FERRIC ANGUIBACTIN-BINDING PROTEIN PRECURSOR.
GN FATB.
OS *Vibrio anguillarum*.
OC Plasmid pW1.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; *Vibrio*.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=775;
RX MEDLINE; 88139336.
RA Accis L.A., Tolmasky M.E., Farrell D.H., Crosa J.H.;
RT "Genetic and molecular characterization of essential components of
RT the *Vibrio anguillarum* plasmid-mediated iron-transport system.";
RL J. Biol. Chem. 263:2853-2860(1988).
RN [2]
RP SEQUENCE OF 1-154 FROM N.A.
RC STRAIN=775;
RX MEDLINE; 92084677.
RA Koester W.L., Actis L.A., Waldbeser L.S., Tolmasky M.E., Crosa J.H.;
RT "Molecular characterization of the iron transport system mediated by
RT the pW1 plasmid in *Vibrio anguillarum* 775.";
RL J. Biol. Chem. 266:23829-23833(1991).
CC -1- FUNCTION: BINDS FERRIC ANGUIBACTIN; PART OF THE BINDING-PROTEIN-
CC DEPENDENT TRANSPORT SYSTEM FOR UPTAKE OF FERRIC ANGUIBACTIN.
CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE INNER MEMBRANE BY A LIPID
CC ANCHOR (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
CC PROTEIN FAMILY 8.
CC -----
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CC -----
DR EMBL; J03529; AAA91580.1; -.
DR

DR EMBL; M74068; AAA25643.1; ALT_INIT.
DR PIR; A29928; A29928.
DR PROSITE; PS0013; PROKAR_LIPOPROTEIN; 1.
DR PFAM; PF01497; Peripla_BP_2; 1.
KW Transport; Iron transport; Signal; Inner membrane; Lipoprotein;
KW Plasmid.
FT SIGNAL 1 22 POTENTIAL.
FT CHAIN 23 322 FERRIC ANGUIBACTIN-BINDING PROTEIN.
FT LIPID 23 23 N-ACYL DIGLYCERIDE (POTENTIAL).
SQ SEQUENCE 322 AA; 35635 MW; FB8674EED5CF73F7 CRC64;

Query Match 65.5%; Score 36; DB 1; Length 322;
Best Local Similarity 75.0%; Pred. No. 7.6;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HHGSPAS 10
|||
Db 203 HHNGSESS 210
|||

RESULT 5
SYE2_RICPR STANDARD; PRT; 470 AA.
ID SYE2_RICPR AC Q9ZCT8;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE 2 (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE 2)
DE (GLURS 2).
GN GLTX2 OR RP623.
OS *Rickettsia prowazekii*.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E.
RX MEDLINE; 99039499.
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sichert-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of *Rickettsia prowazekii* and the origin of
RT mitochondria".
RL Nature 396:133-140(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) -> AMP +
CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; AJ235272; CAA15066.1; -.
DR HSP; P27000; IGLN.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW Aminoacyl-TRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
FT SIMILAR 239 243 "KMSK" REGION.
FT BINDING 242 242 ATP (BY SIMILARITY).
SQ SEQUENCE 470 AA; 53696 MW; DFICE50A20B8A9FD CRC64;

Query Match 65.5%; Score 36; DB 1; Length 470;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSP 8

```
Db 31 ARNHNGSF 38
|||||
RESULT 6
SYE_AQUAE STANDARD; PRT; 473 AA.
AC 067271;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE)
DE (GLURS).
GN GLTX OR AQ_1221.
OS Aquifex aeolicus.
OC Bacteria; Aquificales; Aquificaceae; Aquifex.
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=VF5;
RC MEDLINE; 98196666.
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Anjay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RT "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus."
RL Nature 392:353-358(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA (GLU) = AMP +
CC PYROPHOSPHATE + L-GLUTAMYL-TRNA (GLU).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC -----
DR EMBL; A600729; TRNA07230.1; -.
DR PRINTS; PR00987; TRNASYNTHGLU.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
DR PFAM; PF00749; tRNA-synt.1c; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
FT SIMILAR 242 246 "RMSKS" REGION.
FT BINDING 245 245 ATP (BY SIMILARITY).
SQ SEQUENCE 473 AA; 55121 MW; 5CB4D1590973E07A CRC64;

Query Match 65.5%; Score 36; DB 1; Length 473;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHNGSF 8
|||||
Db 31 ARNHNGGF 38

RESULT 7
EGGS_FASHE STANDARD; PRT; 197 AA.
AC P07915;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PUTATIVE EGG SHELL PROTEIN PRECURSOR.
OS Fasciola hepatica (Liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Echinostomida; Echinostomatidae; Echinostomidae; Fasciolidae;
OC Fasciolidae; Fasciola.
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE; 87175670.
RA Zurita M., Bieber D., Ringold G., Mansour T.E.;
RT "Cloning and characterization of a female genital complex cDNA from
RT the liver fluke Fasciola hepatica."
RL Proc. Natl. Acad. Sci. U.S.A. 84:2340-2344(1987).
CC -----
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CC -----
DR EMBL; M15871; AAA29138.1; -.
DR Eggshell; Signal. 17
FT SIGNAL 18 197 PUTATIVE EGG SHELL PROTEIN.
SQ SEQUENCE 197 AA; 22470 MW; 72033ED203FC1A3E CRC64;

Query Match 63.6%; Score 35; DB 1; Length 197;
Best Local Similarity 75.0%; Pred. No. 7.1;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHNGSF 8
|||||
Db 17 ARNHNGKF 24

RESULT 8
NCAP_CVHOC STANDARD; PRT; 448 AA.
AC P33469;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE NUCLEOCAPSID PROTEIN.
GN N.
OS Human coronavirus (strain OC43).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89243809.
RA Kamahora T., Soe L.H., Lai M.M.C.;
RT "Sequence analysis of nucleocapsid gene and leader RNA of human
RT coronavirus OC43."
RL Virus Res. 12:1-9(1989).
DR PIR; A60003; A60003.
DR PFAM; PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 448 AA; 49316 MW; 5193AB1AE0D75626 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 448;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNHGSF 8
|||||
Db 103 RHNHGSF 109

RESULT 9
CC45_XENLA STANDARD; PRT; 567 AA.
AC Q3YHZ6;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE CDC45-RELATED PROTEIN.
```

GN CDC45.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
 OC Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae;
 OC Xenopus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 98429493.
 RA Mimura S., Takisawa H.;
 RT "Xenopus Cdc45-dependent loading of DNA polymerase alpha onto
 RT chromatin under the control of S-phase Cdk.";
 RL EMBO J. 17:5699-5707(1998).
 CC -1- FUNCTION: REQUIRED FOR INITIATION OF CHROMOSOMAL DNA REPLICATION.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR.
 CC -1- SIMILARITY: BELONGS TO THE CDC45 FAMILY.
 CC
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 CC
 DR EMBL; AF062494; AAC67520.1; -;
 KW DNA replication; Cell cycle; Nuclear protein.
 SQ SEQUENCE 567 AA; 65444 MW; 9A32FB20097F7C86 CRC64;

Query Match 63.6%; Score 35; DB 1; Length 567;
 Best Local Similarity 71.4%; Pred. No. 21;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGS 7

Db 251 SRNHGN 257

RESULT 10

KSYK_RAT
 ID KSYK_RAT STANDARD; PRT; 629 AA.
 AC Q64725;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE TYROSINE-PROTEIN KINASE SYK (EC 2.7.1.112) (SPLEEN TYROSINE KINASE).
 GN SYK.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95279402.
 RA Rowley R.B., Bolen J.B., Fargnoli J.;
 RT "Molecular cloning of rodent p72Syk. Evidence of alternative mRNA
 RT splicing.";
 RL J. Biol. Chem. 270:12659-12664(1995).
 CC -1- FUNCTION: MAY PARTICIPATE IN SIGNALING PATHWAYS. PLAYS A ROLE IN
 CC LYMPHOCYTE ACTIVATION.
 CC -1- CATALYTIC ACTIVITY: ATP + A PROTEIN TYROSINE = ADP + PROTEIN
 CC TYROSINE PHOSPHATE.
 CC -1- ALTERNATIVE PRODUCTS: TWO ISOFORMS; SYK AND SYKB (SHOWN HERE);
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 2 SH2 DOMAINS.
 CC -1- SIMILARITY: TO OTHER PROTEIN-TYROSINE KINASES IN THE CATALYTIC
 CC DOMAIN. BELONGS TO THE SYK/TAP-70 SUBFAMILY.
 CC
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 CC
 DR EMBL; U21684; AAA75167.1; -;
 DR EMBL; U21683; AAA75166.1; -;
 DR HSSP; P43405; ICSY.
 DR PRINTS; PR00401; SH2DOMAIN.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS50001; SH2; 2.
 DR PFAM; PF00017; SH2; 2.
 DR PFAM; PF00069; pkinase; 1.
 KW Transferase; Tyrosine-protein kinase; ATP-binding; Phosphorylation;
 KW SH2 domain; Alternative splicing.
 FT DOMAIN 14 106
 FT DOMAIN 167 258
 FT DOMAIN 365 625
 FT NP_BIND 371 379
 FT BINDING 396 396
 FT ACT_SITE 488 488
 FT MOD_RES 519 519
 FT VARSPPLIC 277 299
 SQ SEQUENCE 629 AA; 71528 MW; 81169A643EC6A6FE CRC64;

Query Match 63.6%; Score 35; DB 1; Length 629;
 Best Local Similarity 77.8%; Pred. No. 24;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSFA 9

Db 195 ARDNNGSFA 203

RESULT 11

PBPL_YEAST
 ID PBPL_YEAST STANDARD; PRT; 722 AA.
 AC P53297;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PAB1-BINDING PROTEIN 1
 GN PBPL OR MRS16 OR YGR178C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Hebling U., Hofmann B., Dellus H.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DMY747;
 RA Mecklenbrauer I.;
 RT "Sequencing and characterization of a suppressor of the pet- phenotype
 RT in a Saccharomyces cerevisiae strain without mitochondrial group II
 RT introns.";
 RL Thesis (1996), Vienna Biocentre, Austria.
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE; 99038243.
 RA Mangus D.A., Amrani N., Jacobson A.;
 RT "Pbplp, a factor interacting with Saccharomyces cerevisiae poly(A)-
 RT binding protein, regulates polyadenylation.";
 RL Mol. Cell. Biol. 18:7383-7396(1998).
 CC -1- FUNCTION: APPEARS TO PROMOTE PROPER POLYADENYLATION. IN THE
 CC ABSENCE OF PBPLP, THE 3'TERMINI OF PRE-MRNAS ARE PROPERLY CLEAVED
 CC BUT LACK FULL-LENGTH POLY(A) TAILS. MAY ACT TO REPRESS THE ABILITY
 CC OF PAB1 TO NEGATIVELY REGULATE POLYADENYLATION.
 CC -1- SUBUNIT: INTERACTS WITH PAB1.
 CC -1- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
 CC

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DR EMBL; 272963; CAA97204.1; -;
 DR EMBL; U46931; AAB94294.1; -;
 DR SGD; L0003967; PBPL.
 KW Nuclear protein.
 SQ SEQUENCE 722 AA; 78781 MW; 92005F3A2346193E CRC64;

Query Match 63.6%; Score 35; DB 1; Length 722;
 Best Local Similarity 85.7%; Pred. No. 27;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RRNHGSF 8
 I I I I I
 DB 474 RRNHGSF 480

RESULT 12
 YNB9_YEAST STANDARD; PRT; 284 AA.

AC P53975;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HYPOTHETICAL 31.3 KD PROTEIN IN HDAL-PUB1 INTERGENIC REGION PRECURSOR.

GN YNL019C OR N2827.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomycetes.

RA Andre B., Iraqi Housaini I., Urrestarazu L.A., Vissers S.;
 RP Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO YEAST YNL033W.

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DR EMBL; 271295; CAA95881.1; -;
 KW Hypothetical protein; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 284 HYPOTHETICAL PROTEIN YNL019C.
 FT CARBOHYD 270 270 POTENTIAL.
 SQ SEQUENCE 284 AA; 31326 MW; 0AD55E3495B2B284 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 284;
 Best Local Similarity 55.6%; Pred. No. 16;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSFA 9
 I I I I I
 DB 194 SHNHGSIS 202

RESULT 13
 YND3_YEAST STANDARD; PRT; 284 AA.
 ID YND3_YEAST
 AC P53964;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHETICAL 31.4 KD PROTEIN IN NCE3-HH72 INTERGENIC REGION PRECURSOR.
 GN YNL033W OR N2743.

OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomycetes.

RN [1]
 RP SEQUENCE FROM N.A.
 RA Dueterhoeft A., Floeth M., Fritz C., Heuss-Neitzel D.,
 RA Hilbert H., Moestl D.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO YEAST YNL019C.

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DR EMBL; 271309; CAA95896.1; -;
 KW Hypothetical protein; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 284 HYPOTHETICAL PROTEIN YNL033W.
 FT CARBOHYD 270 270 POTENTIAL.
 SQ SEQUENCE 284 AA; 31386 MW; 1BC45E3495B2A395 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 284;
 Best Local Similarity 55.6%; Pred. No. 16;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSFA 9
 I I I I I
 DB 194 SHNHGSIS 202

RESULT 14
 IE18_PVKA STANDARD; PRT; 1446 AA.

AC P33479;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE IMMEDIATE-EARLY PROTEIN IE180.

GN IE.
 OS Pseudorabies virus (strain Kaplan) (PRV).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Varicellovirus.

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91021039.
 RA Vicek C., Kozmik Z., Paces V., Schirm S., Schwyzer M.;
 RT "Pseudorabies virus immediate-early gene overlaps with an oppositely
 RT oriented open reading frame: characterization of their promoter and
 RT enhancer regions.";
 RL Virology 179:365-377(1990).

CC -1- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE
 CC OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING
 CC OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.

CC -1- SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.
 CC -1- PTM: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF
 CC PHOSPHORYLATION.

CC -1- SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.

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```
CC -----
DR EMBL; M34651; AAA47470.1; -.
DR PIR; A45344; A45344.
KW Early protein; Transcription regulation; Trans-acting factor;
KW DNA-binding; Phosphorylation; Nuclear protein.
FT DOMAIN 347 354 POLY-SER.
FT DOMAIN 379 397 POLY-SER.
SQ SEQUENCE 1446 AA; 148640 MW; 81F43A3DE3DDA068 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 1446;
Best Local Similarity 75.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGGSF 8
Db 583 APHGGSF 590

RESULT 15
IE18.PRVI
ID IE18.PRVI STANDARD; PRT; 1461 AA.
AC P11675;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE IMMEDIATE-EARLY PROTEIN IE180.
GN IE.
OS Pseudorabies virus (strain Indiana-Funkhauser / Becker) (PRV).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Varicelloviruses.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89315207.
RA Cheung A.K.;
RT "DNA nucleotide sequence analysis of the immediate-early gene of
RT pseudorabies virus.";
RL Nucleic Acids Res. 17:4637-4646(1989).
RN [2]
RP REVISIONS.
RA Cheung A.K.;
RL Submitted (NOV-1989) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE
CC OF MIGRATING TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING
CC OTHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.
CC -!- SUBCELLULAR LOCATION: NUCLEUS OF INFECTED CELLS.
CC -!- PTM: A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF
CC PHOSPHORYLATION.
CC -!- SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X15120; CAA33214.1; -.
DR PIR; S04713; EDBEIF.
KW Early protein; Transcription regulation; Trans-acting factor;
KW DNA-binding; Phosphorylation; Nuclear protein.
FT DOMAIN 390 405 POLY-SER.
FT DOMAIN 958 966 POLY-SER.
SQ SEQUENCE 1461 AA; 149833 MW; 7F31E7ABE403B208 CRC64;

Query Match 61.8%; Score 34; DB 1; Length 1461;
Best Local Similarity 75.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGGSF 8
Db 583 APHGGSF 590
```

Db 594 APHGGSF 601

Search completed: May 27, 2000, 20:45:28
Job time: 2282 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:38:56 ; Search time 34.67 Seconds
(without alignments)
19.998 Million cell updates/sec

Title: US-09-016-061-94
Perfect score: 55
Sequence: 1 ARNHGGSFAS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SPTREMBL_12.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	37	67.3	731	2	Q59369	Q59369 escherichia
2	36	65.5	89	7	O19495	O19495 gallus gall
3	36	65.5	360	3	Q05791	Q05791 saccharomyc
4	36	65.5	470	2	Q9ZCT8	Q9ZCT8 rickettsia
5	35	63.6	272	5	Q24950	Q24950 fasciola he
6	35	63.6	272	5	Q24951	Q24951 fasciola he
7	35	63.6	446	5	O62086	O62086 caenorhabdi
8	35	63.6	538	5	Q21726	Q21726 caenorhabdi
9	35	63.6	567	13	Q9YH26	Q9YH26 xenopus lae
10	35	63.6	615	11	O63614	O63614 rattus norv
11	35	63.6	1291	5	O77261	O77261 drosophila
12	34	61.8	39	7	P79474	P79474 cervus elap
13	34	61.8	39	7	P79477	P79477 cervus elap
14	34	61.8	39	7	P79478	P79478 cervus elap
15	34	61.8	39	7	P79479	P79479 cervus elap
16	34	61.8	82	7	Q30606	Q30606 macaca mula
17	34	61.8	82	7	Q30608	Q30608 macaca mula
18	34	61.8	82	7	Q30637	Q30637 macaca mula
19	34	61.8	82	7	Q30638	Q30638 macaca mula
20	34	61.8	82	7	Q30658	Q30658 macaca mula

21	34	61.8	82	7	Q30659	Q30659 macaca mula
22	34	61.8	82	7	Q30666	Q30666 macaca mula
23	34	61.8	82	7	Q30667	Q30667 macaca mula
24	34	61.8	82	7	Q30668	Q30668 macaca mula
25	34	61.8	82	7	O19287	O19287 macaca mula
26	34	61.8	82	7	O19288	O19288 macaca mula
27	34	61.8	83	7	O98002	O98002 ovis aries
28	34	61.8	85	7	Q30796	Q30796 ovis aries
29	34	61.8	85	7	Q30800	Q30800 ovis aries
30	34	61.8	85	7	Q30803	Q30803 ovis aries
31	34	61.8	85	7	Q30812	Q30812 ovis aries
32	34	61.8	85	7	P79966	P79966 capra aegag
33	34	61.8	85	7	P79967	P79967 capra aegag
34	34	61.8	85	7	P79968	P79968 capra aegag
35	34	61.8	86	7	Q30326	Q30326 bos taurus
36	34	61.8	89	7	O19210	O19210 capra hircu
37	34	61.8	89	7	O19212	O19212 capra hircu
38	34	61.8	89	7	Q30521	Q30521 galago sene
39	34	61.8	89	7	Q30522	Q30522 galago sene
40	34	61.8	89	7	Q30526	Q30526 galago sene
41	34	61.8	89	7	Q30217	Q30217 homo sapien
42	34	61.8	107	7	Q9XRM7	Q9XRM7 phasianus c
43	34	61.8	127	2	Q51713	Q51713 paracoccus
44	34	61.8	225	7	Q30844	Q30844 ovis aries
45	34	61.8	232	7	Q9XRM6	Q9XRM6 phasianus c

ALIGNMENTS

RESULT 1
Q59369 PRELIMINARY; PRT; 731 AA.
ID Q59369
AC Q59369;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE HISTIDINE RICH P TYPE ATPASE.
GN HRA-1.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 95110304.
RA TRENOR C.C., LIN W., ANDREWS N.C.;
RT "Novel bacterial p-type ATPases with histidine-rich heavy-metal-
associated sequences.";
RL Biochem Biophys Res Commun. 205:1644-1650(1994).
DR EMBL; U16658; AAA62113.1; .
DR PROSITE; PS00154; ATPASE_E1_E2; 1.
DR PFAW; PF00122; E1-E2_ATPase; 1.
KW Hydrolase; Transmembrane; Phosphorylation; ATP-binding.
FT MOD_RES 431 431 PHOSPHORYLATION (PROBABLE).
SQ SEQUENCE 731 AA; 78453 MW; 6765E988 CRC32;

Query Match 67.3%; Score 37; DB 2; Length 731;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGGSF 8
+ + + + +
Db 88 AHHHGGSF 95

RESULT 2
O19495 PRELIMINARY; PRT; 89 AA.
ID O19495
AC O19495;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)

DE MHC CLASS II BETA 1 DOMAIN (FRAGMENT).
GN B-LBI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=15.151-5; TISSUE=BURSA;
RA PHARR G.T., DODGSON J.B., HUNT H.D., BACON L.D.;
RL Immunogenetics 47:350-354(1998).
DR ENBL; U91532; AAC15813.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 89 89
SQ SEQUENCE 89 AA; 10724 MW; FDAC6024 CRC32;

Query Match 65.5%; Score 36; DB 7; Length 89;
Best Local Similarity 66.7%; Pred. No. 6.1;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFAS 10
DB 75 RHNYGDFES 83

RESULT 3
Q05791 PRELIMINARY; PRT; 360 AA.
AC Q05791;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE CHROMOSOME XII COSMID 8167.
GN L8167.23.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Hemiascomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RX MEDLINE: 97313267.
RA JOHNSTON M., HILLIER L., RILES L., ALBERMANN K., ANDRE B., ANSORGE W.,
RA BENES V., BRUCKNER M., DELIUS H., DUBOIS E., DUSTERHOFT A.,
RA ENTIAN K.D., FLOETH M., GOFFEAU A., HEBLING U., HEUMANN K.,
RA HEUSS-NEITZEL D., HILBERT H., HILGER F., KLEINE K., KOTTER P.,
RA LOUIS E.J., MESSENGUY F., MEWES H.W., MOSGA T., MOSTL D.,
RA MULLER-AUER S., NENTWICH U., OBERMAYER B., PIRAVANDI E., POHL T.M.,
RA PORTELE D., PURNELLE B., RECHMANN S., RIEGER M., RINKE M., ROSE M.,
RA SCHARFE M., SCHERENS B., SCHOLLER P., SCHWAGER C., SCHWARZ S.,
RA UNDERWOOD A.P., URRESTARAZU L.A., VANDENBOL M., VERHASSELT P.,
RA VIERENDELS F., VOET M., VOLCKAERT G., VOSS H., WAMBUIT R., WEDLER E.,
RA WEDLER H., ZIMMERMANN F.K., ZOLLNER A., HANI J., HOEISEL J.D.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
RL Nature 387:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RA PAULEY A.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RA WATERSTON R.;
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C (AB972);
RA CHERRY J.M.;
RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
DR ENBL; U14913; AAB67444.1; -.
SQ SEQUENCE 360 AA; 41852 MW; BD12B14E CRC32;

Query Match 65.5%; Score 36; DB 3; Length 360;
Best Local Similarity 77.8%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFAS 10
DB 304 RHNGRFAS 312

RESULT 4
Q9ZCT8 PRELIMINARY; PRT; 470 AA.
AC Q9ZCT8;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE (GLTX2).
GN RP623.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E;
RX MEDLINE: 99039499.
RA ANDERSSON S.G.E., ZOMORODIPOUR A., ANDERSSON J.O.,
RA SIKERITZ-PONTEN T., ALSMARK U.C.M., PODOWSKI R.M., NAESLUND A.K.,
RA ERIKSSON A.S., WINKLER H.H., KURLAND C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria.";
RL Nature 396:133-140(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E;
RA ANDERSSON S.G.E.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
DR ENBL; AJ235272; CAA15066.1; -.
DR HSP; P27000; IGLN.
SQ SEQUENCE 470 AA; 53696 MW; A0660D82 CRC32;

Query Match 65.5%; Score 36; DB 2; Length 470;
Best Local Similarity 75.0%; Pred. No. 30;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGFSF 8
DB 31 ARHNGKF 38

RESULT 5
Q24950 PRELIMINARY; PRT; 272 AA.
AC Q24950;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE VITELLINE PROTEIN B1 PRECURSOR.
OS Fasciola hepatica (Liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Echinostomida; Echinostomatidae; Echinostomata; Fasciolidae;
OC Fasciolidae; Fasciola.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 93063029.
RA RICE-FICHT A.C., DUSEK K.A., KOCHVAR G.J., WAITE J.H.;
RT "Eggsheil precursor proteins of Fasciola hepatica, I. Structure and
RT expression of vitelline protein B.";
RL Mol. Biochem. Parasitol. 54:129-141(1992).
DR ENBL; M93024; AAA29143.1; -.
KW Signal.

FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 272 VITELLINE PROTEIN B1.
 SQ SEQUENCE 272 AA; 31211 MW; 892E4D3A CRC32;

Query Match 63.6%; Score 35; DB 5; Length 272;
 Best Local Similarity 75.0%; Pred. No. 28;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARNHGSPF 8

Db 19 ARHPGKPF 26

RESULT 6

ID Q24951 PRELIMINARY; PRT; 272 AA.

AC Q24951;

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)

DE VITELLINE PROTEIN B2 PRECURSOR.

OS Fasciola hepatica (Liver fluke).

OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;

OC Echinostomida; Echinostomatidae; Echinostomata; Fasciolidae;

OC Fasciolidae; Fasciola.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE; 93063029.

RA RICE-FICHT A.C., DUSEK K.A., KOCHVAR G.J., WAITE J.H.;

RT "Eggshell precursor proteins of Fasciola hepatica, I. Structure and

expression of vitelline protein B.";

RL Mol. Biochem. Parasitol. 54:129-141(1992).

DR EMBL; M93025; AAA29144.1; -.

KW Signal.

FT SIGNAL 1 19 POTENTIAL.

FT CHAIN 20 272 VITELLINE PROTEIN B2.

SQ SEQUENCE 272 AA; 31418 MW; EBAF123F CRC32;

Query Match 63.6%; Score 35; DB 5; Length 272;

Best Local Similarity 75.0%; Pred. No. 28;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARNHGSPF 8

Db 19 ARHPGKPF 26

RESULT 7

ID O62086 PRELIMINARY; PRT; 446 AA.

AC O62086;

DT 01-AUG-1998 (TREMBlrel. 07, Created)

DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)

DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)

DE C31H5.6 PROTEIN.

GN C31H5.6.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;

OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

RN [1]

RP SEQUENCE FROM N.A.

RA KERSHAW J.;

RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE; 94150718.

RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,

RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P., III of C.
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL Nature 368:32-38(1994).
 DR EMBL; Z93778; CAB07846.1; -.
 SQ SEQUENCE 446 AA; 50763 MW; B347C0C8 CRC32;

Query Match 63.6%; Score 35; DB 5; Length 446;

Best Local Similarity 66.7%; Pred. No. 45;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNHGSPFAS 10

Db 51 RHNHGSHAA 59

RESULT 8

ID Q21726 PRELIMINARY; PRT; 538 AA.

AC Q21726;

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)

DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)

DE COSMID R04E5.

GN R04E5.2.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;

OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN-BRISTOL N2;

RX MEDLINE; 94150718.

RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M., COULSON A.,

RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., FULTON L.,

RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,

RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,

RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,

RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,

RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,

RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,

RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,

RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P., III of C.
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL Nature 368:32-38(1994).
 RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;

RA MILLER N.;

RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; U41538; AAC48179.1; -.

DR PFAM; PF01595; DUF21; 1.

SQ SEQUENCE 538 AA; 60480 MW; DE87F3F7 CRC32;

Query Match 63.6%; Score 35; DB 5; Length 538;

Best Local Similarity 62.5%; Pred. No. 53;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNHGSPFAS 9

Db 434 KHHGKFA 441

RESULT 9

Q9YH26

ID Q9YH26 PRELIMINARY;

PRT; 567 AA.

AC Q9YH26;

DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE CDC45.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
 OC Batrachia; Anura; Mesobatrachia; Pipidae; Xenopodinae;
 OC Xenopus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 98429493.
 RA MIKURA S., TAKISAWA H.;
 RT "Xenopus Cdc45-dependent loading of DNA polymerase alpha onto
 RT chromatin under the control of S-phase Cdk.";
 RL EMBO J. 17:5699-5707(1998).
 DR EMBL; AF062494; AAC67520.1; -.
 SQ SEQUENCE 567 AA; 65444 MW; F4A7D874 CRC32;

Query Match 63.6%; Score 35; DB 13; Length 567;
 Best Local Similarity 71.4%; Pred. No. 56;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGS 7
 :|||||
 Db 251 SRNHGN 257

RESULT 10
 Q63614
 ID Q63614 PRELIMINARY; PRT; 615 AA.
 AC Q63614;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE TYROSINE KINASE RECEPTOR (FRAGMENT).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=SPLEEN;
 RX MEDLINE; 94043123.
 RA BENHAMOU M., RYBA N.J.P., NISHIKATA H., KIHARA H., SIRAGANIAN R.P.;
 RT "Protein-tyrosine kinase p72syk in high affinity IgE receptor
 RT signaling. Identification as a component of pp72 and association with
 RT the receptor gamma chain after receptor aggregation.";
 RL J. Biol. Chem. 268:23318-23324(1993).
 DR EMBL; L20838; AAA42308.1; -.
 DR HSP; P43405; IAB1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
 DR PFAM; PF00069; pkinase; 1.
 DR PFAM; PF00017; SH2; 2.
 FT NON_TER 1
 FT NON_TER 615 615
 SQ SEQUENCE 615 AA; 70008 MW; 4BDFD84 CRC32;

Query Match 63.6%; Score 35; DB 11; Length 615;
 Best Local Similarity 77.8%; Pred. No. 61;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSFA 9
 |||:||||
 Db 181 ARDNNGSFA 189

RESULT 11
 O77261
 ID O77261 PRELIMINARY; PRT; 1291 AA.
 AC O77261;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE EG:115C2.10 PROTEIN.
 GN EG:115C2.10.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA CATHERINE SALLES, PHILIPPE VALENTI, ARETI DARLAMITSOU,
 RA NADINE HENDERSON, LORNA CAMPBELL, DAVID GLOVER;
 RT "Sequencing the distal x chromosome of Drosophila melanogaster.";
 RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA BENOS P.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL031581; CAA20894.2; -.
 SQ SEQUENCE 1291 AA; 137366 MW; 5ABE146F CRC32;

Query Match 63.6%; Score 35; DB 5; Length 1291;
 Best Local Similarity 75.0%; Pred. No. 1.2e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNHGSFAS 10
 |||||
 Db 554 HNHGQHAS 561

RESULT 12
 P79474
 ID P79474 PRELIMINARY; PRT; 39 AA.
 AC P79474;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervidae; Cervinae; Cervus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SWARBRICK P.A., CRAWFORD A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U63077; AAB37777.1; -.
 KW MHC.
 FT NON_TER 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4767 MW; E01AA287 CRC32;

Query Match 61.8%; Score 34; DB 7; Length 39;
 Best Local Similarity 66.7%; Pred. No. 6.5;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNHGSFAS 10
 |||||
 Db 25 RHNYGVFES 33

RESULT 13
 P79477
 ID P79477 PRELIMINARY; PRT; 39 AA.
 AC P79477;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
 OC Cervinae; Cervus.

RN [1]

RP SEQUENCE FROM N.A.

RA SWARBRICK P.A., CRAWFORD A.M.;

RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U63080; AAB37780.1; -

KW MHC.

FT NON_TER 1 1

FT NON_TER 39 39

SQ SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match

Best Local Similarity 61.8%; Score 34; DB 7; Length 39;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFAS 10

|||||

Db 25 RHNYGVFES 33

RESULT 14

P79478

ID P79478 PRELIMINARY; PRT; 39 AA.

AC P79478;

DT 01-MAY-1997 (TRENBLrel. 03, Created)

DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)

DT 01-AUG-1998 (TRENBLrel. 07, Last annotation update)

DE MHC CLASS II DRB (FRAGMENT).

OS Cervus elaphus (Red deer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;

OC Cervinae; Cervus.

RN [1]

RP SEQUENCE FROM N.A.

RA SWARBRICK P.A., CRAWFORD A.M.;

RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U63081; AAB37781.1; -

KW MHC.

FT NON_TER 1 1

FT NON_TER 39 39

SQ SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match

Best Local Similarity 61.8%; Score 34; DB 7; Length 39;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFAS 10

|||||

Db 25 RHNYGVFES 33

RESULT 15

P79479

ID P79479 PRELIMINARY; PRT; 39 AA.

AC P79479;

DT 01-MAY-1997 (TRENBLrel. 03, Created)

DT 01-MAY-1997 (TRENBLrel. 03, Last sequence update)

DT 01-AUG-1998 (TRENBLrel. 07, Last annotation update)

DE MHC CLASS II DRB (FRAGMENT).

OS Cervus elaphus (Red deer).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;

OC Cervinae; Cervus.

RN [1]

RP SEQUENCE FROM N.A.

RA SWARBRICK P.A., CRAWFORD A.M.;

RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U63082; AAB37782.1; -

KW MHC.

FT NON_TER 1 1

FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match 61.8%; Score 34; DB 7; Length 39;
 Best Local Similarity 66.7%; Pred. No. 6.5;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFAS 10

|||||

Db 25 RHNYGVFES 33

Search completed: May 27, 2000, 19:55:21

Job time: 985 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:21:44 ; Search time 31.68 Seconds
(without alignments)
7.477 Million cell updates/sec

Title: US-09-016-061-94
Perfect score: 55
Sequence: 1 ARHHNGSPAS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	55	100.0	10	1 W76037	LM609 grafted anti
2	51	92.7	10	1 W76020	LM609 grafted anti
3	49	89.1	10	1 W76038	LM609 grafted anti
4	49	89.1	10	1 W76024	LM609 grafted anti
5	46	83.6	10	1 W76025	LM609 grafted anti
6	46	83.6	10	1 W76030	LM609 grafted anti
7	45	81.8	10	1 W76026	LM609 grafted anti
8	45	81.8	10	1 W76027	LM609 grafted anti
9	45	81.8	10	1 W76028	LM609 grafted anti
10	45	81.8	10	1 W76029	LM609 grafted anti
11	45	81.8	10	1 W76010	LM609 grafted anti
12	45	81.8	117	1 W76001	Vitaxin antibody h
13	45	81.8	117	1 W76003	LM609 antibody hea
14	43	78.2	10	1 W76040	LM609 grafted anti
15	42	76.4	10	1 W76021	LM609 grafted anti
16	41	74.5	10	1 W76039	LM609 grafted anti
17	41	74.5	10	1 W76022	LM609 grafted anti
18	41	74.5	10	1 W76023	LM609 grafted anti
19	37	67.3	110	1 W84099	Vitronectin alpha-
20	37	67.3	117	1 W84093	Murine vitronectin
21	37	67.3	117	1 W84097	Humanised anti-arp
22	34	61.8	204	1 W59609	DNA-binding/dimeri
23	34	61.8	358	1 W98649	H. pylori GHPO 403
24	33	60.0	2109	1 W04540	Vesiculovirus larg
25	32	58.2	120	1 R48621	Sequence of the hu
26	32	58.2	121	1 R65173	Region for produci
27	32	58.2	218	1 R94178	Human 35 kDa opson
28	32	58.2	288	1 R94179	Human 35 kDa opson
29	32	58.2	313	1 R94183	Human 35 kDa opson
30	32	58.2	384	1 W14787	FKBP-SYK:SH2 fusio
31	32	58.2	384	1 W96822	A fusion protein o
32	32	58.2	415	1 W33692	Treponema pallidum
33	32	58.2	415	1 W59930	Modified T. pallid
34	32	58.2	415	1 W68498	Treponema pallidum

35 32 58.2 434 1 W59934 Wild type T. palli
36 32 58.2 443 1 R58637 Treponema pallidum
37 32 58.2 443 1 W35744 Treponema pallidum
38 32 58.2 456 1 W33693 Nucleic acid-bound
39 32 58.2 466 1 W22467 Staphylococcus aur
40 32 58.2 466 1 W58529 Staphylococcus aur
41 32 58.2 489 1 W01556 Actavinone C-II hy
42 32 58.2 551 1 W59933 Modified T. pallid
43 32 58.2 612 1 W09321 Human mast cell-de
44 32 58.2 630 1 R62688 Tyrosine-kinase Sy
45 32 58.2 630 1 R64978 Human Syk. Chimeri

ALIGNMENTS

RESULT 1

W76037
ID W76037 standard; Protein; 10 AA.
AC W76037;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #13.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
macular degeneration; osteoporosis; primer; V-H region; CDR;
complementarity determining region.
OS Mus sp.
FN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49874.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
integrin - and related grafted antibodies based on murine monoclonal
LM609, also related nucleic acid, used to treat, prevent or diagnose
angiogenesis or restenosis
Claim 62; Page 43; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
LM609 heavy and light chain variable region. LM609 and the antibody
vitaxin bind selectively to integrin alphavbeta3 and can be used to
inhibit binding of alphavbeta3 to a ligand and thus block
integrin-mediated signal transduction. This is useful in the treatment,
prevention and diagnosis of alphavbeta3-mediated disease, specifically
angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
arthritis, macular degeneration, osteoporosis etc.). The antibodies
contain non-murine framework regions so are suitable for use in humans.
Enhanced types of LM609 have affinity more than 90 times greater than
that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 100.0%; Score 55; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00022;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ARHHNGSPAS 10
| | | | | | | | | |
Db 1 ARHHNGSPAS 10

RESULT 2

W76020
ID W76020 standard; Protein; 10 AA.
AC W76020;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #2.
KW Vitaxin; antibody; variable region; heavy chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49857.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 92.7%; Score 51; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0012;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHHNGSFA 9
 |||||
 DB 1 ARHHNGSFA 9

RESULT 3
 W76038
 ID W76038 standard; Protein; 10 AA.

DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #14.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

OS Mus sp.
 PN WO9833919-A2.

PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.

PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.

DR N-PSDB; V49875.

PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

PS Claim 62; Page 43; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 89.1%; Score 49; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0027;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHHNGSFAS 10
 |||||
 DB 1 ARHHNGSFYS 10

RESULT 4

W76024
 ID W76024 standard; Protein; 10 AA.

AC W76024;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #6.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.

OS Mus sp
 PN WO9833919-A2.

PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.

PR 30-JAN-1997; US-791391.

PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;

DR WPI; 98-437472/37.

DR N-PSDB; V49861.

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis

PS Claim 62; Page 41; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 89.1%; Score 49; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0027;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHHNGSFAS 10
 |||||
 DB 1 ARHHNGSFAS 10

RESULT 5

W76025
 ID W76025 standard; Protein; 10 AA.

W76025;
 CC 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #7.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49862.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 CC Sequence 10 AA;
 SQ

Query Match 83.6%; Score 46; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.0094;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARNHGSPAS 10
 ||||:||||:
 Db 1 ARHNYGSFAA 10

RESULT 6
 W76030
 ID W76030 standard; Protein; 10 AA.
 AC W76030;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #12.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49863.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 CC Sequence 10 AA;
 SQ

Query Match 83.6%; Score 46; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.0094;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARNHGSPAS 10
 ||||:||||:
 Db 1 ARHNYGSFAT 10

RESULT 6
 W76030
 ID W76030 standard; Protein; 10 AA.
 AC W76030;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #12.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49867.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 CC Sequence 10 AA;
 SQ

Query Match 83.6%; Score 46; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.0094;
 Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARNHGSPAS 10
 ||||:||||:
 Db 1 ARHNYGSFAA 10

RESULT 7
 W76026
 ID W76026 standard; Protein; 10 AA.
 AC W76026;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #8.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49863.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 CC Sequence 10 AA;
 SQ

Query Match 81.8%; Score 45; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 0.014;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARNHGSPA 9
 ||||:||||:
 Db 1 ARHNYGSFA 9

```

RESULT 8
W76027
ID W76027 standard; Protein; 10 AA.
AC W76027;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #9.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49864.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 81.8%; Score 45; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.014;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSGFA 9
   ||||:||||
DB 1 ARHNYGSGFA 9

RESULT 10
W76029
ID W76029 standard; Protein; 10 AA.
AC W76029;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #11.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49866.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 81.8%; Score 45; DB 1; Length 10;
Best Local Similarity 88.9%; Pred. No. 0.014;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSGFA 9
   ||||:||||
DB 1 ARHNYGSGFA 9

RESULT 9
W76028
ID W76028 standard; Protein; 10 AA.
AC W76028;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #10.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49865.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

```

QY 1 ARNHGSFA 9
WPI; 98-437472/37.
N-PSDB; V49820.

DR Humanised antibody, Vitaxin, that binds selectively to alphavbeta3 integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose angiogenesis or restenosis

PT Claim 1; Fig 1a; 129pp; English.

PS This sequence represents a fragment of the vitaxin antibody variable heavy chain region. Vitaxin and the antibody LM609 bind selectively to integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.

SQ Sequence 117 AA;

Query Match 81.8%; Score 45; DB 1; Length 117;
Best Local Similarity 88.9%; Pred. No. 0.19;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0

Qy 1 ARNHGSFA 9
|||||
Db 97 ARHNYGSA 105

RESULT 13

W76003 ID W76003 standard; Protein; 117 AA.

AC W76003; 02-NOV-1998 (first entry)

DE LM609 antibody heavy chain variable region protein fragment.

KW Vitaxin; antibody; variable region; heavy chain; light chain; Integrin; LM609; inhibitor; integrin-mediated signal transduction; treatment; diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis.

KW Mus sp.

OS WO9833919-A2.

PN 06-AUG-1998.

PD 30-JAN-1998; U01826.

PF 30-JAN-1997; US-791391.

PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

PI WPI; 98-437472/37.

N-PSDB; V49822.

DR Humanised antibody, Vitaxin, that binds selectively to alphavbeta3 integrin - and related grafted antibodies based on murine monoclonal LM609, also related nucleic acid, used to treat, prevent or diagnose angiogenesis or restenosis

PT Claim 43; Fig 2a; 129pp; English.

PS This sequence represents the LM609 antibody variable heavy chain region. LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3 to a ligand and thus block integrin-mediated signal transduction. This is useful in the treatment, prevention and diagnosis of alphavbeta3-mediated disease, specifically angiogenesis and restenosis (but also e.g. (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis etc.). The antibodies contain non-murine framework regions so are suitable for use in humans. Enhanced types of LM609 have affinity more than 90 times greater than that of parent the parent antibody.

SQ Sequence 117 AA;

Query Match 81.8%; Score 45; DB 1; Length 117;
Best Local Similarity 88.9%; Pred. No. 0.19;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0

Qy 1 ARNHGSFA 9
|||||
Db 1 ARHNYGSA 9

RESULT 12

W76001 ID W76001 standard; Protein; 117 AA.

AC W76001; 02-NOV-1998 (first entry)

DE Vitaxin antibody heavy chain variable region protein fragment.

KW Vitaxin; antibody; variable region; heavy chain; light chain; Integrin; LM609; inhibitor; integrin-mediated signal transduction; treatment; diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy; neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine; macular degeneration; osteoporosis.

KW Mus sp.

OS WO9833919-A2.

PN 06-AUG-1998.

PD 30-JAN-1998; U01826.

PF 30-JAN-1997; US-791391.

PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

QY 1 ARNHGSFA 9
 DB 1 ARHNYGSFA 9

RESULT 11

W76010
 ID W76010 standard; Protein; 10 AA.
 AC W76010;
 DE 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #1.
 DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 PI WPI: 98-437472/37.
 DR N-PSDB; V49847.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 1; Fig 1a; 129pp; English.
 CC This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 SQ Sequence 117 AA;

Query Match 81.8%; Score 45; DB 1; Length 117;
 Best Local Similarity 88.9%; Pred. No. 0.19;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 ARNHGSFA 9
 DB 97 ARHNYGSFA 105

RESULT 13

W76003
 ID W76003 standard; Protein; 117 AA.
 AC W76003;
 DE 02-NOV-1998 (first entry)
 DE LM609 antibody heavy chain variable region protein fragment.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 PI WPI: 98-437472/37.
 DR N-PSDB; V49822.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 43; Fig 2a; 129pp; English.
 CC This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 SQ Sequence 117 AA;

Query Match 81.8%; Score 45; DB 1; Length 117;
 Best Local Similarity 88.9%; Pred. No. 0.19;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 1 ARNHGSFA 9
 DB 1 ARHNYGSFA 9

RESULT 12

W76001
 ID W76001 standard; Protein; 117 AA.
 AC W76001;
 DE 02-NOV-1998 (first entry)
 DE Vitaxin antibody heavy chain variable region protein fragment.
 DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;

Query Match 81.8%; Score 45; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 0.014;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSFA 9
 DB 1 ARHNYGSFA 9

RESULT 12

W76001
 ID W76001 standard; Protein; 117 AA.
 AC W76001;
 DE 02-NOV-1998 (first entry)
 DE Vitaxin antibody heavy chain variable region protein fragment.
 DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;

Query Match 81.8%; Score 45; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 0.014;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSFA 9
 DB 1 ARHNYGSFA 9

RESULT 12

W76001
 ID W76001 standard; Protein; 117 AA.
 AC W76001;
 DE 02-NOV-1998 (first entry)
 DE Vitaxin antibody heavy chain variable region protein fragment.
 DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;

Query Match 81.8%; Score 45; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 0.014;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ARNHGSA 9
DB 97 ARNHGSA 105

RESULT 14
W76040
ID W76040 standard; Protein; 10 AA.
AC W76040;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #16.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
PT N-PSDB; V49877.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related nucleic acid, used to treat, prevent or diagnose
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PS Claim 62; Page 43; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 76.4%; Score 42; DB 1; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.05;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSA 9
DB 1 ARNHGSA 9

Search completed: May 27, 2000, 19:50:46
Job time: 1742 sec

QY 1 ARNHGSA 9
DB 97 ARNHGSA 105

RESULT 15
W76021
ID W76021 standard; Protein; 10 AA.
AC W76021;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #3.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
PT N-PSDB; V49877.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related nucleic acid, used to treat, prevent or diagnose
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PS Claim 62; Page 43; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 78.2%; Score 43; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.033;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSA 10
DB 1 ARNHGSA 10

RESULT 15
W76021
ID W76021 standard; Protein; 10 AA.
AC W76021;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #3.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
PT N-PSDB; V49877.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related nucleic acid, used to treat, prevent or diagnose
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PS Claim 62; Page 43; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 76.4%; Score 42; DB 1; Length 10;
Best Local Similarity 77.8%; Pred. No. 0.05;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSA 9
DB 1 ARNHGSA 9

Search completed: May 27, 2000, 19:50:46
Job time: 1742 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:52:02 ; Search time 29.7 Seconds
(without alignments)
19.741 Million cell updates/sec

Title: US-09-016-061-96

Perfect score: 58

Sequence: 1 ARHNGSFYS 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

PIR_53:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	40	69.0	555	2 T21028	hypothetical prote
2	39	67.2	350	2 S76212	hypothetical prote
3	39	67.2	470	2 H71667	glutamate--trNA li
4	38	65.5	196	2 H64968	acetyl CoA acetyl
5	38	65.5	722	2 S64492	hypothetical prote
6	37	63.8	530	2 T01030	hypothetical prote
7	37	63.8	731	1 JC2464	probable copper-tr
8	36	62.1	275	2 S75190	hypothetical prote
9	36	62.1	473	2 D70405	glutamate--trNA li
10	36	62.1	548	1 B44511	fumarate hydratase
11	35	60.3	108	2 C72852	AcOrf-19 protein -
12	35	60.3	108	2 D44221	orf4 protein - Aut
13	35	60.3	110	2 T41765	AcMNPV orf19 - Bom
14	35	60.3	113	2 S26468	Ig heavy chain V I
15	35	60.3	272	2 S27819	vitelline B1 precu
16	35	60.3	272	2 S27820	vitelline B2 precu
17	35	60.3	349	2 S15011	mbhl protein - mou
18	35	60.3	352	1 A39834	actin-capping prot
19	35	60.3	448	1 A60003	nucleocapsid prote
20	35	60.3	543	2 T27190	hypothetical prote
21	35	60.3	552	2 T27191	hypothetical prote
22	35	60.3	659	2 S30859	hypothetical prote
23	35	60.3	1466	2 T31138	CL1AA protein - ra
24	35	60.3	1467	2 T18411	latrophilin-1, bra
25	35	60.3	1471	2 T17149	CL1BA protein - ra
26	35	60.3	1472	2 T18413	latrophilin-1, bra
27	35	60.3	1510	2 T17145	CL1AB protein - ra
28	35	60.3	1515	2 T17156	CL1BB protein - ra
29	35	60.3	2470	2 I50726	cation-independent
30	34	58.6	139	2 G29380	Ig heavy chain pre

31 34 58.6 140 2 I37782 Ig variable region
32 34 58.6 236 2 S16389 sporamin - sweet p
33 34 58.6 379 1 F64633 site-specific DNA-
34 34 58.6 381 2 A71882 type II DNA modifi
35 34 58.6 466 2 JC5897 killer cell inhibi
36 34 58.6 467 2 T40348 hypothetical prote
37 34 58.6 604 2 S05447 finger protein gla
38 34 58.6 813 2 A72203 cellobiose-phospho
39 34 58.6 1012 2 T23160 hypothetical prote
40 34 58.6 1446 1 A45344 immediate-early pr
41 34 58.6 1460 1 ED8E1F immediate-early pr
42 34 58.6 1615 2 B49502 protein-tyrosine-p
43 34 58.6 1767 2 A49502 protein-tyrosine-p
44 33 56.9 81 2 T15314 hypothetical prote
45 33 56.9 89 2 S38688 MHC class II histo

ALIGNMENTS

RESULT 1

T21028

hypothetical protein F16H6.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T21028

R:Matthews, L.

submitted to the EMBL Data Library, November 1996

A:Reference number: Z19362

A:Accession: T21028

A>Status: preliminary; translated from GB/EMBL/DDBB

A:Molecule type: DNA

A:Residues: 1-555 <WIL>

A:Cross-references: EMBL:Z01506; PIDN:CAB04128.1; GSPDB:GN00023; CESP:F16H6.1

A:Experimental source: clone F16H6

C:Genetics:

A:Gene: CESP:F16H6.1

A:Map position: 5

A:Introns: 123/1; 318/3

Query Match 69.0%; Score 40; DB 2; Length 555;
Best Local Similarity 87.5%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFYS 10

Db 314 HNHGSFYS 321

RESULT 2

S76212

hypothetical protein - Synechocystis sp. (strain PCC 6803)

C:Species: Synechocystis sp.

A:Variety: PCC 6803

C>Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999

C:Accession: S76212

R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Miyajima, Y.;

O. K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas

DNA Res. 3, 109-136, 1996

A>Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocys

s.

A:Reference number: S74322; MUID:97061201

A:Accession: S76212

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-350 <KAN>

A:Cross-references: EMBL:P90914; GB:AB001339; NID:g1653477; PIDN:BAA18471.1; PID:d101

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 67.2%; Score 39; DB 2; Length 350;

Best Local Similarity 71.4%; Pred. No. 11;

Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNHGSFY 9

Db 247 HNHGNTY 253
||||:|

RESULT 3

H71667
glutamate--tRNA ligase (EC 6.1.1.17) (gitX2) RP623 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C>Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 08-Oct-1999
C:Accession: H71667
R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, T.; Nare 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499
A:Accession: H71667

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-470 <AND>

A:Cross-references: GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAAL5066.1; PID:el34291
A:Experimental source: Strain Madrid E

C:Genetics:

A:Gene: gitX2; RP623

C:Superfamily: glutamate--tRNA ligase; glutamine--tRNA ligase homology
C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 67.2%; Score 39; DB 2; Length 470;

Best Local Similarity 66.7%; Pred. No. 15;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGSFY 9

Db 31 ARNHNGKF 39
||||:|

RESULT 4

H64968
acetyl CoA acetyltransferase - Escherichia coli
C:Species: Escherichia coli
C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 18-Jun-1999
C:Accession: H64968; I69646; I69656
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617

A:Accession: H64968

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-196 <BLAT>

A:Cross-references: GB:AE000294; GB:U00096; NID:g1788338; PIDN:AACT5094.1; PID:g1788345;
A:Experimental source: strain K-12, substrain MG1655

R:Yao, Z.; Valvano, M.A.

J. Bacteriol. 176, 4133-4143, 1994

A:Title: Genetic analysis of the O-specific lipopolysaccharide biosynthesis region (rfb)
erotypes Y and 4a.

A:Reference number: I55053; MUID:94292434

A:Accession: I69646

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-167, 'LFRKYCHC', 177-186, 'IMR', 190-196 <RES>

A:Cross-references: EMBL:U03041; NID:g501028; PIDN:AACT5094.1; PID:g510256

R:Stevenson, G.; Neal, B.; Liu, D.; Hobbs, M.; Packer, N.H.; Batley, M.; Redmond, J.W.;

J. Bacteriol. 176, 4144-4156, 1994

A:Title: Structure of the O antigen of Escherichia coli K-12 and the sequence of its rfb

A:Reference number: I55054; MUID:94292435

A:Accession: I69656

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-167, 'LFRKYCHC', 177-186, 'IMR', 190-196 <RE2>

A:Cross-references: EMBL:U09876; NID:g508236; PID:g508245
C:Genetics:

A:Gene: yefH

A:Map position: 45 min

C:Superfamily: galactoside acetyltransferase

Query Match 65.5%; Score 38; DB 2; Length 196;

Best Local Similarity 100.0%; Pred. No. 9.5;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNHGSF 8

Db 105 HNHGSF 110
|||||

RESULT 5

S64492

hypothetical protein YGR178c - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein G7139

C:Species: Saccharomyces cerevisiae

C>Date: 17-May-1996 #sequence_revision 17-May-1996 #text_change 29-Oct-1999

C:Accession: S64492

R:Hebling, U.; Hofmann, B.; Delius, H.

submitted to the Protein Sequence Database, May 1996

A:Reference number: S64003

A:Accession: S64492

A:Molecule type: DNA

A:Residues: 1-722 <HEB>

A:Cross-references: EMBL:Z72963; NID:g1323314; PIDN:CAA97204.1; PID:e243559; PID:g132

A:Experimental source: strain S288C

C:Genetics:

A:Gene: SGD:PBP1

A:Cross-references: SGD:S0003410; MIPS:YGR178c

A:Map position: 7R

Query Match 65.5%; Score 38; DB 2; Length 722;

Best Local Similarity 75.0%; Pred. No. 34;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNHGSFY 9

Db 474 RHNHGSFF 481
|||||

RESULT 6

T01030

hypothetical protein YUP8H12R.13 - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 22-Oct-1999

C:Accession: T01030

R:Theologis, A.; Vysotskaya, V.S.; Osborne, B.I.; Schwartz, J.R.; Federspiel, N.A.; K

Oefner, P.; Davis, R.W.

submitted to the EMBL Data Library, May 1998

A:Description: Arabidopsis thaliana chromosome 1 YAC YUP8H12R sequence.

A:Reference number: Z14227

A:Accession: T01030

A:Status: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-530 <THE>

A:Cross-references: EMBL:AC002986; NID:g2494106; PID:g3152559; GSPDB:GN00059; ATSP:YU

C:Genetics:

A:Gene: YUP8H12R.13

A:Map position: 1

A:Introns: 37/3; 77/1; 100/3; 219/3; 380/3; 451/3; 499/3

Query Match 63.8%; Score 37; DB 2; Length 530;

Best Local Similarity 62.5%; Pred. No. 38;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFYS 10

Db 192 HNHNNYS 199
||| :||
RESULT 7
JC2464
Probable copper-transporting ATPase (EC 3.6.1.-) HRA-1 - Enterobacteriaceae spp.
C:Species: Enterobacteriaceae spp.
C:Date: 16-Oct-1998 #sequence_revision 16-Oct-1998 #text_change 18-Jun-1999
C:Accession: JC2464
R:Trenor III., C.; Lin, W.; Andrews, N.C.
Biochem. Biophys. Res. Commun. 205, 1644-1650, 1994
A:Title: Novel bacterial P-type ATPases with histidine-rich heavy-metal-associated sequence
A:Reference number: JC2464; MUID:95110304
A:Accession: JC2464
A:Molecule type: mRNA
A:Residues: 1-731 <TRE>
A:Cross-references: GB:U16658; NID:643612; PIDN:AA62113.1; PID:643613
A:Experimental source: human small intestine cDNA library
A:Note: the source species is uncertain; the cloned sequence did not hybridize with human
C:Superfamily: Enterococcus copper-transporting ATPase copB; ATPase nucleotide-binding
C:Keywords: ATP; copper transport; hydrolase; ion transport; phosphoprotein; transmembrane
F:7-92/Region: His-rich
F:135-477/Domain: ATPase transduction domain homology <ATT>
F:544-685/Domain: ATPase nucleotide-binding domain homology <ATN>
F:287/Active site: Glu #status predicted
F:431/Active site: Asp (aspartylphosphate intermediate) #status predicted

Query Match 63.8%; Score 37; DB 1; Length 731;
Best Local Similarity 75.0%; Pred. No. 52;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ARNHGSGF 8
| | :|||
Db 88 AHHHGSF 95

RESULT 8
S75190
Hypothetical protein slr2042 - Synecchocystis sp. (strain PCC 6803)
C:Species: Synecchocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S75190
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecchocystis
S.
A:Reference number: S74322; MUID:97061201
A:Accession: S75190
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-275 <KAN>
A:Cross-references: EMBL:D90903; GB:AB001339; NID:q1652127; PIDN:BAAL17104.1; PID:d101783
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 62.1%; Score 36; DB 2; Length 275;
Best Local Similarity 62.5%; Pred. No. 30;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 RHNHGSFY 9
:||| |
Db 253 QHNGQLY 260

RESULT 9
D70405
glutamate--trRNA ligase (EC 6.1.1.17) - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999

C:Accession: D70405
R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666
C:Accession: D70405
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-473 <AQE>
A:Cross-references: GB:AE000729; NID:92983659; PIDN:AC07230.1; PID:g2983664; GB:AE00
A:Experimental source: strain VF5
C:Genetics:
A:Gene: gltX
C:Superfamily: glutamate--trRNA ligase; glutamine--trRNA ligase homology
C:Keywords: aminoacyl-trRNA synthetase; ligase; protein biosynthesis

Query Match 62.1%; Score 36; DB 2; Length 473;
Best Local Similarity 75.0%; Pred. No. 51;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 ARNHGSGF 8
| | :|||
Db 31 ARHNGGF 38

RESULT 10
B44511
fumarate hydratase (EC 4.2.1.2) fumb, iron-dependent - Escherichia coli
N:Alternate names: fumarase B
C:Species: Escherichia coli
C:Date: 03-Mar-1993 #sequence_revision 10-Oct-1997 #text_change 18-Jun-1999
C:Accession: A65222; B44511; S56351
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.;
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: A65222
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-548 <BLAT>
A:Cross-references: GB:AE000485; GB:U00096; NID:q1790563; PIDN:AACT7083.1; PID:gl7905
A:Experimental source: strain K-12, substrain MG1655
R:Bell, P.J.; Andrews, S.C.; Sivak, M.N.; Guest, J.R.
J. Bacteriol. 171, 3494-3503, 1989
A:Title: Nucleotide sequence of the FNR-regulated fumarase gene (fumb) of Escherichia
A:Reference number: A44511; MUID:89255123
A:Accession: B44511
A:Molecule type: DNA
A:Residues: 1-49, 'V', 51-548 <BEL>
A:Cross-references: EMBL:M27058; NID:q146046; PIDN:AAA23827.1; PID:q146048
R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A:Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from
A:Reference number: S56314; MUID:95334362
A:Accession: S56351
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-49, 'X', 51-548 <BUR>
A:Cross-references: EMBL:U14003; NID:q1263172; PIDN:AAA97022.1; PID:g536967
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
C:Comment: In E. coli, three fumarate hydratase genes (fuma, fumb, and fumC) have bee
class I hydratase.
C:Genetics:
A:Gene: fumb
A:Map position: 93.5 min
A:Complex: homodimer
C:Function:
A:Description: catalyzes the stereospecific interconversion of fumarate and L-malate
A:Note: expressed at higher level under anaerobic conditions
C:Superfamily: iron-dependent fumarate hydratase; iron-dependent tartrate dehydratase

C:Keywords: 4Fe-4S; carbon-oxygen lyase; homodimer; hydro-lyase; iron-sulfur protein; md
 F:2-548/Product: fumarate hydratase fumb, iron-dependent #status predicted <WAT>
 F:93-300/Domain: iron-dependent tartrate dehydratase alpha chain homology <TTDA>
 F:373-537/Domain: iron-dependent tartrate dehydratase beta chain homology <TTDB>

Query Match 62.1%; Score 36; DB 1; Length 548;
 Best Local Similarity 66.7%; Pred. No. 59;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGGSFY 9
 | | | | |
 Db 473 ACHKHGGFY 481

RESULT 11

C72852
 AcOrf-19 protein - Autographa californica nuclear polyhedrosis virus

C:Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
 A:Note: dsDNA virus

C:Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 12-Nov-1999
 C:Accession: C72852

R:Ayres, M.D.; Howard, S.C.; Kuzio, J.; Lopez-Ferber, M.; Possee, R.D.
 Virology 202, 586-605, 1994

A:Title: The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.
 A:Reference number: A72850; MUID:94303173

A:Accession: C72852

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-108 <AYR>

A:Cross-references: GB:L22858; NID:9510708; PIDN:AAA66649.1; PID:9559088

C:Genetics:

A:Gene: AcOrf-19

Query Match 60.3%; Score 35; DB 2; Length 108;
 Best Local Similarity 66.7%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGGSFY 9
 | | | | |
 Db 25 ANRNHSSFY 33

RESULT 12

D44221
 orf4 protein - Autographa californica nuclear polyhedrosis virus

C:Species: Autographa californica nuclear polyhedrosis virus, AcMNPV
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993

C:Accession: D44221

R:Braunagel, S.C.; Daniel, K.D.; Reilly, L.M.; Guarino, L.A.; Hong, T.; Summers, M.D.
 Virology 191, 1003-1008, 1992

A:Title: Sequence, genomic organization of the EcoRI-A fragment of Autographa californica
 VP8 of rotavirus.

A:Reference number: A44221; MUID:93079853

A:Accession: D44221

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-108 <BRA>

A:Cross-references: GB:S52569

Query Match 60.3%; Score 35; DB 2; Length 108;
 Best Local Similarity 66.7%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGGSFY 9
 | | | | |
 Db 25 ANRNHSSFY 33

RESULT 13

T41765

C:Keywords: 4Fe-4S; carbon-oxygen lyase; homodimer; hydro-lyase; iron-sulfur protein; md
 F:2-548/Product: fumarate hydratase fumb, iron-dependent #status predicted <WAT>
 F:93-300/Domain: iron-dependent tartrate dehydratase alpha chain homology <TTDA>
 F:373-537/Domain: iron-dependent tartrate dehydratase beta chain homology <TTDB>

Query Match 62.1%; Score 36; DB 1; Length 548;
 Best Local Similarity 66.7%; Pred. No. 59;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

AcMNPV orf19 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
 C:Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV
 A:Variety: isolate T3
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T41765

R:Gomi, S.; Majima, K.; Maeda, S.
 J. Gen. Virol. 80, 1323-1337, 1999

A:Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
 A:Reference number: 222020

A:Accession: T41765

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-110 <KAM>

A:Cross-references: EMBL:L33180; PIDN:AAC63694.1

A:Experimental source: isolate T3

C:Genetics:

A:Note: Orf_11

Query Match 60.3%; Score 35; DB 2; Length 110;
 Best Local Similarity 66.7%; Pred. No. 18;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGGSFY 9
 | | | | |
 Db 27 ANRNHSSFY 35

RESULT 14

S26468

Ig heavy chain V region - mouse

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999

C:Accession: S26468

R:Kavaler, J.
 submitted to the EMBL Data Library, April 1991

A:Reference number: S26459

A:Accession: S26468

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-113 <XAV>

A:Cross-references: EMBL:X59107; NID:951944; PIDN:CAA41833.1; PID:951945

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 60.3%; Score 35; DB 2; Length 113;
 Best Local Similarity 50.0%; Pred. No. 19;
 Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARNHGGSFY 10
 | | | | |
 Db 93 ARHPYGNYYA 102

RESULT 15

S27819

vitellogenin B1 precursor - liver fluke

N:Alternate names: eggshell protein B1

C:Species: Fasciola hepatica (liver fluke)

C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 15-Oct-1999

C:Accession: A48436; S27819

R:Rice-Ficht, A.C.; Dusek, K.A.; Kochevar, G.J.; Waite, J.H.
 Mol. Biochem. Parasitol. 54, 129-141, 1992

A:Title: Eggshell precursor proteins of Fasciola hepatica, I. Structure and expressio

A:Reference number: A48436; MUID:93063029

A:Accession: A48436

A:Molecule type: mRNA; protein

A:Residues: 1-272 <RI2>

A:Cross-references: EMBL:M93024; NID:q159065; PID:q159066

A:Note: sequence extracted from NCBI backbone (NCBIN:117208, NCBIIP:117210)

C:Keywords: egg shell

F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-272/Product: vitelline B1 #status predicted <MAT>

Query Match 60.3%; Score 35; DB 2; Length 272;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNHGSF 8
 | | | | |
Db 19 ARHPHGKF 26

Search completed: May 27, 2000, 19:52:03
Job time: 1506 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 20:45:28 ; Search time 48.34 Seconds
(without alignments)
6.300 Million cell updates/sec

Title: US-09-016-061-96
Perfect score: 58
Sequence: 1 ARNHGFSFY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	67.2	470	1 SYE2_RICPR	Q9ZCT8 rickettsia
2	38	65.5	196	1 WBBJ_ECOLI	P37750 escherichia
3	38	65.5	722	1 PBP1_YEAST	P53297 saccharomyc
4	36	62.1	275	1 YK42_SYNV3	P73079 synechocyst
5	36	62.1	473	1 SVE_AQUAE	O67271 aquifex aeo
6	36	62.1	548	1 FUMB_ECOLI	P14407 escherichia
7	35	60.3	108	1 Y019_NPVAC	P41424 autographa
8	35	60.3	197	1 EGG5_FASHE	P07915 fasciola he
9	35	60.3	218	1 Y4VH_RHISN	O53216 rhizobium s
10	35	60.3	352	1 CAPG_MOUSE	P24452 mus musculus
11	35	60.3	448	1 NCAP_CVHOC	P33469 human coron
12	35	60.3	567	1 CC45_XENLA	Q9YH26 xenopus lae
13	35	60.3	659	1 RA24_YEAST	P32641 saccharomyc
14	34	58.6	349	1 F16P_NOSPU	P48847 nostoc punc
15	34	58.6	435	1 PURA_SPICI	P52150 spiroplasma
16	34	58.6	604	1 GLAS_DROME	P13360 drosophila
17	34	58.6	718	1 LSP2_DROME	Q24388 drosophila
18	34	58.6	1446	1 IE18_PRVKA	P33479 pseudorabie
19	34	58.6	1461	1 IE18_PRVIF	P11675 pseudorabie
20	33	56.9	81	1 YWR4_CAEEL	Q10927 caenorhabdi
21	33	56.9	225	1 CD9_MOUSE	P02400 mus musculus
22	33	56.9	284	1 YNB9_YEAST	P53975 saccharomyc
23	33	56.9	284	1 YND3_YEAST	P53964 saccharomyc
24	33	56.9	322	1 FATB_VIBAN	P11460 vibrio angu
25	33	56.9	347	1 UL33_HSV6U	P52380 herpes simp
26	33	56.9	394	1 IPOU_DROME	P24350 drosophila
27	33	56.9	480	1 SVE_HAEIN	P43818 haemophilus
28	33	56.9	486	1 GATC_DROME	P91623 drosophila
29	33	56.9	502	1 KIR3_MOUSE	Q61288 mus musculus
30	33	56.9	503	1 KIR3_HUMAN	P37023 homo sapien
31	33	56.9	505	1 KIR3_RAT	P80203 rattus norv
32	33	56.9	596	1 GLMS_HELPY	O26060 h glucosami
33	33	56.9	692	1 ANO1_PICAN	P12807 pichia angu
34	33	56.9	767	1 AMDM_SCHPO	P50998 schizosacch

35	33	56.9	783	1 FAND_ECOLI	P12050 escherichia
36	33	56.9	798	1 YLFN_CAEEL	Q20296 caenorhabdi
37	33	56.9	966	1 M172_HUMAN	Q14596 homo sapien
38	33	56.9	1046	1 POL_FENV1	P31792 feline endo
39	33	56.9	1189	1 POL_BAEVM	P10272 baboon endo
40	32	55.2	117	1 GVPK_HALME	Q02236 halobacteri
41	32	55.2	129	1 YP36_MYCTU	Q50742 mycobacteri
42	32	55.2	166	1 YO21_BPHP1	P51723 bacterioph
43	32	55.2	174	1 YO30_BPHP1	P51734 bacterioph
44	32	55.2	190	1 SLVD_HAEIN	P44830 haemophilus
45	32	55.2	194	1 PTH_SALTI	Q60001 salmonella

ALIGNMENTS

```
RESULT 1
SYE2_RICPR
ID SYE2_RICPR STANDARD; PRT; 470 AA.
AC Q9ZCT8;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE 2 (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE 2)
DE (GLURS 2).
GN GLTX2 OR RP623.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MADRID E.
RX MEDLINE; 95039499.
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Scharitz-Ponten T., Almark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria".
RL Nature 396:133-140(1998).
CC -|- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) -> AMP +
CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -|- SUBUNIT: MONOMER (BY SIMILARITY).
CC -|- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -|- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
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CC
CC EMBL; AJ235272; CAA15066.1; -.
CC HSP; P27000; IGLN.
CC PROSITE; P500178; AA_TRNA_LIGASE_I; FALSE_NEG.
CC Aminoacyl-TRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
CC SIMILAR 10 20 "HIGH" REGION.
CC SIMILAR 239 243 "KMSKS" REGION.
CC BINDING 242 242 ATP (BY SIMILARITY).
CC SEQUENCE 470 AA; 53696 MW; DFICE50A20B8A9FD CRC64;
```

Query Match 67.2%; Score 39; DB 1; Length 470;
Best Local Similarity 66.7%; Pred. No. 4.9;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 ARNHGFSFY 9
|||||:
Db 31 ARHNKGKFF 39
RESULT 2

WBBJ_ECOLI STANDARD; PRT; 196 AA.
ID WBBJ_ECOLI
AC P3750; P76375;
DT 01-OCT-1994 (Rel. 30, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE PUTATIVE LIPOLYSACCHARIDE BIOSYNTHESIS O-ACETYL TRANSFERASE WBBJ
DE (EC 2.3.1.-).
GN WBBJ.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / W3110;
RX MEDLINE; 94292434.
RA Yao Z., Valvano M.A.;
RT "Genetic analysis of the O-specific lipopolysaccharide biosynthesis
RT region (rfb) of Escherichia coli K-12 W3110: identification of genes
RT that confer group 6 specificity to Shigella flexneri serotypes Y and
RT 4a";
RL J. Bacteriol. 176:4133-4143(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / W31;
RX MEDLINE; 94292435.
RA Stevenson G., Neal B., Liu D., Hobbs M., Packer N.H., Batley M.,
RA Redmond J.W., Lindquist L., Reeves P.R.;
RT "Structure of the O antigen of Escherichia coli K-12 and the sequence
RT of its rfb gene cluster";
RL J. Bacteriol. 176:4144-4156(1994).
RN [3]
RP REVISIONS TO 168-176 AND 187-189.
RC STRAIN-K12 / W31;
RX Stevenson G.;
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE; 97426617.
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12";
RL Science 277:1233-1238(1997).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN-K12;
RX MEDLINE; 97251358.
RA Itoh T., Alba H., Baba T., Fujita K., Hayashi K., Inada T.,
RA Isono K., Kasai H., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T.,
RA Saito N., Sampei G., Seki Y., Sivasubramanian S., Tagami H.,
RA Takeda J., Takemoto K., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 40.1-50.0 min region on the linkage map";
RL DNA Res. 3:379-392(1996).
RN [6]
RP FUNCTION: PUTATIVE O-ACETYLTRANSFERASE THAT TRANSFERS AN O-ACETYL
ON THE O ANTIGEN.
CC
CC -1- PATHWAY: LIPOLYSACCHARIDE BIOSYNTHESIS.
CC -1- SIMILARITY: BELONGS TO THE CYSE/LACA/LPXA/NDL FAMILY OF
CC ACETYLTRANSFERASES. COMPOSED OF MULTIPLE REPEATS OF [LIV]-G-X(4).
CC
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CC

DR EMBL; U03041; AAC31635.1; -;
DR EMBL; U09876; AAB88406.1; -;
DR EMBL; AE000294; AAC75094.1; -;
DR EMBL; D90841; CAB21803.1; -;
DR EMBL; D90842; CAB21811.1; -;
DR EMBL; EG11984; WBBJ
DR EMBL; PS00101; HEXAPEP_TRANSFERASES; FALSE_NEG.
DR PFAM; PF00132; hexapep; 1.
KW Lipopolysaccharide biosynthesis; Transferase; Acyltransferase; Repeat.
FT CONFLICT 168 176 SIPENTVIA -> LFRKYCHC (IN REF. 1).
FT CONFLICT 187 189 NHE -> IMR (IN REF. 1).
SQ SEQUENCE 196 AA; 21675 MW; DIC2FA7D3B29A1BI CRC64;

Query Match 65.5%; Score 38; DB 1; Length 196;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 HHGGSF 8
DB 105 HHGGSF 110
| | | | |
| | | | |

RESULT 3
PBPI_YEAST
ID PBPI_YEAST STANDARD; PRT; 722 AA.
AC P53297;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE PAB1-BINDING PROTEIN 1.
GN PBPI OR MRS16 OR YGR178C.
OS Saccharomyces cerevisiae (Baker's Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RA Hebling U., Hofmann B., Delius H.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-DBY747;
RA Mecklenbrauker I.;
RT "Sequencing and characterization of a suppressor of the pet- phenotype
RT in a Saccharomyces cerevisiae strain without mitochondrial group II
RT introns";
RL Thesis (1996), Vienna Biocentre, Austria.
RN [3]
RP CHARACTERIZATION.
RX MEDLINE; 99038243.
RA Mangus D.A., Amrani N., Jacobson A.;
RT "Pbpi, a factor interacting with Saccharomyces cerevisiae poly(A)-
RT binding protein, regulates polyadenylation.";
RL Mol. Cell. Biol. 18:7383-7396(1998).
CC -1- FUNCTION: APPEARS TO PROMOTE PROPER POLYADENYLATION. IN THE
CC ABSENCE OF PBPI, THE 3' TERMINI OF PRE-MRNAs ARE PROPERLY CLEAVED
CC BUT LACK FULL-LENGTH POLY(A) TAILS. MAY ACT TO REPRESS THE ABILITY
CC OF PAB1 TO NEGATIVELY REGULATE POLYADENYLATION.
CC -1- SUBUNIT: INTERACTS WITH PAB1.
CC -1- SUBCELLULAR LOCATION: NUCLEAR AND CYTOPLASMIC.
CC
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CC
CC EMBL; Z72963; CAA97204.1; -;
DR EMBL; U46931; AAB94294.1; -;
DR SGD; L0003967; PBPI.
KW Nuclear protein.

AS AN

CC -!- CATALYTIC ACTIVITY: L-MALATE = FUMARATE + H(2)O.
 CC -!- COFACTOR: BINDS A 4FE-4S CLUSTER.
 CC -!- ENZYME REGULATION: SUBJECT TO ANAEROBIC REPRESSION.
 CC -!- PATHWAY: FERMENTATIVE PATHWAY THAT LEADS TO THE PRODUCTION OF
 CC SUCCINATE.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- SIMILARITY: 79% IDENTITY WITH E.COLI FUM.
 CC -!- SIMILARITY: TO OTHER THERMOLABILE CLASS I FUMARASES.
 CC -----
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 CC -----
 DR EMBL; M27058; AAA23827.1; -;
 DR EMBL; U14003; AAA97022.1; -;
 DR EMBL; AE000485; AAC77083.1; -;
 DR PIR; B44511; B44511.
 DR ECOGENE; EG10357; FUMB.
 DR PROSITE; PS00163; FUMARATE_LYASES; 1.
 DR PFAM; PF00206; lyase_1; 1.
 DR Lysase; Tricarboxylic acid cycle; Iron-sulfur; 4Fe-4S.
 KW METAL 318 318 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
 FT ACT_SITE 397 397 POTENTIAL.
 FT BINDING 463 463 CARBOXYL GROUP (POTENTIAL).
 FT CONFLICT 50 50 V -> L (IN AAC77083).
 FT CONFLICT 50 50 V -> L (IN AAC77083).
 SQ SEQUENCE 548 AA; 60091 MW; 336854D8FA5551AB CRC64;

 Query Match 62.1%; Score 36; DB 1; Length 548;
 Best Local Similarity 66.7%; Pred. No. 21;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

 QY 1 ARHNHGSFY 9
 | | | | |
 Db 473 ACHKHGGFY 481

 RESULT 7
 Y019.NPVAC
 ID Y019.NPVAC STANDARD; PRT; 108 AA.
 AC P41424;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DE 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHETICAL 12.2 KD PROTEIN IN EGT-IAP1 INTERGENIC REGION (ORF4).
 OS Autographa californica nuclear polyhedrosis virus (ACMPNV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C6;
 RX MEDLINE; 94303173.
 RA Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
 RT "The complete DNA sequence of Autographa californica nuclear
 RT polyhedrosis virus."
 RL Virology 202:586-605(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E2;
 RX MEDLINE; 93079853.
 RA Braunagel S.C., Daniel K.D., Reilly L.M., Guarino L.A., Hong T.,
 RA Summers M.D.;
 RT "Sequence, genomic organization of the EcoRI-A fragment of Autographa
 RT californica nuclear polyhedrosis virus, and identification of a
 RT viral-encoded protein resembling the outer capsid protein VP8 of
 RT rotavirus."
 RL Virology 191:1003-1008(1992).
 CC -!- SIMILARITY: TO CORRESPONDING ORF IN OPMNPV.
 CC -----

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 CC -----
 DR EMBL; L22858; AAA66649.1; -;
 DR EMBL; M96361; AAA66789.1; -;
 DR PIR; D44221; D44221.
 KW Hypothetical protein.
 FT CONFLICT 6 6 A -> R (IN REF. 2).
 SQ SEQUENCE 108 AA; 12162 MW; 8363B15DF72486A1 CRC64;

 Query Match 60.3%; Score 35; DB 1; Length 108;
 Best Local Similarity 66.7%; Pred. No. 5.6;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

 QY 1 ARHNHGSFY 9
 | | | | |
 Db 25 ANRHNSSFY 33

 RESULT 8
 EGGS_FASHE
 ID EGGS_FASHE STANDARD; PRT; 197 AA.
 AC P07915;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE PUTATIVE EGGSHELL PROTEIN PRECURSOR.
 OS Fasciola hepatica (liver fluke).
 OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
 OC Echinostomida; Echinostomatidae; Echinostomata; Fascioloidae;
 OC Fasciolidae; Fasciola.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 87175670.
 RA Zurita M., Bieber D., Ringold G., Mansour T.E.;
 RT "Cloning and characterization of a female genital complex cDNA from
 RT the liver fluke Fasciola hepatica."
 RL Proc. Natl. Acad. Sci. U.S.A. 84:2340-2344(1987).
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 CC -----
 DR EMBL; M15871; AAA29138.1; -;
 KW Eggshell; Signal.
 FT SIGNAL 1 17
 FT CHAIN 18 197 PUTATIVE EGGSHELL PROTEIN.
 SQ SEQUENCE 197 AA; 22470 MW; 72033ED203FC1A3E CRC64;

 Query Match 60.3%; Score 35; DB 1; Length 197;
 Best Local Similarity 75.0%; Pred. No. 11;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

 QY 1 ARHNHGSF 8
 | | | | |
 Db 17 ARPHGKF 24

 RESULT 9
 Y4VH_RHISN
 ID Y4VH_RHISN STANDARD; PRT; 218 AA.
 AC Q53216;

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DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE HYPOTHETICAL 24.6 KD PROTEIN Y4VH.
GN Y4VH.
OS Rhizobium sp. (strain NGR234).
OC Plasmid sym NGR234a.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE; 97305956.
RA Freiberg C.A., Fellay R., Bairoch A., Broughton W.J., Rosenthal A.,
RA Perret X.;
RT "Molecular basis of symbiosis between Rhizobium and legumes.";
RL Nature 387:394-401(1997).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE; 96389014.
RA Freiberg C., Perret X., Broughton W.J., Rosenthal A.;
RT "Sequencing the 500-kb GC-rich symbiotic replicon of Rhizobium sp.
RT NGR234 using dye terminators and a thermostable 'sequenase'; a
RT beginning.";
RL Genome Res. 6:590-600(1996).
CC -!- SIMILARITY: NONE OBVIOUS.
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CC -----
DR EMBL; Z69203; CAA92423.1; -
DR EMBL; AE00101; AAB91896.1; -
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 218 AA; 24594 MW; 501C6CB38A09A2E5 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 218;
Best Local Similarity 75.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGFSF 8
Db || |||||
68 ARDNHGSY 75

RESULT 10
CAPG_MOUSE STANDARD; PRT; 352 AA.
AC P24452;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE MACROPHAGE CAPPING PROTEIN (MYC BASIC MOTIF HOMOLOG-1) (ACTIN-CAPPING
DE PROTEIN GCAP39).
GN CAPG OR MBH1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=NIH.
RX MEDLINE; 91184120.
RA Prendergast G.C., Ziff E.B.;
RT "Mbh 1: a novel gelsolin/severin-related protein which binds actin in
RT vitro and exhibits nuclear localization in vivo.";
RL EMBO J. 10:757-766(1991).
RN [2]
RN SEQUENCE FROM N.A.
RC TISSUE=KIDNEY;

```

```

RX MEDLINE; 91075231.
RA Yu F.-X., Johnston P.A., Suedhof T.C., Yin H.L.;
RT "Gcap39, a calcium ion- and polyphosphoinositide-regulated actin
RT capping protein.";
RL Science 250:1413-1415(1990).
RN [3]
RN PARTIAL SEQUENCE.
RX MEDLINE; 91009264.
RA Johnston P.A., Yu F.-X., Reynolds G.A., Yin H.L., Moomaw C.R.,
RA Slaughter C.A., Suedhof T.C.;
RT "Purification and expression of gcap39. An intracellular and secreted
RT Ca2(+)-dependent actin-binding protein enriched in mononuclear
RT phagocytes.";
RL J. Biol. Chem. 265:17946-17952(1990).
RN [4]
RN SUBCELLULAR LOCATION.
RX MEDLINE; 94123352.
RA Onoda K., Yu F.-X., Yin H.L.;
RT "Gcap39 is a nuclear and cytoplasmic protein.";
RL Cell Motil. Cytoskeleton 26:227-238(1993).
CC -!- FUNCTION: CALCIUM-SENSITIVE PROTEIN WHICH REVERSIBLY BLOCKS THE
CC BARBED ENDS OF ACTIN FILAMENTS BUT DOES NOT SEVER PREFORMED ACTIN
CC FILAMENTS. MAY PLAY AN IMPORTANT ROLE IN MACROPHAGE FUNCTION. MAY
CC PLAY A ROLE IN REGULATING CYTOPLASMIC AND/OR NUCLEAR STRUCTURES
CC THROUGH POTENTIAL INTERACTIONS WITH ACTIN. MAY BIND DNA. UNCAPPING
CC OCCURS EITHER WHEN CA(2+) FALLS OR WHEN THE CONCENTRATION OF
CC POLYPHOSPHOINOSITIDE RISES, BOTH AT LOW AND HIGH CA(2+).
CC -!- SUBCELLULAR LOCATION: NUCLEAR, CYTOPLASMIC AND SECRETED. NUCLEAR
CC GCAP39 REDISTRIBUTES THROUGHOUT THE CYTOPLASM DURING MITOSIS AND
CC IS EXCLUDED FROM REGIONS CONTAINING CHROMOSOMES.
CC -!- TISSUE SPECIFICITY: PRESENT IN A LARGE VARIETY OF TISSUES AND IS
CC PARTICULARLY ABUNDANT IN KIDNEY AND LUNG.
CC -!- PTM: PHOSPHORYLATED. NUCLEAR GCAP39 IS MORE HIGHLY PHOSPHORYLATED
CC THAN CYTOPLASMIC GCAP39.
CC -!- SIMILARITY: BELONGS TO THE VILIN/GELSOLIN FAMILY.
CC -----
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CC -----
DR EMBL; X54511; CAA38370.1; -
DR PIR; A39834; A39834.
DR PIR; S15011; S15011.
DR HSP; P10733; 1SVQ.
DR MGD; MGI:1098259; CAPG.
DR PFAM; PF00626; Gelsolin; 3.
KW Nuclear protein; Actin-binding; Repeat; Phosphorylation.
FT DOMAIN 139 148 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT REPEAT 32 310 3 X APPROXIMATE REPEATS.
FT REPEAT 32 78 1.
FT REPEAT 155 192 2.
FT REPEAT 267 312 3.
FT CONFLICT 32 32 V -> W (IN REF. 1).
FT CONFLICT 98 98 V -> L (IN REF. 1).
FT CONFLICT 117 117 MISSING (IN REF. 1).
FT CONFLICT 122 135 VESAFHKTSGARG -> GRVGISQDNLRATP (IN
FT CONFLICT 156 156 REF. 1).
FT CONFLICT 245 245 P -> A (IN REF. 1).
FT CONFLICT 247 248 Q -> E (IN REF. 3).
FT CONFLICT 295 296 MISSING (IN REF. 1 AND 3).
FT CONFLICT 336 336 AQ -> GK (IN REF. 1).
FT CONFLICT 352 AA; 39240 MW; 332CF78CD43B8057 CRC64;
SQ SEQUENCE 352 AA; 39240 MW; 332CF78CD43B8057 CRC64;

```

Query Match 60.3%; Score 35; DB 1; Length 352;
 Best Local Similarity 60.0%; Pred. No. 20;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 ARHNHGSFYS 10
DB 35 ARESHGIFTS 44

RESULT 11
NCAP_CVHOC
ID NCAP_CVHOC STANDARD; PRT; 448 AA.
AC P33469;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE NUCLEOCAPSID PROTEIN.
GN N.
OS Human coronavirus (strain OC43).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
OC Coronaviridae; Coronavirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89243809.
RA Kamahora T., Soe L.H., Lai M.M.C.;
RT "Sequence analysis of nucleocapsid gene and leader RNA of human
RT coronavirus OC43.";
RL Virus Res. 12:1-9(1989).
DR PIR; A60003; A60003.
DR PFAM; PF00937; Corona_nucleoca; 1.
KW Nucleocapsid.
SQ SEQUENCE 448 AA; 49316 MW; 5193AB1AE0D75626 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 448;
Best Local Similarity 85.7%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNHGSF 8
DB 103 RHNHGSF 109

RESULT 12
CC45_XENLA
ID CC45_XENLA STANDARD; PRT; 567 AA.
AC Q9YH26;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE CDC45-RELATED PROTEIN.
GN CDC45.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae;
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98429493.
RA Mimura S., Takisawa H.;
RT "Xenopus Cdc45-dependent loading of DNA polymerase alpha onto
RT chromatin under the control of S-phase Cdk.";
RL EMBO J. 17:5699-5707(1998).
CC -!- FUNCTION: REQUIRED FOR INITIATION OF CHROMOSOMAL DNA REPLICATION.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- SIMILARITY: BELONGS TO THE CDC45 FAMILY.
CC -----
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CC -----
DR EMBL; AF062494; AAC67520.1; -.
KW DNA replication; Cell cycle; Nuclear protein.

```

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SQ SEQUENCE 567 AA; 65444 MW; 9A32FB20097F7C86 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 567;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGS 7
DB 251 SRHNHGN 257

RESULT 13
RA24_YEAST
ID RA24_YEAST STANDARD; PRT; 659 AA.
AC P32641;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE CHECKPOINT PROTEIN RAD24.
GN RAD24 OR YER173W OR SYGP-ORF60.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomycetes.
RN [1]
RP SEQUENCE FROM N.A.
RA Mulligan J.T., Dietrich F.S., Hennessey K.M., Sehl P., Komp C.,
RA Wei Y., Taylor P., Nakahara K., Roberts D., Davis R.W.;
RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-S288C / AB972;
RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
RA Chung E., Duncan A., Guzman E., Hartzell G., Hunnicke-Smith S.,
RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Norgren R., Oefner P., Oh C.,
RA Petel F.X., Roberts D., Sehl P., Schramm S., Shogren T., Smith V.,
RA Taylor P., Wei Y., Yelton M., Botstein D., Davis R.W.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP IDENTIFICATION.
RX MEDLINE; 96112796.
RA Weinert T.;
RL Unpublished results, cited by:
RL Griffiths D.J.F., Barbet N.C., McCready S., Lehmann A.R.,
RL Carr A.M.;
RL EMBO J. 14:5812-5823(1995).
CC -!- FUNCTION: PARTICIPATES IN CHECKPOINT PATHWAYS ARREST OF THE CELL
CC CYCLE. A MECHANISM THAT ALLOWS THE DNA REPAIR PATHWAYS TO ACT TO
CC RESTORE THE INTEGRITY OF THE DNA PRIOR TO DNA SYNTHESIS OR
CC SEPARATION OF THE REPLICATED CHROMOSOMES.
CC -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -!- SIMILARITY: TO S.POMBE RAD17 AND SOME SIMILARITY TO ACTIVATOR 1 36
CC -----
CC TO 40 KD SUBUNITS FAMILY.
CC -----
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CC -----
DR EMBL; U18922; AAB64700.1; -.
DR PIR; S30859; S30859.
KW DNA damage; DNA repair; Nuclear protein; Cell cycle.
SQ SEQUENCE 659 AA; 75726 MW; 130FE54875CAA930 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 659;
Best Local Similarity 71.4%; Pred. No. 39;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

QY 3 HHGFSFY 9
 ||||| I
 Db 436 HHGTVY 442

RESULT 14
 F16P_NOSPU STANDARD; PRT; 349 AA.
 AC P48847;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 13-DEC-1998 (Rel. 37, Last annotation update)
 DE FRUCTOSE-1,6-BISPHOSPHATASE (EC 3.1.3.11) (D-FRUCTOSE-1,6-BISPHOSPHATE
 DE 1-PHOSPHOHYDROLASE) (FBPASE).
 GN FBP.
 OS Nostoc punctiforme.
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.

[1]
 RN SEQUENCE FROM N.A.
 RC STRAIN-ATCC 29133 / PCC 73102;
 RA Summers M.L., Wolf R.E. Jr., Chu S., Meeks J.C.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: D-FRUCTOSE 1,6-BISPHOSPHATE + H(2)O =
 CC D-FRUCTOSE 6-PHOSPHATE + ORTHOPHOSPHATE.
 CC -1- PATHWAY: KEY ENZYME OF THE REDUCTIVE CARBON DIOXIDE ASSIMILATION.
 CC OR CALVIN CYCLE OF PHOTOSYNTHETIC CARBON DIOXIDE ASSIMILATION.
 CC -1- SIMILARITY: BELONGS TO THE FBPASE FAMILY.

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 CC -----

DR EMBL; L32796; AAA50768.1; -;
 DR HSP; P00636; 3FBP
 DR PRINTS; PR00115; FBPHPTASE.
 DR PRINTS; PR00377; INFBPHPTASE.
 DR PROSITE; PS00124; FBPAASE; 1.
 DR PFAM; PF00316; FBPAse; 1.
 KW Hydrolase; Carbohydrate metabolism; Calvin cycle; Photosynthesis.
 FT ACT_SITE 288 288 BY SIMILARITY.
 SQ SEQUENCE 349 AA; 38618 MW; 6720CF7C8F36127E CRC64;

Query Match 58.6%; Score 34; DB 1; Length 349;
 Best Local Similarity 85.7%; Pred. No. 30;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 HHGFSYS 10
 ||||| I
 Db 222 HHGVSYS 228

RESULT 15
 PURA_SPICI STANDARD; PRT; 435 AA.
 AC P52150;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE ADENYLOSUCCINATE SYNTHETASE (EC 6.3.4.4) (IMP---ASPARTATE LIGASE)
 DE (ADSS) (AMPSASE).
 GN PURA.
 OS Spiroplasma citri.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Spiroplasmataceae; Spiroplasma.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-R8A2HP;

RA Citti C., Saillard C., Bove J.M.;
 RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE DE NOVO PATHWAY OF PURINE
 CC NUCLEOTIDE BIOSYNTHESIS
 CC -1- CATALYTIC ACTIVITY: GTP + IMP + L-ASPARTATE = GDP + ORTHOPHOSPHATE
 CC + ADENYLOSUCCINATE.
 CC -1- PATHWAY: FIRST COMMITTED STEP IN AMP BIOSYNTHESIS.
 CC -1- SIMILARITY: BELONGS TO THE ADENYLOSUCCINATE SYNTHETASE FAMILY.
 CC -----
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 CC -----

DR EMBL; L22971; AAA26586.1; -;
 DR HSP; P12283; 1ADI.
 DR PROSITE; PS00513; ADENYLOSUCCIN_SYN_2; 1.
 DR PROSITE; PS01266; ADENYLOSUCCIN_SYN_1; 1.
 DR PFAM; PF00709; Adenylsucc_synt; 1.
 KW Lyase; Purine biosynthesis; Ligase; GTP-binding.
 FT NP_BIND 17 23
 FT ACT_SITE 146 146 BY POTENTIAL.
 FT ACT_SITE 153 153 BY SIMILARITY.
 SQ SEQUENCE 435 AA; 49609 MW; 74EB74E7B5A2091A CRC64;

Query Match 58.6%; Score 34; DB 1; Length 435;
 Best Local Similarity 66.7%; Pred. No. 38;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNHGSFY 9
 | | | | |
 Db 217 AIHNHGFY 225

Search completed: May 27, 2000, 20:45:29
 Job time: 2283 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:55:21 ; Search time 34.67 Seconds
(without alignments)
19.998 Million cell updates/sec

Title: US-09-016-061-96
Perfect score: 58
Sequence: 1 ARNHGSEFYS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

SPTREMBL_12.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	40	69.0	555	Q9XV91	Q9XV91 caenorhabdi
2	39	67.2	350	P74376	P74376 synecocyst
3	39	67.2	470	Q9ZC78	Q9ZC78 rickettsia
4	37	63.8	530	Q64526	Q64526 arabidopsis
5	37	63.8	731	Q29369	Q29369 escherichia
6	36	62.1	339	Q9XD85	Q9XD85 corynebacte
7	36	62.1	463	Q4923	Q4923 caenorhabdi
8	36	62.1	627	Q24474	Q24474 abies grand
9	35	60.3	89	Q19495	Q19495 gallus gall
10	35	60.3	110	Q92387	Q92387 bombyx mori
11	35	60.3	272	Q24950	Q24950 fasciola he
12	35	60.3	272	Q24951	Q24951 fasciola he
13	35	60.3	552	Q9XW65	Q9XW65 caenorhabdi
14	35	60.3	567	Q9YR26	Q9YR26 xenopus lae
15	35	60.3	1467	Q97830	Q97830 bos taurus
16	35	60.3	1472	Q97831	Q97831 bos taurus
17	35	60.3	1474	Q94910	Q94910 homo sapien
18	35	60.3	1515	Q88917	Q88917 rattus norv
19	35	60.3	2470	Q90681	Q90681 gallus gall
20	34	58.6	151	Q99702	Q99702 homo sapien

21	34	58.6	236	10	Q40088	Q40088 ipomoea bat
22	34	58.6	371	5	Q94707	Q94707 physarum po
23	34	58.6	379	2	O25568	O25568 helicobacte
24	34	58.6	381	2	O92KT9	O92KT9 helicobacte
25	34	58.6	385	9	O64373	O64373 lactobacill
26	34	58.6	449	5	Q9XYC7	Q9XYC7 plasmodium
27	34	58.6	450	3	O93934	O93934 botrytis ci
28	34	58.6	467	3	O43038	O43038 schizosacch
29	34	58.6	483	4	O75020	O75020 homo sapien
30	34	58.6	611	2	O9X5S2	O9X5S2 streptomyce
31	34	58.6	715	5	O61270	O61270 halocynthia
32	34	58.6	807	2	O66383	O66383 clostridium
33	34	58.6	813	2	O87964	O87964 thermotoga
34	34	58.6	813	2	O9X2G3	O9X2G3 thermotoga
35	34	58.6	883	5	O9XYX1	O9XYX1 drosophila
36	34	58.6	1012	5	Q21075	Q21075 caenorhabdi
37	34	58.6	1767	5	Q24495	Q24495 drosophila
38	33	56.9	39	7	P79474	P79474 cervus elap
39	33	56.9	39	7	P79477	P79477 cervus elap
40	33	56.9	39	7	P79478	P79478 cervus elap
41	33	56.9	39	7	P79479	P79479 cervus elap
42	33	56.9	73	12	O56648	O56648 human cytom
43	33	56.9	79	7	O19398	O19398 felis silve
44	33	56.9	82	7	Q30606	Q30606 macaca mula
45	33	56.9	82	7	Q30608	Q30608 macaca mula

ALIGNMENTS

RESULT 1
Q9XV91 PRELIMINARY; PRT; 555 AA.
AC Q9XV91;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE F16H6.1 PROTEIN.
GN F16H6.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA MATTHEWS L.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans";
RT Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
elegans";
RL Nature 368:32-38(1994).
DR EMBL; 281506; CAB04128.1;
SQ SEQUENCE 555 AA; 60401 MW; F0504B72 CRC32;

Query Match 69.0%; Score 40; DB 5; Length 555;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFYS 10
 Db 314 HNHGSFYS 321

RESULT 2
 P74376 PRELIMINARY; PRT; 350 AA.
 ID P74376
 AC P74376;
 DT 01-FEB-1997 (TREMBlrel. 02, Created)
 DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
 DT 01-JAN-1999 (TREMBlrel. 09, Last annotation update)
 DE HYPOTHETICAL 40.3 KD PROTEIN.
 OS Synechocystis sp. (strain PCC 6803).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC6803;
 RA TABATA S.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PCC6803;
 RX MEDLINE; 97061201.
 RA KANEKO T., SATO S., KOTANI H., TANAKA A., ASAMIZU E., NAKAMURA Y.,
 RA MIYAJIMA N., HIROSAWA M., SUGIURA M., SASAMOTO S., KIMURA T.,
 RA HOSOUCHI T., MATSUO A., MURAKI A., NAKAZAKI N., NARUO K., OKUMURA S.,
 RA SHIMO S., TAKEUCHI C., WADA T., WATANABE A., YAMADA M., YASUDA M.,
 RA TABATA S.;
 RT "Sequence analysis of the genome of the unicellular cyanobacterium
 RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
 RT entire genome and assignment of potential protein-coding regions.";
 RL DNA Res. 3:109-136(1996).
 DR EMBL; D90914; BAA18471.1;
 KW Hypothetical protein.
 SQ SEQUENCE 350 AA; 40262 MW; B68C9003 CRC32;

Query Match 67.2%; Score 39; DB 2; Length 350;
 Best Local Similarity 71.4%; Pred. No. 10;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNHGSFY 9
 Db 247 HNHGNY 253

RESULT 3
 Q9ZCT8 PRELIMINARY; PRT; 470 AA.
 ID Q9ZCT8
 AC Q9ZCT8;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE GLUTAMYL-TRNA SYNTHETASE (GLTX2).
 GN RP623.
 OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MADRID E;
 RX MEDLINE; 99039499.
 RA ANDERSSON S.G.E., ZOMORODIPOUR A., ANDERSSON J.O.,
 RA SICKERITZ-PONTEN T., ALSMARK U.C.M., PODOWSKI R.M., NAESLUND A.K.,
 RA ERIKSSON A.S., WINKLER H.H., KUHLAND C.G.;
 RT "The genome sequence of Rickettsia prowazekii and the origin of
 RT mitochondria.";
 RL Nature 396:133-140(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MADRID E;
 RA ANDERSSON S.G.E.;

RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ235272; CAA15066.1;
 DR HSSP; P27000; IGLN.
 SQ SEQUENCE 470 AA; 53696 MW; A0660D82 CRC32;

Query Match 67.2%; Score 39; DB 2; Length 470;
 Best Local Similarity 66.7%; Pred. No. 14;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNHGSFY 9
 Db 31 ARHNHNGKEF 39

RESULT 4
 O64526 PRELIMINARY; PRT; 530 AA.
 ID O64526
 AC O64526;
 DT 01-AUG-1998 (TREMBlrel. 07, Created)
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE YUP8H12R.13 PROTEIN.
 GN YUP8H12R.13.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
 OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
 OC Arabidopsis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA THEOLOGIS A., VYSOTSKAYA V.S., OSBORNE B.I., SCHWARTZ J.R.,
 RA FEDERSPIEL N.A., KWAN A., TORIUMI M., YU G., OJI, O., ARAUJO R.,
 RA CHUNG E., DEWER K., DIETRICH F., ECKER J.R., MARZIALI A., OEFNER P.,
 RA DAVIS R.W.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA THEOLOGIS A.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA THEOLOGIS A.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA THEOLOGIS A.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA;
 RA THEOLOGIS;
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AC002986; AAC17040.1;
 DR MENDEL; 29344; Arath;3318;29344.
 SQ SEQUENCE 530 AA; 59679 MW; 62FDB0B1 CRC32;

Query Match 63.8%; Score 37; DB 10; Length 530;
 Best Local Similarity 62.5%; Pred. No. 36;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNHGSFYS 10
 Db 192 HNHNNYS 199

RESULT 5
 Q59369

ID Q59369 PRELIMINARY; PRT; 731 AA.
 AC Q59369;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE HISTIDINE RICH P TYPE ATPASE.
 DE HRA-1.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 95110304.
 RA TRENNOR C.C., LIN W., ANDREWS N.C.;
 RT "Novel bacterial P-type ATPases with histidine-rich heavy-metal-
 associated sequences.";
 RL Biochem Biophys Res Commun. 205:1644-1650(1994).
 DR EMBL; U16658; AAA62113.1; -. E2; 1.
 DR PROSITE; PS00154; ATPASE_E1_E2; 1.
 DR PFAM; PF00122; E1-E2_ATPase; 1.
 KW Hydrolase; Transmembrane; Phosphorylation; ATP-binding.
 FT MOD_RES 431 431 PHOSPHORYLATION (PROBABLE).
 SQ SEQUENCE 731 AA; 78453 MW; 6765E988 CRC32;

Query Match 63.8%; Score 37; DB 2; Length 731;
 Best Local Similarity 75.0%; Pred. No. 49;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNHGSF 8
 | :|:|:|
 Db 88 AHHHGSF 95

RESULT 6
 Q9XD85 PRELIMINARY; PRT; 339 AA.
 AC Q9XD85;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DE SECRETED PROTEIN PRECURSOR.
 OC Corynebacterium diphtheriae.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Corynebacterineae; Corynebacteriaceae;
 OC Corynebacterium.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C7(-);
 RA DRAZEK E.S., SCHMITT M.P.;
 RT "Identification of Corynebacterium diphtheriae genes required for
 acquisition of iron from heme and hemoglobin that are homologous to
 ABC transporters.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF109162; AAD37497.1; -.
 KW Signal.
 FT SIGNAL 1 31 POTENTIAL.
 FT CHAIN 32 339 SECRETED PROTEIN.
 SQ SEQUENCE 339 AA; 37116 MW; 2023490C CRC32;

Query Match 62.1%; Score 36; DB 2; Length 339;
 Best Local Similarity 85.7%; Pred. No. 35;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NHGSFYS 10
 :|:|:|:|
 Db 120 HHGSFYS 126

RESULT 7
 O44923 PRELIMINARY; PRT; 463 AA.
 ID O44923

AC O44923;
 DT 01-JUN-1998 (TrEMBLrel. 06, Created)
 DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE COSMID W10G11.
 DE W10G11.19.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
 OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN-BRISTOL N2;
 RX MEDLINE; 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA WILSON R., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIBERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 RL Nature 368:32-38(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA GOELA D., SCHEET P.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA WATERSTON R.;
 RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF040661; AAB95082.1; -.
 SQ SEQUENCE 463 AA; 53300 MW; 8C669F8E CRC32;

Query Match 62.1%; Score 36; DB 5; Length 463;
 Best Local Similarity 66.7%; Pred. No. 48;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNHGSFY 9
 | :|:|:|
 Db 121 ARENHGRFH 129

RESULT 8
 O24474 PRELIMINARY; PRT; 627 AA.
 AC O24474;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
 DE MYRCENE SYNTHASE.
 GN AG2.2.
 OS Abies grandis.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
 OC Abies.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 97413772.
 RA BOHLMANN J., STEELE C.L., CROTEAU R.;
 RT "Monoterpene synthases from grand fir (Abies grandis). cDNA isolation,
 RT characterization, and functional expression of myrcene synthase, (-)-
 RT (4S)-limonene synthase, and (-)-(1S,5S)-pinene synthase.";
 RL J. Biol. Chem. 272:21784-21792(1997).
 DR EMBL; U87908; AAB71084.1; -.
 DR HSSP; Q40577; SEAT.
 DR MENDEL; 27003; Abigr; 2508; 27003.

DR PFAM: PF01397; Terpene synth; 1.
SQ SEQUENCE 627 AA; 72478 MW; 8741AC4F CRC32;

Query Match 62.1%; Score 36; DB 10; Length 627;
Best Local Similarity 60.0%; Pred. No. 64;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGGSFYS 10
||| | ||:
Db 340 ARHRHVEFT 349

RESULT 9
O19495
ID O19495 PRELIMINARY; PRT; 89 AA.
AC O19495;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS II BETA 1 DOMAIN (FRAGMENT).
GN B-LBI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=I5.151-5; TISSUE=BURSA;
RA PHARR G.T.; DODGSON J.B.; HUNT H.D.; BACON L.D.;
RL Immunogenetics 47:350-354(1998).
DR EMBL; U91532; AAC15813.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 89 89
SQ SEQUENCE 89 AA; 10724 MW; FDAC6024 CRC32;

Query Match 60.3%; Score 35; DB 7; Length 89;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNHGSFYS 10
||| | ||:
Db 75 RHNHGSFYS 83

RESULT 10
O92387
ID O92387 PRELIMINARY; PRT; 110 AA.
AC O92387;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE ACMPNP ORF19.
OS Bombyx mori nuclear polyhedrosis virus (BmNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=T3;
RX MEDLINE; 97329351.
RA KAMITA S.G.; MAEDA S.;
RT "Sequencing of the putative DNA helicase-encoding gene of the Bombyx mori nuclear polyhedrosis virus and fine-mapping of a region involved in host range expansion.";
RT RT
RL Gene 190:173-179(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=T3;
RA GOMI S.; MAJIMA K.; MAEDA S.;
RT "Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.";

RL Submitted (OCT-1998) to the EMBL/GenBank/DBDJ databases.
DR EMBL; L33180; AAC63694.1; -.
SQ SEQUENCE 110 AA; 12506 MW; 1AC8E69C CRC32;

Query Match 60.3%; Score 35; DB 12; Length 110;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGGSF 9
| | | | |
Db 27 ANRHSSFY 35

RESULT 11
Q24950
ID Q24950 PRELIMINARY; PRT; 272 AA.
AC Q24950;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE VITELLINE PROTEIN B1 PRECURSOR.
OS Fasciola hepatica (Liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Echinostomida; Echinostomatidae; Echinostomata; Fascioloidae;
OC Fasciolidae; Fasciola.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93063029.
RA RICE-FICHT A.C.; DUSEK K.A.; KOCHVAR G.J.; WAITE J.H.;
RT "Eggshell precursor proteins of Fasciola hepatica, I. Structure and expression of vitelline protein B.";
RL Mol. Biochem. Parasitol. 54:129-141(1992).
DR EMBL; M93024; AAA29143.1; -.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 272 VITELLINE PROTEIN B1.
SQ SEQUENCE 272 AA; 31211 MW; 892E4D3A CRC32;

Query Match 60.3%; Score 35; DB 5; Length 272;
Best Local Similarity 75.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGGSF 8
| | | | |
Db 19 ARPHGKGF 26

RESULT 12
Q24951
ID Q24951 PRELIMINARY; PRT; 272 AA.
AC Q24951;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE VITELLINE PROTEIN B2 PRECURSOR.
OS Fasciola hepatica (Liver fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;
OC Echinostomida; Echinostomatidae; Echinostomata; Fascioloidae;
OC Fasciolidae; Fasciola.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 93063029.
RA RICE-FICHT A.C.; DUSEK K.A.; KOCHVAR G.J.; WAITE J.H.;
RT "Eggshell precursor proteins of Fasciola hepatica, I. Structure and expression of vitelline protein B.";
RL Mol. Biochem. Parasitol. 54:129-141(1992).
DR EMBL; M93025; AAA29144.1; -.
KW Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 272 VITELLINE PROTEIN B2.
SQ SEQUENCE 272 AA; 31418 MW; EBAF123F CRC32;

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RX MEDLINE: 98429493.
RA MIMURA S., TAKISAWA H.;
RT "Xenopus Cdc45-dependent loading of DNA polymerase alpha onto
RT chromatin under the control of S-phase Cdk.";
RL EMBO J. 17:5699-5707(1998).
DR EMBL: AF062494; AAC67520.1; -.
SQ SEQUENCE 567 AA; 65444 MW; F4A7D874 CRC32;

Query Match 60.3%; Score 35; DB 13; Length 567;
Best Local Similarity 71.4%; Pred. No. 89;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSGF 7
Db 251 SRNHGNC 257
:|||||:

RESULT 15
O97830 PRELIMINARY; PRT; 1467 AA.
ID O97830:
AC O97830:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE LATROPHILIN-1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE: 97407945.
RA LELIANOVA V.G., DAVLETOV B.A., STERLING A., RAHMAN M.A., GRISHIN E.V.,
RA TOTTY N.F., USHKARYOV Y.A.;
RT "Alpha-latrotoxin receptor, latrophilin, is a novel member of the
RT secretin family of G protein-coupled receptors.";
RL J. Biol. Chem. 272:21504-21508(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RX MEDLINE: 99148828
RA MATSUSHITA H., LELIANOVA V.G., USHKARYOV Y.A.;
RT "The latrophilin family: multiply spliced G protein-coupled receptors
RT with differential tissue distribution.";
RL FEBS Lett. 443:348-352(1999).
DR EMBL: AF111097; AAD09191.1; -.
SQ SEQUENCE 1467 AA; 161606 MW; F922F459 CRC32;

Query Match 60.3%; Score 35; DB 6; Length 1467;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARNHGSGFYS 10
Db 553 ARHTRGSIYA 562
|||||:

Search completed: May 27, 2000, 19:55:22
Job time: 986 sec

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RX MEDLINE: 98429493.
RA MIMURA S., TAKISAWA H.;
RT "Xenopus Cdc45-dependent loading of DNA polymerase alpha onto
RT chromatin under the control of S-phase Cdk.";
RL EMBO J. 17:5699-5707(1998).
DR EMBL: AF062494; AAC67520.1; -.
SQ SEQUENCE 567 AA; 65444 MW; F4A7D874 CRC32;

Query Match 60.3%; Score 35; DB 5; Length 272;
Best Local Similarity 75.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARNHGSGF 8
Db 19 ARHPHGKF 26
|||||:

RESULT 13
O9XWG6 PRELIMINARY; PRT; 552 AA.
ID O9XWG6:
AC O9XWG6:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE Y55D9A.2B PROTEIN.
GN Y55D9A.2B.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RX WALLIS J.;
RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE: 94150718.
RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHNING J., LLOYD C., McMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
DR EMBL: AL032649; CAA21703.1; -.
SQ SEQUENCE 552 AA; 62840 MW; 3FD398F1 CRC32;

Query Match 60.3%; Score 35; DB 5; Length 552;
Best Local Similarity 62.5%; Pred. No. 87;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNHGSGFYS 10
Db 36 HEHGMFYN 43
|||||:

RESULT 14
O9YH26 PRELIMINARY; PRT; 567 AA.
ID O9YH26:
AC O9YH26:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE CDC45.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
OC Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae;
OC Xenopus.
RN [1]
RP SEQUENCE FROM N.A.

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:50:46 ; Search time 31.68 Seconds
(without alignments)
7.477 Million cell updates/sec

Title: US-09-016-061-96
Perfect score: 58
Sequence: 1 ARNHGSPYS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	10	1 W76038	LM609 grafted anti
2	52	89.7	10	1 W76040	LM609 grafted anti
3	49	84.5	10	1 W76037	LM609 grafted anti
4	48	82.8	10	1 W76039	LM609 grafted anti
5	48	82.8	10	1 W76023	LM609 grafted anti
6	47	81.0	10	1 W76020	LM609 grafted anti
7	43	74.1	10	1 W76024	LM609 grafted anti
8	41	70.7	10	1 W76022	LM609 grafted anti
9	41	70.7	10	1 W76025	LM609 grafted anti
10	41	70.7	10	1 W76026	LM609 grafted anti
11	41	70.7	10	1 W76027	LM609 grafted anti
12	41	70.7	10	1 W76028	LM609 grafted anti
13	41	70.7	10	1 W76029	LM609 grafted anti
14	41	70.7	10	1 W76030	LM609 grafted anti
15	41	70.7	10	1 W76010	LM609 grafted anti
16	41	70.7	117	1 W76001	Vitaxin antibody h
17	41	70.7	117	1 W76003	LM609 antibody hea
18	38	65.5	10	1 W76021	LM609 grafted anti
19	35	60.3	352	1 R53686	38KD HR1 factor. N
20	35	60.3	353	1 R53687	38KD HR2 factor. N
21	35	60.3	659	1 W26662	Yeast checkpoint c
22	35	60.3	659	1 W73892	Yeast RAD24 protei
23	35	60.3	1471	1 W74585	Calcium indepen
24	34	58.6	204	1 W59609	DNA-binding/dimeri
25	34	58.6	358	1 W98649	H. pylori GHPO 403
26	34	58.6	483	1 W82550	Human LIR-pbmhh pr
27	34	58.6	514	1 W69235	EcR-V protein sequ
28	33	56.9	110	1 W84099	Vitronectin alpha-
29	33	56.9	117	1 W84093	Murine vitronectin
30	33	56.9	117	1 W84097	Humanised anti-alp
31	33	56.9	318	1 W06405	Verotoxigenic E. c
32	33	56.9	326	1 W06409	Histidine tagged v
33	33	56.9	329	1 W06414	Flag tag/VT2 A sub
34	33	56.9	502	1 R55371	Mouse Activin rece

35	33	56.9	503	1 R55366	Human Activin rece
36	33	56.9	503	1 R55210	Human ALK-1. Ident
37	33	56.9	503	1 R94602	TAR-3 polypeptide.
38	33	56.9	503	1 W27507	Human activin rece
39	33	56.9	505	1 R41922	MISR3. New recepto
40	33	56.9	505	1 W03761	Mullerian inhibiti
41	33	56.9	711	1 W06412	Maltose binding pr
42	32	55.2	30	1 W39403	H. horridum extendi
43	32	55.2	30	1 W39346	H. horridum extendi
44	32	55.2	148	1 W89953	Antigen from clust
45	32	55.2	271	1 R41891	Pcp A. Novel prote

ALIGNMENTS

RESULT 1

W76038
ID W76038 standard; Protein; 10 AA.
AC W76038;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #14.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN W09833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998: U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49875.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
integrin - and related grafted antibodies based on murine monoclonal
LM609, also related nucleic acid, used to treat, prevent or diagnose
angiogenesis or restenosis
Claim 62: Page 43; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
LM609 heavy and light chain variable region. LM609 and the antibody
vitaxin bind selectively to integrin alphavbeta3 and can be used to
inhibit binding of alphavbeta3 to a ligand and thus block
integrin-mediated signal transduction. This is useful in the treatment,
prevention and diagnosis of alphavbeta3-mediated disease, specifically,
angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
arthritis, macular degeneration, osteoporosis etc.). The antibodies
contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 100.0%; Score 58; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00024;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ARNHGSPYS 10
Db 1 ARNHGSPYS 10
|||||||

RESULT 2

W76040
ID W76040 standard; Protein; 10 AA.
AC W76040;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #16.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49877.
 DR Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 43; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 89.7%; Score 52; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0025;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARNHGSEYS 10
 DB 1 ARNHGSEYS 10
 ||||:||||

RESULT 3
 W76037
 ID W76037 standard; Protein; 10 AA.
 AC W76037;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #13.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49874.
 DR Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 43; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 84.5%; Score 49; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0082;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 ARNHGSEYS 10
 DB 1 ARNHGSEFS 10
 ||||:||||

RESULT 4
 W76039
 ID W76039 standard; Protein; 10 AA.
 AC W76039;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #15.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49876.
 DR Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 43; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 82.8%; Score 48; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 0.012;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARNHGSEFY 9
 DB 1 ARNHGSEFY 9
 ||||:||||

RESULT 5
 W76023
 ID W76023 standard; Protein; 10 AA.

AC W76023;
 DE 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #5.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49860.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 82.8%; Score 48; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 0.012; Indels 0; Gaps 0;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSFY 9
 |||||
 DB 1 ARHNHGSFY 9

RESULT 6
 W76020
 ID W76020 standard; Protein; 10 AA.
 AC W76020;
 DE 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #2.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49857.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 81.0%; Score 47; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.018; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSF 8
 |||||
 DB 1 ARHNHGSF 8

RESULT 7
 W76024
 ID W76024 standard; Protein; 10 AA.
 AC W76024;
 DE 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #6.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49861.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 74.1%; Score 43; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.087; Indels 1; Gaps 0;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNHGSFYS 10
 |||||
 DB 1 ARHNHGSFAS 10

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RESULT 8
W76022
ID W76022 standard; Protein; 10 AA.
AC W76022:
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #4.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49859.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62: Page 41: 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 70.7%; Score 41; DB 1; Length 10;
Best Local Similarity 87.5%; Pred. No. 0.19;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSF 8
Db 1 ARHNYGSF 8

RESULT 10
W76026
ID W76026 standard; Protein; 10 AA.
AC W76026:
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #8.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49863.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62: Page 41: 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 70.7%; Score 41; DB 1; Length 10;
Best Local Similarity 87.5%; Pred. No. 0.19;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSF 8
Db 1 ARHNYGSF 8

RESULT 9
W76025
ID W76025 standard; Protein; 10 AA.
AC W76025:
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #7.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49862.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

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QY 1 ARHNHGSF 8
 ||||:||||
 Db 1 ARHNHGSF 8

RESULT 11

W76027 ID W76027 standard; Protein; 10 AA.

AC W76027; 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #9.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 LM609; inhibitor; integrin-mediated signal transduction; treatment;
 diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 macular degeneration; osteoporosis; primer; V-H region; CDR;
 complementarity determining region.

OS Mus sp.

PN WO9833919-A2.

PD 06-AUG-1998.

PF 30-JAN-1998; U01826.

PR 30-JAN-1997; US-791391.

PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

DR WPI; 98-437472/37.

DR N-PSDB; V49864.

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT Integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

PS Claim 62; Page 41; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody

CC vitaxin bind selectively to integrin alphavbeta3 and can be used to

CC inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies

CC contain non-murine framework regions so are suitable for use in humans.

CC Enhanced types of LM609 have affinity more than 90 times greater than

CC that of parent the parent antibody.

SQ Sequence 10 AA;

Query Match 70.7%; Score 41; DB 1; Length 10;

Best Local Similarity 87.5%; Pred. No. 0.19;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSF 8
 ||||:||||
 Db 1 ARHNHGSF 8

RESULT 12

W76028 ID W76028 standard; Protein; 10 AA.

AC W76028;

DE LM609 grafted antibody V-H region CDR3 protein fragment #10.

DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

LM609; inhibitor; integrin-mediated signal transduction; treatment;

diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

macular degeneration; osteoporosis; primer; V-H region; CDR;

complementarity determining region.

OS Mus sp.

PN WO9833919-A2.

PD 06-AUG-1998.

PF 30-JAN-1998; U01826.

PR 30-JAN-1997; US-791391.

PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.

DR N-PSDB; V49865.

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT Integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

PS Claim 62; Page 41; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody

CC vitaxin bind selectively to integrin alphavbeta3 and can be used to

CC inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies

CC contain non-murine framework regions so are suitable for use in humans.

CC Enhanced types of LM609 have affinity more than 90 times greater than

CC that of parent the parent antibody.

SQ Sequence 10 AA;

Query Match 70.7%; Score 41; DB 1; Length 10;

Best Local Similarity 87.5%; Pred. No. 0.19;

Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNHGSF 8

||||:||||

Db 1 ARHNHGSF 8

RESULT 13

W76029 ID W76029 standard; Protein; 10 AA.

AC W76029;

DE LM609 grafted antibody V-H region CDR3 protein fragment #11.

DE Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

LM609; inhibitor; integrin-mediated signal transduction; treatment;

diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

macular degeneration; osteoporosis; primer; V-H region; CDR;

complementarity determining region.

OS Mus sp.

PN WO9833919-A2.

PD 06-AUG-1998.

PF 30-JAN-1998; U01826.

PR 30-JAN-1997; US-791391.

PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

DR WPI; 98-437472/37.

DR N-PSDB; V49866.

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT Integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

PS Claim 62; Page 41; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody

CC LM609 heavy and light chain variable region. LM609 and the antibody

CC vitaxin bind selectively to integrin alphavbeta3 and can be used to

CC inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,

CC prevention and diagnosis of alphavbeta3-mediated disease, specifically

CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,

CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid

CC arthritis, macular degeneration, osteoporosis etc.). The antibodies

CC contain non-murine framework regions so are suitable for use in humans.

CC Enhanced types of LM609 have affinity more than 90 times greater than

CC that of parent the parent antibody.

SQ Sequence 10 AA;

Query Match 70.7%; Score 41; DB 1; Length 10;
 Best Local Similarity 87.5%; Pred. No. 0.19;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSF 8
 ||||:||||
 Db 1 ARHNYGSF 8

RESULT 14
 W76030
 ID W76030 standard; Protein; 10 AA.
 AC W76030;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #12.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSV-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49867.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 integrin - and related grafted antibodies based on murine monoclonal
 LM609, also related nucleic acid, used to treat, prevent or diagnose
 angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC LM6007-W76040 are protein fragments of the grafted monoclonal antibody
 LM609 heavy and light chain variable region. LM609 and the antibody
 vitaxin bind selectively to integrin alphavbeta3 and can be used to
 inhibit binding of alphavbeta3 to a ligand and thus block
 integrin-mediated signal transduction. This is useful in the treatment,
 prevention and diagnosis of alphavbeta3-mediated disease, specifically
 angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 arthritis, macular degeneration, osteoporosis etc.). The antibodies
 contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 70.7%; Score 41; DB 1; Length 10;
 Best Local Similarity 87.5%; Pred. No. 0.19;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSF 8
 ||||:||||
 Db 1 ARHNYGSF 8

RESULT 15
 W76010
 ID W76010 standard; Protein; 10 AA.
 AC W76010;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #1.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.

PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSV-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49847.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 integrin - and related grafted antibodies based on murine monoclonal
 LM609, also related nucleic acid, used to treat, prevent or diagnose
 angiogenesis or restenosis
 PS Disclosure; Page 40; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 LM609 heavy and light chain variable region. LM609 and the antibody
 vitaxin bind selectively to integrin alphavbeta3 and can be used to
 inhibit binding of alphavbeta3 to a ligand and thus block
 integrin-mediated signal transduction. This is useful in the treatment,
 prevention and diagnosis of alphavbeta3-mediated disease, specifically
 angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 arthritis, macular degeneration, osteoporosis etc.). The antibodies
 contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 70.7%; Score 41; DB 1; Length 10;
 Best Local Similarity 87.5%; Pred. No. 0.19;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARNHGSF 8
 ||||:||||
 Db 1 ARHNYGSF 8

Search completed: May 27, 2000, 19:50:47
 Job time: 1743 sec

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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:52:03 ; Search time 29.7 Seconds
(without alignments)
19.741 Million cell updates/sec

Title: US-09-016-061-98
Perfect score: 58
Sequence: 1 ARHNYGSFY 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR_63:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	39	67.2	113	2 S26468	Ig heavy chain V r
2	38	65.5	275	2 D71087	probable translati
3	38	65.5	275	2 G75130	translation initia
4	38	65.5	402	2 T25001	hypothetical prote
5	37	63.8	134	2 B72651	hypothetical prote
6	37	63.8	385	2 S51436	probable membrane
7	37	63.8	388	1 JC5461	cellulase (EC 3.2.
8	37	63.8	388	1 S43920	cellulase (EC 3.2.
9	37	63.8	2288	2 T29999	hypothetical prote
10	36	62.1	82	2 I51106	Major Histocompat
11	36	62.1	89	2 S38688	MHC class II histo
12	36	62.1	89	2 S38683	MHC class II histo
13	36	62.1	89	2 S38684	MHC class II histo
14	36	62.1	225	2 I47095	MHC class II histo
15	36	62.1	446	2 T19625	hypothetical prote
16	36	62.1	470	2 H71667	glutamate--tRNA li
17	36	62.1	785	2 S37031	probable succinogl
18	35	60.3	9	2 S36850	Ig heavy chain V r
19	35	60.3	167	2 T16454	hypothetical prote
20	35	60.3	210	1 B69265	conserved hypoten
21	35	60.3	230	2 S46332	homeotic protein G
22	35	60.3	255	2 B71273	probable methionin
23	35	60.3	296	2 H55118	hypothetical adenil
24	35	60.3	326	2 S47248	site-specific DNA-
25	35	60.3	378	2 T11713	probable alpha-1,2
26	35	60.3	555	2 T21028	hypothetical prote
27	35	60.3	575	2 T12094	beta-fructofuranos
28	35	60.3	583	2 S56680	beta-fructofuranos
29	35	60.3	592	2 J00991	beta-fructofuranos
30	35	60.3	592	2 S56681	beta-fructofuranos

31 35 60.3 592 2 S61503 beta-fructofuranos
32 35 60.3 593 2 T01575 beta-fructofuranos
33 35 60.3 686 2 D71292 probable DNA recom
34 35 60.3 790 2 S67803 probable membrane
35 34 58.6 80 2 S25050 Ig heavy chain V r
36 34 58.6 102 2 S25025 Ig heavy chain - m
37 34 58.6 106 2 S25036 Ig heavy chain V r
38 34 58.6 107 2 PL0080 Ig kappa chain V r
39 34 58.6 108 2 C72852 AcOrf-19 protein -
40 34 58.6 108 2 D44221 orf4 protein - Aut
41 34 58.6 110 2 T41765 AcMNPV orf19 - Bom
42 34 58.6 111 2 S25052 Ig heavy chain V r
43 34 58.6 111 2 S25055 Ig heavy chain V r
44 34 58.6 111 2 S25054 Ig heavy chain V r
45 34 58.6 111 2 S25031 Ig heavy chain V r

ALIGNMENTS

RESULT 1

S26468
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26468
R.Kavaler, J.
submitted to the EMBL Data Library, April 1991

A:Reference number: S26459
A:Accession: S26468
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <NAV>

A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945
C:Superfamily: Immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 67.2%; Score 39; DB 2; Length 113;
Best Local Similarity 66.7%; Pred. No. 3;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
||| ||:|
Db 93 ARHPYGNYY 101

RESULT 2

D71087
probable translation initiation factor eIF-2 alpha chain - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 26-Aug-1999
C:Accession: D71087
R.Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Halkawa, Y.; Hino, Y.; Yamamoto, S.; Se
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophil
A:Reference number: A71000; MUID:98344137

A:Accession: D71087
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-275 <KAW>

A:Cross-references: GB:AP000004; NID:g3236131; PIDN:BAA30058.1; PID:d1031001; PID:g32
A:Experimental source: strain OT3
A>Note: this accession replaces an Interim accession for a sequence replaced by GenBa
C:Genetics:
C:Gene: PH0961

C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 65.5%; Score 38; DB 2; Length 275;
Best Local Similarity 75.0%; Pred. No. 11;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFY 10
|||||

Db 23 HNYGAFLE 30

RESULT 3

G75130
translation initiation factor aif-2, subunit alpha (aif2a) PAB0568 - Pyrococcus abyssi

C:Species: Pyrococcus abyssi

C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 24-Nov-1999

C:Accession: G75130

R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome structure

A:Reference number: A75001

A:Accession: G75130

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-275 <RAW>

A:Cross-references: GB:AJ248285; GB:AL096836; NID:g5458067; PIDN:CAB49760.1; PID:e151565

A:Experimental source: strain Orsay

C:Genetics:

A:Gene: aif2A; PAB0568

C:Superfamily: translation initiation factor eIF-2 alpha chain

Query Match 65.5%; Score 38; DB 2; Length 275;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFY 10
|||||

Db 23 HNYGAFLE 30

RESULT 4

T25001
hypothetical protein T19C9.8 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T25001

R:Matthews, L.
submitted to the EMBL Data Library, March 1997

A:Reference number: Z19967

A:Accession: T25001

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-402 <WIL>

A:Cross-references: EMBL:292972; PIDN:CAB07486.1; GSPDB:GN00023; CESP:T19C9.8

A:Experimental source: clone T19C9

C:Genetics:

A:Gene: CESP:T19C9.8

A:Map position: 5

A:Introns: 54/1; 229/2; 337/2

Query Match 65.5%; Score 38; DB 2; Length 402;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFY 10
|||||

Db 261 HDYNSFY 268

RESULT 5

B72651
hypothetical protein APE0639 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999

C:Accession: B72651

R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J. DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero

A:Reference number: A72450; MUID:99310339

A:Accession: B72651

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-134 <RAW>

A:Cross-references: DDBJ:AP000060; NID:g5104188; PIDN:BAA79610.1; PID:d1043396; PID:g

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE0639

Query Match 63.8%; Score 37; DB 2; Length 134;
Best Local Similarity 75.0%; Pred. No. 8.3;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFY 10
|||||

Db 26 HNYGNFY 33

RESULT 6

S51436
probable membrane protein YLR191w - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein L9470.1

C:Species: Saccharomyces cerevisiae

C>Date: 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 06-Feb-1998

C:Accession: S51436

R:Wohldmann, P.
submitted to the EMBL Data Library, November 1994

A:Description: The sequence of S. cerevisiae cosmid 9470.

A:Reference number: S51414

A:Accession: S51436

A:Molecule type: DNA

A:Residues: 1-386 <WOH>

A:Cross-references: EMBL:U17246; NID:g577192; PID:g577193; MIPS:YLR191w

C:Genetics:

A:Gene: SGD:PEX13

A:Cross-references: SGD:S0004181; MIPS:YLR191w

A:Map position: 12R

C:Superfamily: SH3 homology

C:Keywords: transmembrane protein

F:284-280/Domain: transmembrane #status predicted <TMM>

F:313-367/Domain: SH3 homology <SH3>

Query Match 63.8%; Score 37; DB 2; Length 386;
Best Local Similarity 85.7%; Pred. No. 24;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSFY 9
|||||

Db 117 NNYGSFY 123

RESULT 7

JC5461
cellulase (EC 3.2.1.4) precursor - imperfect fungus (Humicola grisea)

N:Alternate names: endo-1,4-beta-glucanase; endoglucanase

C:Species: Humicola grisea var. thermolidea

C>Date: 11-Sep-1998 #sequence_revision 11-Sep-1998 #text_change 18-Jun-1999

C:Accession: JC5461

R:Takashima, S.; Nakamura, A.; Masaki, H.; Uozumi, T.
Biosci. Biotechnol. Biochem. 61, 245-250, 1997

A:Title: Cloning, sequencing, and expression of a thermostable cellulase gene of Humi

A:Reference number: JC5461; MUID:97212020

A:Accession: JC5461

A:Molecule type: DNA

A:Residues: 1-388 <TAK>

A:Cross-references: DDBJ:D84470; NID:q1304101; PIDN:BAAL2676.1; PID:d1013356; PID:q13

A:Experimental source: strain IFO9854

C:Genetics:

A:Gene: egl2

A:Introns: 120/3; 369/1

C:Function:

A:Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as cel-

A:Pathway: cellulose degradation

C:Superfamily: Trichoderma cellulase III; fungal cellulose-binding domain homology

C:Keywords: glycosidase; hydrolase; polysaccharide degradation

F:1-16/Domain: signal sequence #status predicted <SIG>

F:17-388/Product: cellulase #status predicted <MAT>

F:21-52/Domain: fungal cellulose-binding domain homology <FCB>

Query Match 63.8%; Score 37; DB 1; Length 388;
Best Local Similarity 62.5%; Pred. No. 24;
Matches 5; Conservative 2; Mismatches 1; Indels 1; Gaps 0;

QY 3 HNYGSFYE 10

||| :||
Db 175 HNFGRYVE 182

RESULT 8

S43920

cellulase (EC 3.2.1.4) precursor - imperfect fungus (Humicola insolens)

N:Alternate names: endo-1,4-beta-glucanase; endoglucanase

C:Species: Humicola insolens

C:Date: 11-Sep-1998 #sequence_revision 11-Sep-1998 #text_change 18-Jun-1999

C:Accession: S43920

R:Dalboge, H.; Helldt-Hansen, H.P.

Mol. Gen. Genet. 243, 253-260, 1994

A:Title: A novel method for efficient expression cloning of fungal enzyme genes.

A:Reference number: S43919; MUID:94247364

A:Accession: S43920

A:Molecule type: mRNA

A:Residues: 1-388 <DAL>

A:Cross-references: EMBL:X76046; NID:g505194; PIDN:CAA53631.1; PID:g505195

C:Genetics:

A:Gene: CMC3

C:Function:

A:Description: hydrolysis of 1,4-beta-D-glucosidic linkages in beta-D-glucans such as cel-

A:Pathway: cellulose degradation

C:Superfamily: Trichoderma cellulase III; fungal cellulose-binding domain homology

C:Keywords: glycosidase; hydrolase; polysaccharide degradation

F:1-16/Domain: signal sequence #status predicted <SIG>

F:17-388/Product: cellulase #status predicted <MAT>

F:21-52/Domain: fungal cellulose-binding domain homology <FCB>

Query Match 63.8%; Score 37; DB 1; Length 388;
Best Local Similarity 62.5%; Pred. No. 24;
Matches 5; Conservative 2; Mismatches 1; Indels 1; Gaps 0;

QY 3 HNYGSFYE 10

||| :||
Db 175 HNFGRYVE 182

RESULT 9

T29999

hypothetical protein ZC8.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T29999

R:Latreille, P.; Bradshaw, H.

submitted to the EMBL Data Library, July 1996

A:Description: The sequence of C. elegans cosmid ZC8.

A:Reference number: Z20719

A:Accession: T29999

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-2288 <LAT>

A:Cross-references: EMBL:D64862; PIDN:AAB52624.1; GSPDB:GN00028; CESP:ZC8.4
A:Experimental source: strain Bristol N2; clone ZC8

C:Genetics:

A:Gene: CESP:ZC8.4

A:Map position: 10

A:Introns: 43/2; 80/3; 110/3; 153/2; 274/3; 738/2; 1249/1; 1392/3; 1454/1; 1602/1; 16

Query Match 63.8%; Score 37; DB 2; Length 2288;
Best Local Similarity 66.7%; Pred. No. 1.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9

:| ||| ||
Db 34 SRSNYGEFY 42

RESULT 10

I51106

Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)

C:Species: Phasianus colchicus (ring-necked pheasant)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999

C:Accession: I51106

R:Wittzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.

Immunogenetics 39, 395-403, 1994

A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-ne

A:Reference number: I51103; MUID:94245280

A:Accession: I51106

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-82 <WIT>

A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 62.1%; Score 36; DB 2; Length 82;
Best Local Similarity 85.7%; Pred. No. 7.8;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

||||| |
Db 75 RHNYGVF 81

RESULT 11

S38688

MHC class II histocompatibility antigen HLA-DR-08 beta chain - Galago senegalensis (f

C:Species: Galago senegalensis

C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997

C:Accession: S38688

R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.

submitted to the EMBL Data Library, November 1993

A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduce

A:Reference number: S38676

A:Accession: S38688

A:Molecule type: DNA

A:Residues: 1-89 <FIG>

A:Cross-references: EMBL:Z27158

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 62.1%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8

||||| |
Db 75 RHNYGVF 81

RESULT 12

S38683

MHC class II histocompatibility antigen HLA-DR-03 beta chain - Galago senegalensis (f

C:Species: Galago senegalensis
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997
C:Accession: S38683
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from
A:Reference number: S38676
A:Accession: S38683
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27153
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 62.1%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 75 RHNYGVF 81

RESULT 13

S38684
MHC class II histocompatibility antigen HLA-DR-04 beta chain - Galago senegalensis (fragment)
C:Species: Galago senegalensis
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997
C:Accession: S38684
R:Figuerola, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced from
A:Reference number: S38676
A:Accession: S38684
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:Z27154
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 62.1%; Score 36; DB 2; Length 89;
Best Local Similarity 85.7%; Pred. No. 8.5;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 75 RHNYGVF 81

RESULT 14

I47095
MHC class II OVAR-DR-beta-3 - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 23-Jul-1999
C:Accession: I47095
R:Fabb, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.
Anim. Genet. 24, 249-255, 1993
A:Title: Isolation, characterization and evolution of ovine major histocompatibility complex
A:Reference number: I47095
A:Accession: I47095
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-225 <FAB>
A:Cross-references: GB:L04790; NID:g458880; PIDN:AAA16562.1; PID:g458881
C:Genetics:
A:Gene: OVAR-DRB3
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 62.1%; Score 36; DB 2; Length 225;
Best Local Similarity 85.7%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
|||||
Db 68 RHNYGVF 74

RESULT 15

T19625
hypothetical protein C31H5.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19625
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19625
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-446 <WIL>
A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6
A:Experimental source: clone C31H5
C:Genetics:
A:Gene: CESP:C31H5.6
A:Map position: 1
A:Introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3

Query Match 62.1%; Score 36; DB 2; Length 446;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGS 7
|||||
Db 51 RHNYGS 56

Search completed: May 27, 2000, 19:52:03
Job time: 1506 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 20:45:29 ; Search time 48.34 Seconds
(without alignments)
6.300 Million cell updates/sec

Title: US-09-016-061-98
Perfect score: 58
Sequence: 1 ARHNYGSFYE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	65.5	275	1 IF2A_PYRHO	O58655 pyrococcus
2	37	63.8	386	1 PEXD_YEAST	P06677 saccharomyc
3	36	62.1	470	1 SYE2_RICPR	Q92ct8 rickettsia
4	36	62.1	786	1 EXOP_THIME	P33698 rhizobium m
5	35	60.3	255	1 AMPM_TREPA	O83814 treponema p
6	35	60.3	294	1 YHDJ_ECOLI	P28638 escherichia
7	35	60.3	361	1 LIM4_MOUSE	P53776 mus musculus
8	35	60.3	583	1 INV3_DAUCA	Q39693 daucus caro
9	35	60.3	592	1 INV1_DAUCA	P27692 daucus caro
10	35	60.3	592	1 INV2_DAUCA	Q39692 daucus caro
11	35	60.3	686	1 RECG_TREPA	P96130 treponema p
12	34	58.6	108	1 Y019_NPVAC	P41424 autographa
13	34	58.6	284	1 IPYR_PICPA	O13505 pichia past
14	34	58.6	286	1 IPYR_KLGLA	P13998 kluyveromyc
15	34	58.6	286	1 IPYR_YEAST	P00817 saccharomyc
16	34	58.6	564	1 LDHD_HAEIN	P45295 haemophilus
17	34	58.6	718	1 LSP2_DROME	Q24388 drosophila
18	34	58.6	887	1 QVAL_DROME	Q23989 drosophila
19	33	56.9	89	1 CFA_CITFR	P45509 citrobacter
20	33	56.9	347	1 UL33_HSV6U	P52380 herpes simp
21	33	56.9	364	1 SUCC_METJA	O57663 methanococc
22	33	56.9	448	1 NCAP_CVHOC	P33469 human coron
23	33	56.9	473	1 SYE_AQUAE	O67271 aquifex aeo
24	33	56.9	494	1 RNHI_CRIFA	Q07762 crithidia f
25	33	56.9	512	1 PNTA_HAEIN	P43842 haemophilus
26	33	56.9	514	1 LIM_HALRO	Q25132 halocynthia
27	33	56.9	713	1 HS90_EIMTE	O44001 elmeria ten
28	33	56.9	715	1 ADSV_BOVIN	Q28046 bos taurus
29	33	56.9	725	1 SPEI_DIACA	Q96412 dianthus ca
30	33	56.9	826	1 VILI_CHICK	P02640 gallus gall
31	33	56.9	1386	1 RPOD_MARPO	P06274 marchantia
32	33	56.9	1394	1 ITA2_DROME	P12080 drosophila
33	33	56.9	2184	1 RPPL_CDVO	P24658 canine dist
34	32.5	56.0	2148	1 VITI_AEDAE	Q16927 aedes aegyp

35	32	55.2	65	1 CCSA_OENBE	P31565 oenothera b
36	32	55.2	65	1 CCSA_PEA	P31172 pisum sativ
37	32	55.2	119	1 V120_ASFL5	P26704 african swi
38	32	55.2	194	1 PTH_SALTI	O60001 salmonella
39	32	55.2	196	1 WBJI_ECOLI	P37750 escherichia
40	32	55.2	198	1 HB2C_HUMAN	P01911 homo sapien
41	32	55.2	209	1 Y038_NPVOP	Q05125 orgyia pseu
42	32	55.2	266	1 HB2A_HUMAN	P01913 homo sapien
43	32	55.2	266	1 HB2B_HUMAN	P01912 homo sapien
44	32	55.2	266	1 HB2C_HUMAN	P01914 homo sapien
45	32	55.2	266	1 HB2D_CANFA	P18470 canis famil

ALIGNMENTS

RESULT	1				
IF2A_PYRHO					
ID	IF2A_PYRHO	STANDARD;	PRT;	275 AA.	
AC	O58655;				
DT	15-DEC-1998 (Rel. 37, Created)				
DT	15-DEC-1998 (Rel. 37, Last sequence update)				
DT	15-FEB-2000 (Rel. 39, Last annotation update)				
DE	PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).				
GN	PH0961.				
OS	Pyrococcus horikoshii.				
OC	Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=OT3;				
RX	MEDLINE; 98344137.				
RA	Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,				
RA	Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,				
RA	Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,				
RA	Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,				
RA	Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,				
RA	Masuchi Y., Shizuya H., Kikuchi H.;				
RT	*Complete sequence and gene organization of the genome of a hyper-				
RT	thermophilic archaeobacterium, Pyrococcus horikoshii OT3.;				
RL	DNA Res. 5:55-76(1998).				
CC	-1- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS				
CC	BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA				
CC	(BY SIMILARITY).				
CC	-1- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA				
CC	CHAIN (BY SIMILARITY).				
CC	-----				
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; AP000004; BAA30058.1; -				
DR	PFAM; PF00575; S1; 1.				
KW	Initiation factor; Protein biosynthesis.				
SQ	SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;				

Query Match 65.5%; Score 38; DB 1; Length 275;
Best Local Similarity 75.0%; Pred. No. 3.6;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYE 10
|||||
Db 23 HNYGAFLE 30

RESULT

PEXD_YEAST	2				
ID	PEXD_YEAST	STANDARD;	PRT;	386 AA.	
AC	P80667;				

DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE PEROXISOMAL MEMBRANE PROTEIN PAS20 (PEROXIN-13).
 GN PEX13 OR PAS20 OR YLR191W OR L9470.1.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomyces.
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE; 97011156.
 RA Elgersma Y., Kwast L., Klein A., Voorn-Brouwer T., van den Berg M.,
 RA Tabak H.F., Distel B.;
 RT "The SH3 domain of the Saccharomyces cerevisiae peroxisomal membrane
 RT protein Pex13p functions as a docking site for Pex5p, a mobile
 RT receptor for the Import PTS1-containing proteins.";
 RL J. Cell Biol. 135:97-109(1996).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
 RA Favell A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,
 RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
 RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,
 RA Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,
 RA Taich A., Trevasakis E., Vignati D., Wilcox L., Wohlman P., Vaudin M.,
 RA Wilson R., Waterston R.;
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN PARTIAL SEQUENCE, AND CHARACTERIZATION.
 RC STRAIN=S288C;
 RX MEDLINE; 97011157.
 RA Erdmann R., Blobel G.;
 RT Identification of Pex13p as a peroxisomal membrane receptor for the
 RT PTS1 recognition factor.";
 RL J. Cell Biol. 135:111-121(1996).
 CC -1- FUNCTION: COMPONENT OF THE PEROXISOMAL TRANSLOCATION MACHINERY
 CC WITH PEX14 AND PEX17. INTERACTS WITH THE PTS1 RECEPTOR
 CC (PAS10/PEX5).
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PEROXISOMAL.
 CC -1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
 CC -----
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 CC -----
 DR EMBL; S82971; AAB46885.1; -;
 DR EMBL; U37420; AAY9308.1; -;
 DR EMBL; U17246; AAB67453.1; -;
 DR EMBL; U14913; AAB67448.1; -;
 DR HSSP; Q06187; 1AWW.
 DR SGD; L0003024; PAS20.
 DR PRINTS; PR00452; SH3DOMAIN.
 DR PROSITE; PS50002; SH3; 1.
 DR PFAM; PF00018; SH3; 1.
 KW Peroxisome; Transport; Protein transport; Transmembrane; SH3 domain.
 FT DOMAIN 1 263 LUMENAL (POTENTIAL).
 FT TRANSMEM 264 280 POTENTIAL.
 FT DOMAIN 281 386 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 306 372 SH3.
 SQ SEQUENCE 386 AA; 42706 MW; DBEA9A2372185860 CRC64;
 Query Match 63.8%; Score 37; DB 1; Length 386;
 Best Local Similarity 85.7%; Pred. No. 8.1;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 HNYGSFY 9
 :|||||

Db 117 NNYGSFY 123
 RESULT 3
 SYE2_RICPR STANDARD; PRT; 470 AA.
 AC Q9ZCT8;
 DT 15-FEB-2000 (Rel. 39, Created)
 DT 15-FEB-2000 (Rel. 39, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE GLUTAMYL-TRNA SYNTHETASE 2 (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE 2)
 DE (GLURS 2).
 GN GLTX2 OR RP623.
 OS Rickettsia prowazekii.
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
 OC Rickettsiaceae; Rickettsieae; Rickettsia.
 RN [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=MADRID E;
 RX MEDLINE; 99039499.
 RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
 RA Sicheit-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
 RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
 RT "The genome sequence of Rickettsia prowazekii and the origin of
 RT mitochondria.";
 RL Nature 396:133-140(1998).
 CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) = AMP +
 CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
 CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; AJ235272; CAAL5066.1; -;
 DR HSSP; P27000; 1GLN.
 DR PROSITE; PS00178; AA-TRNA_LIGASE_I; FALSE_NEG.
 KW Aminoacyl-TRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
 FT SIMILAR 10 20 "HIGH" REGION.
 FT SIMILAR 239 243 "KMSKS" REGION.
 FT BINDING 242 242 ATP (BY SIMILARITY).
 SQ SEQUENCE 470 AA; 53696 MW; DFICE50A20B9A9FD CRC64;
 Query Match 62.1%; Score 36; DB 1; Length 470;
 Best Local Similarity 66.7%; Pred. No. 16;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 ARHNYGSFY 9
 ||||| |:
 Db 31 ARHNGKFF 39
 RESULT 4
 EXOP_RHIME STANDARD; PRT; 786 AA.
 AC P33698;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE SUCCINOGLYCAN BIOSYNTHESIS TRANSPORT PROTEIN EXOP.
 GN EXOP.
 OS Rhizobium meliloti.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 RN [1]
 RN SEQUENCE FROM N.A.

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RC STRAIN-1021;
RX MEDLINE; 94042869.
RA Glucksmann M.A., Reuber T.L., Walker G.C.;
RT "Family of glycosyl transferases needed for the synthesis of
RL succinoglycan by Rhizobium meliloti.";
RL J. Bacteriol. 175:7033-7044(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-1021;
RX MEDLINE; 94042870.
RA Glucksmann M.A., Reuber T.L., Walker G.C.;
RT "Genes needed for the modification, polymerization, export, and
RL processing of succinoglycan by Rhizobium meliloti: a model for
RN succinoglycan biosynthesis.";
RN J. Bacteriol. 175:7045-7055(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-2011;
RX MEDLINE; 94067019.
RA Becker A., Kleickmann A., Keller M., Arnold W., Puehler A.;
RT "Identification and analysis of the Rhizobium meliloti exoAMONP genes
RL involved in exopolysaccharide biosynthesis and mapping of promoters
RN located on the exoKLANONP fragment.";
RN Mol. Gen. Genet. 241:367-379(1993).
CC -1- PATHWAY: EXOPOLYSACCHARIDE BIOSYNTHESIS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
CC -1- SIMILARITY: SOME, TO B. SOLANACEARUM EPSB.
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-----
DR EMBL; L20758; AAA16042.1; -.
DR EMBL; Z22636; CAA80349.1; -.
DR PIR; B49349; B49349.
DR PIR; S37031; S37031.
DR PIR; S39960; S39960.
KW Exopolysaccharide synthesis; Transport; Transmembrane; ATP-binding.
FT DOMAIN 1 42
FT TRANSMEM 43 66
FT POTENTIAL.
FT DOMAIN 67 689
FT PERIPLASMIC (POTENTIAL).
FT TRANSMEM 690 711
FT POTENTIAL.
FT DOMAIN 712 786
FT CYTOPLASMIC (POTENTIAL).
FT NP_BIND 583 590
FT ATP (POTENTIAL).
SQ SEQUENCE 786 AA; 86123 MW; E19E771E31F2030C CRC64;

Query Match 62.1%; Score 36; DB 1; Length 786;
Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9
| | | | |
Db 768 RHRYGKY 775

RESULT 5
AMPM_TREPA
ID AMPM_TREPA STANDARD; PRT; 255 AA.
AC O83814;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE METHIONINE AMINOPEPTIDASE (EC 3.4.11.18) (MAP) (PEPTIDASE M).
GN MAP OR TP0842.
OS Treponema pallidum.
OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN-NICHOLS;
RX MEDLINE; 98332770.
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artlach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete.";
RT Science 281:375-388(1998).
CC -1- FUNCTION: REMOVES THE AMINO-TERMINAL METHIONINE FROM NASCENT
CC PROTEINS.
CC -1- CATALYTIC ACTIVITY: L-METHIONYLPEPTIDE + H(2)O = L-METHIONINE +
CC PEPTIDE.
CC -1- COFACTOR: COBALT (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M24; ALSO KNOWN AS THE
CC MAP FAMILY 1.
-----
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-----
DR EMBL; AE001255; AAC65810.1; -.
DR TIGR; TP0842; -.
DR PRINTS; PR00599; MAPPEPTIDASE.
DR PROSITE; PS00680; MAP_1; 1.
DR PFAM; PF00557; Peptidase_M24; 1.
KW Amino-peptidase; Hydrolase; Cobalt.
FT METAL 93 93
FT METAL 104 104
FT METAL 174 174
FT METAL 201 201
FT METAL 233 233
FT SEQUENCE 255 AA; 27316 MW; 4EDE582C67F3526A CRC64;

Query Match 60.3%; Score 35; DB 1; Length 255;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 10
| | | | |
Db 154 ARHFGVYVE 163

RESULT 6
YHDJ_ECOLI
ID YHDJ_ECOLI STANDARD; PRT; 294 AA.
AC P28638;
DT 01-DEC-1992 (Rel. 24, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE HYPOTHETICAL ADENINE-SPECIFIC METHYLASE IN FIS-ENVR INTERGENIC REGION
DE (EC 2.1.1.72) (ORF2).
GN YHDJ.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-K12 / MG1655;
RX MEDLINE; 97426617.
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner F.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";

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RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE OF 1-98 FROM N.A.
RX MEDLINE; 93094136.
RA Ball C.A., Osuna R., Ferguson K.C., Johnson R.C.:
RT "Dramatic changes in Fis levels upon nutrient upshift in Escherichia
RT coli.";
RL J. Bacteriol. 174:8043-8056(1992).
RN [3]
RP SEQUENCE OF 1-11 FROM N.A.
RC STRAIN=K12;
RX MEDLINE; 88217925.
RA Johnson R.C., Ball C.A., Pfeffer D., Simon M.I.;
RT "Isolation of the gene encoding the Hin recombinational enhancer
RT binding protein.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:3484-3488(1988).
CC -1- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA ADENINE =
CC S-ADENOSYL-L-HOMOCYSTEINE + DNA 6-METHYLAMINOPURINE.
CC -1- SIMILARITY: BELONGS TO THE N-6 ADENINE-SPECIFIC DNA METHYLASE
CC FAMILY.
CC
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CC
DR EMBL; U18997; AAA58066.1; ALT_INIT.
DR EMBL; AE000405; AAC76294.1; ALT_INIT.
DR EMBL; M95784; AAA23784.1; ALT_INIT.
DR EMBL; J03245; AAA83857.1;
DR PIR; D47043; D47043.
DR HSP; P11409; IB00.
DR ECOGENE; EGI1498; YHDI.
DR PRINTS; PR00506; D21NGMTFRASE.
DR PRINTS; PR00508; S21NAMTFRASE.
DR PROSITE; PS00092; N6_MTASE; 1.
DR PFAM; PF01355; N6_N4_Mtase; 1.
KW Hypothetical protein; Transferase; Methyltransferase.
FT CONFLICT 28 28 K -> N (IN REF. 2).
SQ SEQUENCE 294 AA; 33397 MW; 6BCC49D9A571884B CRC64;

Query Match 60.3%; Score 35; DB 1; Length 294;
Best Local Similarity 60.0%; Pred. No. 15;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFYE 10
Db 119 AKRHGSMYE 128
| : |||||
| : |||||

RESULT 7
LIM4_MOUSE
ID LIM4_MOUSE STANDARD; PRT; 361 AA.
AC P53776; O08916;
DT 01-OCT-1996 (Rel. 34, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE LIM HOMEOBOX PROTEIN 4 (FRAGMENT).
GN LHX4 OR GSH4 OR GSH-4.
OS LHX4 musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE OF 1-190 FROM N.A.
RC STRAIN=FVB/N; TISSUE=EMBRYO;
RX MEDLINE; 97432832.
RA Yamashita T., Moriyama K., Sheng H.Z., Westphal H.;
RT "Lhx4, a LIM homeobox gene.";
RL Genomics 44:144-146(1997).
```

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[2]
RN SEQUENCE OF 130-361 FROM N.A.
RP MEDLINE; 94298779.
RA Li H., Witte D.P., Branford W.W., Aronow B.J., Weinstein M., Kaur S.,
RA Wert S., Singh G., Schreiner C.M., Whitsett J.A., Scott W.J. Jr.,
RA Potter S.S.;
RT "Gsh-4 encodes a LIM-type homeodomain, is expressed in the developing
RT central nervous system and is required for early postnatal
RT survival.";
RL EMBO J. 13:2876-2885(1994).
CC -1- FUNCTION: MAY PLAY A CRITICAL ROLE IN THE DEVELOPMENT OF
CC RESPIRATORY CONTROL MECHANISMS AND IN THE NORMAL GROWTH AND
CC MATURATION OF THE LUNG.
CC -1- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
CC -1- TISSUE SPECIFICITY: TRANSIENT EXPRESSION IN VENTROLATERAL REGIONS
CC OF THE DEVELOPING NEURAL TUBE AND HINDBRAIN.
CC -1- SIMILARITY: TO OTHER HOMEOBOX DOMAINS. BELONGS TO THE LIM
CC SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
CC IONS.
CC
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CC
DR EMBL; U89343; AAC53336.1;
DR EMBL; S71659; AAB31260.1;
DR HSP; P02836; 1HDD.
DR MGD; MGI-101776; LHX4.
DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
DR PROSITE; PS00023; LIM_DOMAIN_2; 2.
DR PROSITE; PS00027; HOMEOBOX_1; 1.
DR PROSITE; PS00071; HOMEOBOX_2; 1.
DR PFAM; PF00046; homeobox; 1.
DR PFAM; PF00412; LIM; 2.
KW Homeobox; DNA-binding; Nuclear protein; Repeat; LIM motif;
KW Metal-binding; Zinc; Transcription regulation.
FT NON_TER 1 52 LIM.
FT DOMAIN 1 60 115 LIM.
FT DOMAIN 128 187 HOMEOBOX.
FT DNA_BIND 128 187
SQ SEQUENCE 361 AA; 40086 MW; 09535343C7990FED CRC64;

Query Match 60.3%; Score 35; DB 1; Length 361;
Best Local Similarity 55.6%; Pred. No. 18;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYE 10
Db 192 RHRWGQFYK 200
| : | | |
| : | | |

RESULT 8
INV3_DAUCA
ID INV3_DAUCA STANDARD; PRT; 583 AA.
AC Q39693;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 3 PRECURSOR (EC 3.2.1.26)
DE (SUCROSE-6-PHOSPHATE HYDROLASE 3) (INVERTASE 3) (CELL WALL BETA-
DE FRUCTOSIDASE 3).
GN INV3.
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
RN [1]
```

RP SEQUENCE FROM N.A.
RC STRAIN-CV. QUEEN ANNE'S LACE;
RX MEDLINE; 95306787.
RA Lorenz K., Lienhard S., Sturm A.;
RT "Structural organization and differential expression of carrot beta-fructofuranosidase genes: identification of a gene coding for a flower bud-specific isozyme.";
RT Plant Mol. Biol. 28:189-194(1995).
RL
CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN PHLOEM UNLOADING AND IN STRESS RESPONSE.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING BETA-D-FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES.
CC -1- SUBCELLULAR LOCATION: IONICALLY BOUND TO THE CELL WALL.
CC -1- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
CC
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CC
CC EMBL; X78423; CAA55188.1; -;
DR PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.
DR PFAM; PF00251; Glyco_hydro_32; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Cell wall; zymogen; Signal.
FT SIGNAL 1 ?
FT PROPEP ? ? POTENTIAL.
FT CHAIN ? 583 BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 3.
FT CARBOHYD 164 164 POTENTIAL.
FT CARBOHYD 280 280 POTENTIAL.
FT CARBOHYD 303 303 POTENTIAL.
FT CARBOHYD 340 340 POTENTIAL.
FT CARBOHYD 561 561 POTENTIAL.
SQ SEQUENCE 583 AA; 66381 MW; 1DBF591CD94749AF CRC64;

Query Match 60.3%; Score 35; DB 1; Length 583;
Best Local Similarity 62.5%; Pred. No. 31;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 RHNYGSFY 9
Db 313 RYDYGNY 320

RESULT 9
ID INV1_DAUCA STANDARD; PRT; 592 AA.
AC P26792;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 1 PRECURSOR (EC 3.2.1.26)
DE (SUCROSE-6-PHOSPHATE HYDROLASE 1) (INVERTASE 1) (CELL WALL BETA-FRUCTOSIDASE 1).
GN INV1.
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
[1]
RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RP STRAIN-CV. QUEEN ANNE'S LACE;
RX MEDLINE; 93005650.
RA Sturm A., Chrispeels M.J.;
RT "cDNA cloning of carrot extracellular beta-fructosidase and its expression in response to wounding and bacterial infection.";
RL Plant Cell 2:1107-1119(1990).
RN [2]
RP SEQUENCE FROM N.A.

RX MEDLINE; 94035200.
RA Ramloch-Lorenz K., Knudsen S., Sturm A.;
RT "Molecular characterization of the gene for carrot cell wall beta-fructosidase.";
RT Plant J. 4:545-554(1993).
RL
CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN PHLOEM UNLOADING AND IN STRESS RESPONSE.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING BETA-D-FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES.
CC -1- SUBCELLULAR LOCATION: IONICALLY BOUND TO THE CELL WALL.
CC -1- TISSUE SPECIFICITY: IN LEAVES AND ROOTS OF YOUNG PLANTS.
CC -1- INDUCTION: IN RESPONSE TO WOUNDING AND BACTERIAL INFECTION.
CC -1- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
CC
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CC
CC EMBL; M58362; AAA03516.1; -;
DR EMBL; J69321; CAA49162.1; -;
DR PIR; JQ0991; JQ0991.
DR PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.
DR PFAM; PF00251; Glyco_hydro_32; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Cell wall; zymogen; Signal.
FT SIGNAL 1 31 OR 39 (POTENTIAL).
FT PROPEP 32 48 OR 40 (POTENTIAL).
FT CHAIN 49 592 BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 1.
FT ACT_SITE 74 74 BY SIMILARITY.
FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (COMPLEX).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 311 311 N-LINKED (GLCNAC. . .) (COMPLEX).
FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (HIGH MANNOSE).
FT CARBOHYD 570 570 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 133 133 R -> W (IN REF. 2).
FT CONFLICT 487 487 A -> V (IN REF. 2).
SQ SEQUENCE 592 AA; 66813 MW; E3DF85355D277D0C CRC64;

Query Match 60.3%; Score 35; DB 1; Length 592;
Best Local Similarity 62.5%; Pred. No. 31;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 RHNYGSFY 9
Db 321 RYDYGNY 328

RESULT 10
ID INV2_DAUCA STANDARD; PRT; 592 AA.
AC Q39692;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 2 PRECURSOR (EC 3.2.1.26)
DE (SUCROSE-6-PHOSPHATE HYDROLASE 2) (INVERTASE 2) (CELL WALL BETA-FRUCTOSIDASE 2).
GN INV2.
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
[1]
RN SEQUENCE FROM N.A.
RP STRAIN-CV. QUEEN ANNE'S LACE;
RX MEDLINE; 95306787.
RA Lorenz K., Lienhard S., Sturm A.;
RT "Structural organization and differential expression of carrot beta-

fructofuranosidase genes: identification of a gene coding for a flower bud-specific isozyme.";
 Plant Mol. Biol. 28:189-194(1995).
 -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN PHLOEM UNLOADING AND IN STRESS RESPONSE.
 -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING BETA-D-FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES.
 -1- SUBCELLULAR LOCATION: IONICALLY BOUND TO THE CELL WALL.
 -1- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.

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EMBL; X78424; CAA55189.1;
 PROSITE; PS00609; GLYCOSYL-HYDROL_F32; 1.
 PFAM; PF00251; Glyco_hydro_32; 1.
 Hydrolase; Glycosidase; Glycoprotein; Cell wall; Zymogen; Signal.
 SIGNAL 1 ? POTENTIAL.
 PROPEP ? ? POTENTIAL.
 FT CHAIN ? 592 BETA-FRUCTOFURANOSIDASE, INSOLUBLE
 FT ACT-SITE 75 75 BY SIMILARITY.
 FT CARBOHYD 171 171 POTENTIAL.
 FT CARBOHYD 195 195 POTENTIAL.
 FT CARBOHYD 310 310 POTENTIAL.
 FT CARBOHYD 347 347 POTENTIAL.
 FT CARBOHYD 568 568 POTENTIAL.
 SQ SEQUENCE 592 AA; 67397 MW; 2734603836709133 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 592;
 Best Local Similarity 62.5%; Pred. No. 31;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9
 {}::|||
 DB 320 RYDYGNEY 327

RESULT 11
 RECG_TREPA STANDARD; PRT; 686 AA.
 AC P96130;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE ATP-DEPENDENT DNA HELICASE RECG (EC 3.6.1.-).
 GN RECG OR TP0687.
 OS Treponema pallidum.
 OC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NICHOLS;
 RA Stamm L.V., Barnes N.Y.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NICHOLS;
 RX MEDLINE; 98332770.
 RA Dodson R., Norris S.J., Weinstock G.M., White O., Sutton G.G., Fraser C.M., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Artach P., Bowman J.K., Chidambaram M., Utterback T., McDonald L., Artach P., Howell J.K., Chidambaram M., Utterback T., Hatcher B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.;
 RA "Complete genome sequence of Treponema pallidum, the syphilis spirochete.";

RL Science 281:375-388(1998).
 CC -1- FUNCTION: CRITICAL ROLE IN RECOMBINATION AND DNA REPAIR. HELP
 CC PROCESS HOLLIDAY JUNCTION INTERMEDIATES TO MATURE PRODUCTS BY
 CC CATALYSING BRANCH MIGRATION. HAS A DNA UNWINDING ACTIVITY
 CC CHARACTERISTIC OF A DNA HELICASE WITH A 3' TO 5' POLARITY. RECG
 CC UNWIND BRANCHED DUPLEX DNA (Y-DNA) (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE RECG SUBFAMILY OF HELICASES.

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 EMBL; U70661; AAB38707.1; -;
 DR EMBL; AE001243; AAC65656.1; -;
 DR TIGR; TP0687;
 DR PFAM; PF00270; DEAD; 1.
 DR PFAM; PF00271; helicase.C; 1.
 KW Helicase; DNA repair; ATP-binding; DNA recombination; DNA-binding.
 FT NP_BIND 298 305 ATP (POTENTIAL).
 FT SITE 399 402 DEQH BOX.
 SQ SEQUENCE 686 AA; 77196 MW; B05AFDC6FA046B0 CRC64;

Query Match 60.3%; Score 35; DB 1; Length 686;
 Best Local Similarity 100.0%; Pred. No. 36;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 YGSFYE 10
 |||||
 DB 116 YGSFYE 121

RESULT 12
 Y019_NPVAC STANDARD; PRT; 108 AA.
 AC P41424;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE HYPOTHETICAL 12.2 KD PROTEIN IN EGT-IAP1 INTERGENIC REGION (ORF4).
 OS Autographa californica nuclear polyhedrosis virus (ACNPV).
 OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
 OC Nucleopolyhedrovirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C6;
 RX MEDLINE; 94303173.
 RA Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
 RT "The complete DNA sequence of Autographa californica nuclear polyhedrosis virus.";
 RL Virology 202:586-605(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E2;
 RX MEDLINE; 93079853.
 RA Braunagel S.C., Daniel K.D., Reilly L.M., Guarino L.A., Hong T., Summers M.D.;
 RT "Sequence, genomic organization of the EcoRI-A fragment of Autographa californica nuclear polyhedrosis virus, and identification of a viral-encoded protein resembling the outer capsid protein VP8 of rotavirus.";
 RL Virology 191:1003-1008(1992).
 CC -1- SIMILARITY: TO CORRESPONDING ORF IN OPMPV.

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 CC -----

DR EMBL; L22858; AAA66649.1; -;
 DR EMBL; M66361; AAA66789.1; -;
 DR PIR; D44221; D44221.
 KW Hypothetical protein.
 FT CONFLICT 6
 FT SEQUENCE 108 AA; 12162 MW; 8363B15DF72486A1 CRC64;
 SQ

Query Match 58.6%; Score 34; DB 1; Length 108;
 Best Local Similarity 60.0%; Pred. No. 7.6;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 ARHNGSFYE 10
 | | | | |
 Db 25 ANRHSFYE 34

RESULT 13
 IPYR_PICPA STANDARD; PRT; 284 AA.
 ID IPYR_PICPA
 AC Q13505;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI.
 OS Pichia pastoris (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Pichia.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NRRL Y-11430;
 RX MEDLINE; 99034033.
 RA Cosano I.C., Alvarez P., Molina M., Nombela C.;
 RT "Cloning and sequence analysis of the Pichia pastoris TRP1, IPPI and
 RT HIS3 genes";
 RL Yeast 14:861-867(1998).

CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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 CC -----

DR EMBL; A001000; CAA04453.1; -;
 DR HSSP; P00817; IWGI.
 DR PROSITE; PS00387; PPASE; 1.
 DR PFAM; PF00719; Pyrophosphatase; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 284 AA; 31937 MW; 3DAD27970D775D6 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 284;
 Best Local Similarity 83.3%; Pred. No. 22;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
 | | | | |

Db 91 HNYGAF 96

RESULT 14
 IPYR_KLULA STANDARD; PRT; 286 AA.
 ID IPYR_KLULA
 AC P13998;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPPI OR IPP.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Kluyveromyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89189093.
 RA Stark M.J.R., Milner J.S.;
 RT "Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a
 RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
 RT and histone H3";
 RL Yeast 5:35-50(1989).
 RN [2]
 RP SIMILARITY TO E.COLI AND YEAST PPASES.
 RX MEDLINE; 90254161.
 RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihtinen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RT "Conservation of functional residues between yeast and E. coli
 RT inorganic pyrophosphatases";
 RL Biochim. Biophys. Acta 1038:338-345(1990).

CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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 CC -----

DR EMBL; X14230; CAA32446.1; -;
 DR PIR; S07894; PMVKL.
 DR HSSP; P00817; IWGI.
 DR PROSITE; PS00387; PPASE; 1.
 DR PFAM; PF00719; Pyrophosphatase; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 286 AA; 32034 MW; 11647F4ABD916A2F CRC64;

Query Match 58.6%; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 22;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
 | | | | |

Db 91 HNYGAF 96
 RESULT 15
 IPYR_YEAST STANDARD; PRT; 286 AA.
 ID IPYR_YEAST
 AC P00817;
 DT 21-JUL-1986 (Rel. 01, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
DE HYDROLASE) (PBASE).
GN IPP1 OR PPA1 OR PPA OR YBR011C OR YBR0202.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Saccharomyces.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=X2180.
RX MEDLINE: 89083474.
RA Kolakowski L.F. Jr., Schloesser M., Cooperman B.S.;
RT "Cloning, molecular characterization and chromosome localization of
RT the inorganic pyrophosphatase (PPA) gene from *S. cerevisiae*.";
RL Nucleic Acids Res. 16:10441-10452(1988).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Entian K.-D., Koetter P., Rose M., Li Z., Thermann R., Brendel M.,
RA Baur A., Boles E., Miosga T., Schaaff-Gerstenschlaeger I.,
RA Zimmermann F.K.;
RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE.
RX MEDLINE: 78087552.
RA Cohen S.A., Sterner R., Keim P.S., Heinrikson R.L.;
RT "Covalent structural analysis of yeast inorganic pyrophosphatase.";
RL J. Biol. Chem. 253:899-897(1978).
RN [4]
RP SEQUENCE OF 25-35 AND 239-251.
RC STRAIN=S288C;
RX MEDLINE: 95203288.
RA Garrels J.I., Fletcher B., Kobayashi R., Latter G.I., Schwender B.,
RA Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a Saccharomyces cerevisiae protein
RT database.";
RN [5]
RP Electrophoresis 15:1466-1486(1994).
RC SEQUENCE OF 239-249.
RC STRAIN=ATCC 38531 / Y41;
RX MEDLINE: 97089742.
RA Norbeck J., Blomberg A.;
RT "Protein expression during exponential growth in 0.7 M NaCl medium of
RT Saccharomyces cerevisiae";
RL FEMS Microbiol. Lett. 137:1-8(1996).
RN [6]
RP ACTIVE SITE.
RX MEDLINE: 80109718.
RA Bond M.W., Chiu N.Y., Cooperman B.S.;
RT "Identification of an arginine important for enzymatic activity
RT within the covalent structure of yeast inorganic pyrophosphatase.";
RL Biochemistry 19:94-102(1980).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
RA Arutunian E.G., Terzian S.S., Voronova A.A., Kuranova I.P.,
RA Smirnova E.A., Vainstein B.K., Hohn W.E., Hansen G.;
RT "X-ray diffraction study of inorganic pyrophosphatase from baker's
RT yeast at the 3-A resolution.";
RL Dokl. Akad. Nauk SSSR 258:1481-1492(1981).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
RX MEDLINE: 97148342.
RA Heikinheimo P., Lehtonen J., Baykov A., Lahti R., Cooperman B.S.,
RA Goldman A.;
RT "The structural basis for pyrophosphatase catalysis.";
RL Structure 4:1491-1508(1996).
RN [9]
RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
RA Swaminathan K., Cooperman B.S., Lahti R., Voet D.;
RL Submitted (DEC-1997) to the PDB data bank.
RN [10]
RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF MUTANTS LYS-78 AND LYS-117.
RX MEDLINE: 99096888.
RA Tuominen V., Heikinheimo P., Kajander T., Torkkel T., Hyytiä T.,
RA Kypälä J., Lahti R., Cooperman B.S., Goldman A.;
RT "The R78K and D117E active-site variants of Saccharomyces cerevisiae
RT soluble inorganic pyrophosphatase: structural studies and mechanistic
RT implications.";
RL J. Mol. Biol. 284:1565-1580(1998).
RN [11]
RP SIMILARITY TO E-COLI AND K-LACTIS PBASES.
RX MEDLINE: 90254161.
RA Lahti R., Kolakowski L.F. Jr., Heinonen J., Vihinen M., Pohjanoksa K.,
RA Cooperman B.S.;
RT "Conservation of functional residues between yeast and *E. coli*
RT inorganic pyrophosphatases.";
RL Biochim. Biophys. Acta 1038:338-345(1990).
CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY. IT BINDS UP TO 4 DIVALENT
CC CATIONS PER SUBUNIT, WITH THREE REQUIRED FOR ACTIVITY.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE PBASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X13253; CAA31629.1; -;
DR EMBL: Z35880; CAA84949.1; -;
DR PIR: S45864; PWEY.
DR PDB: 1YPY; 15-OCT-91.
DR PDB: 1YPP; 07-DEC-96.
DR PDB: 1WGI; 19-NOV-97.
DR PDB: 1WGI; 19-NOV-97.
DR PDB: 1WGI; 19-NOV-97.
DR PDB: 1H0J; 08-APR-98.
DR PDB: 1H0J; 08-APR-98.
DR PDB: 1HUK; 08-APR-98.
DR PDB: 117E; 23-DEC-98.
DR PDB: 8PRK; 23-DEC-98.
DR PDB: 8PRK; 23-DEC-98.
DR SWISS-2DPAGE; P00817; YEAST.
DR YEPD; 7305; -;
DR SGD: L0000872; IPP1.
DR PROSITE: PS00387; PBASE; 1.
DR PFAM: PF00719; Pyrophosphatase; 1.
DR KW Hydrolyase; Magnesium; 3D-structure.
FT INIT_MET 0
FT ACT_SITE 56 56 PROBABLE.
FT BINDING 78 78 INORGANIC PYROPHOSPHATE.
FT CONFLICT 40 40 N -> D (IN REF. 3).
FT CONFLICT 71 71 D -> N (IN REF. 3).
FT CONFLICT 74 74 MISSING (IN REF. 3).
FT CONFLICT 123 123 E -> Q (IN REF. 3).
FT CONFLICT 136 136 Q -> E (IN REF. 3).
FT CONFLICT 186 186 N -> D (IN REF. 3).
FT CONFLICT 224 224 D -> N (IN REF. 3).
FT CONFLICT 266 266 L -> P (IN REF. 2).
FT STRAND 4 7
FT STRAND 16 20
FT STRAND 25 25
FT TURN 28 30
FT TURN 38 41
FT STRAND 45 45
FT STRAND 55 55
FT STRAND 79 79
FT TURN 97 98
FT TURN 111 112
FT STRAND 121 123
FT TURN 131 132
FT STRAND 135 135
FT STRAND 138 145

FT STRAND 151 158
 FT TURN 160 161
 FT TURN 165 167
 FT HELIX 172 175
 FT TURN 176 177
 FT TURN 179 180
 FT HELIX 182 197
 FT STRAND 203 203
 FT HELIX 205 207
 FT STRAND 210 210
 FT HELIX 212 230
 FT TURN 231 231
 FT TURN 245 246
 FT TURN 248 249
 FT TURN 251 252
 FT TURN 255 260
 FT TURN 274 275
 SQ SEQUENCE 286 AA; 32184 MW; F29390260B60C8E2 CRC64;

Query Match 58.6%; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 22;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
 Db 91 HNYGAF 96

Search completed: May 27, 2000, 20:45:30
 Job time: 2284 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:55:22 ; Search time 34.67 Seconds
(without alignments)
19,998 Million cell updates/sec

Title: US-09-016-061-98
Perfect score: 58
Sequence: 1 ARHNYGSFYE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues
Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SPTREMBL_12:
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	38	65.5	89	7	O19495 gallus gall
2	38	65.5	402	5	O45792 caenorhabdi
3	37	63.8	134	1	Q9YED6 aeryopyrum p
4	37	63.8	149	2	Q9ZBB5 streptococc
5	37	63.8	388	3	Q12620 humicola gr
6	37	63.8	388	3	Q12624 humicola in
7	37	63.8	483	10	O22861 arabidopsis
8	37	63.8	2288	5	Q23081 caenorhabdi
9	36	62.1	39	7	P79474 cervus elap
10	36	62.1	39	7	P79477 cervus elap
11	36	62.1	39	7	P79478 cervus elap
12	36	62.1	39	7	P79479 cervus elap
13	36	62.1	78	6	O97835 ovnis aries
14	36	62.1	78	6	O97839 ovnis aries
15	36	62.1	78	6	O97844 ovnis aries
16	36	62.1	78	6	O97968 ovnis aries
17	36	62.1	79	7	O19191 prionailuru
18	36	62.1	79	7	O19192 prionailuru
19	36	62.1	79	7	O19380 felis silve
20	36	62.1	79	7	O19381 felis silve

21	36	62.1	79	7	O19382 felis silve
22	36	62.1	79	7	O19396 felis silve
23	36	62.1	79	7	O19397 felis silve
24	36	62.1	79	7	O19405 felis silve
25	36	62.1	79	7	O19406 felis silve
26	36	62.1	79	7	O19407 felis silve
27	36	62.1	79	7	O19408 felis silve
28	36	62.1	79	7	O19435 felis silve
29	36	62.1	81	7	Q30568 macaca fasc
30	36	62.1	81	7	Q30571 macaca fasc
31	36	62.1	81	7	Q30737 macaca neme
32	36	62.1	81	7	Q30739 macaca neme
33	36	62.1	81	7	Q30563 macaca fasc
34	36	62.1	81	7	Q30740 macaca neme
35	36	62.1	82	7	Q95598 phasianus c
36	36	62.1	82	7	Q30606 macaca mula
37	36	62.1	82	7	Q30608 macaca mula
38	36	62.1	82	7	Q30637 macaca mula
39	36	62.1	82	7	Q30638 macaca mula
40	36	62.1	82	7	Q30658 macaca mula
41	36	62.1	82	7	Q30659 macaca mula
42	36	62.1	82	7	Q30666 macaca mula
43	36	62.1	82	7	Q30667 macaca mula
44	36	62.1	82	7	Q30668 macaca mula
45	36	62.1	82	7	O19287 macaca mula

ALIGNMENTS

RESULT 1					
O19495					
ID O19495	PRELIMINARY;	PRT;	89 AA.		
AC O19495					
DT O1-JAN-1998	(TREMBLrel. 05, Created)				
DT O1-JAN-1998	(TREMBLrel. 05, Last sequence update)				
DT O1-NOV-1998	(TREMBLrel. 08, Last annotation update)				
DE MHC CLASS II BETA 1 DOMAIN (FRAGMENT).					
GN B-LBI.					
OS Gallus gallus (Chicken).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;					
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.					
RN [1]					
RP SEQUENCE FROM N.A.					
RC STRAIN=15.151-5; TISSUE=BURSA;					
RA PHARR G.T., DODGSON J.B., HUNT H.D., BACON L.D.;					
RL Immunogenetics 47:350-354(1998).					
DR EMBL; U91532; AAC15813.1; -.					
DR PFAM; PF00969; MHC_II_beta; 1.					
KW MHC.					
FT NON_TER 1					
FT NON_TER 89					
SQ SEQUENCE 89 AA; 10724 MW; FDAC6024 CRC32;					

Query Match 65.5%; Score 38; DB 7; Length 89;
Best Local Similarity 85.7%; Pred. No. 4.1;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 75 RHNYGDF 81

RESULT 2					
O45792	PRELIMINARY;	PRT;	402 AA.		
ID O45792					
AC O45792					
DT O1-JUN-1998	(TREMBLrel. 06, Created)				
DT O1-JUN-1998	(TREMBLrel. 06, Last sequence update)				
DT O1-JAN-1999	(TREMBLrel. 09, Last annotation update)				
DE T19C9.8 PROTEIN.					
GN T19C9.8.					

OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
 OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MATTHEWS L.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94150718.
 RA WILSON R., AINSCOUGH R., ANDERSON K., BAYNES C., BEKES M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRATON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RT elegans.";
 RL Nature 368:32-38(1994).
 DR EMBL: Z92972; CAB07486.1; -.
 SQ SEQUENCE 402 AA; 45029 MW; 0AD4E30B CRC32;

Query Match 65.5%; Score 38; DB 5; Length 402;
 Best Local Similarity 75.0%; Pred. No. 21;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYE 10
 | : | | | | |
 Db 261 HDYNSFYE 268

RESULT 3
 ID QYVED6 PRELIMINARY; PRT; 134 AA.
 AC QYVED6;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE 134AA LONG HYPOTHETICAL PROTEIN.
 GN APE0639.
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Aeropyrum.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K1.
 RX MEDLINE: 99310339.
 RA KAWABAYASHI Y., HINO Y., HORIKAWA H., YAMAZAKI S., HAIKAWA Y.,
 RA JIN-NO K., TAKAHASHI M., SEKINE M., BABA S., ANKAI A., KOSUGI H.,
 RA HOSIYAMA A., FUKUI S., NAGAI Y., NISHIJIMA K., NAKAZAWA H.,
 RA TAKAMIYA M., MASUDA S., FUNAHASHI T., TANAKA T., KUDOH Y.,
 RA YAMAZAKI J., KUSHIDA N., OGUCHI A., AOKI K., KUBOTA K., NAKAMURA Y.,
 RA NOMURA N., SAKO Y., KIKUCHI H.;
 RT "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1.";
 RL DNA Res. 6:83-101(1999).
 DR EMBL: AP000060; BAA79610.1; -.
 SQ SEQUENCE 134 AA; 14845 MW; AE28BEF6 CRC32;

Query Match 63.8%; Score 37; DB 1; Length 134;
 Best Local Similarity 75.0%; Pred. No. 9.7;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYE 10
 | : | | | | |
 Db 26 HVGNFYE 33

RESULT 4.
 Q92BB5
 ID Q92BB5 PRELIMINARY; PRT; 149 AA.
 AC Q92BB5;
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)
 DE HYPOTHETICAL 17.5 KD PROTEIN.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Streptococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SP1000; TRANSPOSON-TN5252;
 RX MEDLINE: 98154299.
 RA SAMPATH J., VIJAYAKUMAR M.N.;
 RT "Identification of a DNA cytosine methyltransferase gene in
 RT conjugative transposon Tn5252.";
 RL Plasmid 39:63-76(1998).
 DR EMBL: L29323; AAC98423.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 149 AA; 17465 MW; DA75330A CRC32;

Query Match 63.8%; Score 37; DB 2; Length 149;
 Best Local Similarity 66.7%; Pred. No. 11;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 HNYGSFYE 10
 | : | | | | |
 Db 52 KHNYPLEYE 60

RESULT 5
 Q12620
 ID Q12620 PRELIMINARY; PRT; 388 AA.
 AC Q12620;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBlrel. 12, Last annotation update)
 DE CELLULOSE (EC 3.2.1.4) (ENDOGLUCANASE) (ENDO-1,4-BETA-GLUCANASE)
 DE (CARBOXYMETHYL CELLULOSE).
 OS Humicola grisea.
 OC Eukaryota; Fungi; Ascomycota; Euascomycetes; Pyrenomycetes;
 OC anamorphic Pyrenomycetes; Humicola.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-IFO9854;
 RA TAKASHIMA S., NAKAMURA A., MASAKI H., UOZUMI T.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-GLUCOSIDIC
 CC LINKAGES IN CELLULOSE.
 DR EMBL: D84470; BAA12676.1; -.
 DR HSSP: P00725; IAZH.
 DR PROSITE: PS00562; CBD_FUNGAL; 1.
 DR PFAM: PF00734; CBD_1; 1.
 DR PFAM: PF00150; cellulase; 1.
 KW Hydrolase; Glycosidase.
 SQ SEQUENCE 388 AA; 42606 MW; DDAF83CE CRC32;

Query Match 63.8%; Score 37; DB 3; Length 388;
 Best Local Similarity 62.5%; Pred. No. 30;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYE 10
 | : | | | | |
 Db 175 HNGRYE 182

RESULT 6
 Q12624
 ID Q12624 PRELIMINARY; PRT; 388 AA.

```

AC Q12624;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE CELLULOSE PRECURSOR (EC 3.2.1.4) (ENDOGLUCANASE)
DE (ENDO-1,4-BETA-GLUCANASE) (CARBOXYMETHYL CELLULOSE).
GN CMC3.
OS Humicola insolens.
OC Eukaryota; Fungi; Ascomycota; Euascomycetes; Pyrenomycetes;
OC anamorphic Pyrenomycetes; Humicola.
RN [1]
RX MEDLINE; 94247364.
RA DALBOGE H., HANSEN H.P.H.;
RT "A novel method for efficient expression cloning of fungal enzyme
RT genes.";
RL Mol. Gen. Genet. 243:253-260(1994).
CC -1- CATALYTIC ACTIVITY: ENDOHYDROLYSIS OF 1,4-BETA-D-GLUCOSIDIC
CC LINKAGES IN CELLULOSE.
DR EMBL; X76046; CAAS3631.1; -.
DR HSSP; P00725; IAZH.
DR PROSITE; PS00562; CBD_FUNGAL; 1.
DR PFAM; PF00734; CBD_1; 1.
DR PFAM; PF00150; cellulase; 1.
DR PSM; Hydrolase; Glycosidase.
KW Signal; 16 POTENTIAL.
FT SIGNAL 1 16
SQ SEQUENCE 388 AA; 42563 MW; 7FD8C7AC CRC32;

Query Match 63.8%; Score 37; DB 3; Length 388;
Best Local Similarity 62.5%; Pred. No. 30;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYE 10
Db 175 HNFGRYVE 182

RESULT 7
O22861 PRELIMINARY; PRT; 483 AA.
AC O22861;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JAN-1998 (TrEMBLrel. 05, Last annotation update)
DE HYPOTHETICAL PROTEIN.
GN T01024.21.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
OC Arabidopsis.
RN [1]
RX SEQUENCE FROM N.A.
RC STRAIN=CV, COLUMBIA;
RA ROUNSLEY S.D., TSCHUDY M.M., LIN X., KETCHUM K.A., CROSBY M.L.,
RA BRANDON R.C., SPRIGGS T.A., MASON T.M., KERLAVAGE A.R., ADAMS M.D.,
RA SOMERVILLE C.R., VENTER J.C.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC002335; AAB64341.1; -.
SQ SEQUENCE 483 AA; 54491 MW; 1450A846 CRC32;

Query Match 63.8%; Score 37; DB 10; Length 483;
Best Local Similarity 75.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 HNYGSFYE 10
Db 288 HQYASFYE 295

RESULT 8

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Q23081 PRELIMINARY; PRT; 2288 AA.
AC Q23081;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE CODED FOR BY C. ELEGANS CDNA YK33H8.3.
GN ZC8.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditida;
OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RX SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RX MEDLINE; 94150718.
RA WILSON R., AINSKOUGH R., ANDERSON K., BAYNES C., BERKS M.,
RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
RA CRATON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULTON J.,
RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
RN [2]
RX SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA LATREILLE P., BRADSHAW H.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RX SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RX SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA WATERSTON R.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U64862; AAB52624.1; -.
SQ SEQUENCE 2288 AA; 262172 MW; 6AD20DAC CRC32;

Query Match 63.8%; Score 37; DB 5; Length 2288;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNYGSFY 9
Db 34 SRSNYGEFY 42

RESULT 9
P79474 PRELIMINARY; PRT; 39 AA.
AC P79474;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-AUG-1998 (TrEMBLrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
OC Cervinae; Cervus.
RN [1]
RX SEQUENCE FROM N.A.
RA SWABRICK P.A., CRAWFORD A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63077; AAB37777.1; -.

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KW MHC.
FT NON_TER 1
   NON_TER 39
SQ SEQUENCE 39 AA; 4767 MW; E01AA287 CRC32;

Query Match
Best Local Similarity 62.1%; Score 36; DB 7; Length 39;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 10
P79477
ID P79477 PRELIMINARY; PRT; 39 AA.
AC P79477;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea; Cervidae;
OC Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.
RA SWABRICK P.A., CRAWFORD A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63080; AAB37780.1; -.
KW MHC.
FT NON_TER 1
   NON_TER 39
SQ SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match
Best Local Similarity 62.1%; Score 36; DB 7; Length 39;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 11
P79478
ID P79478 PRELIMINARY; PRT; 39 AA.
AC P79478;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea; Cervidae;
OC Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.
RA SWABRICK P.A., CRAWFORD A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63081; AAB37781.1; -.
KW MHC.
FT NON_TER 1
   NON_TER 39
SQ SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match
Best Local Similarity 62.1%; Score 36; DB 7; Length 39;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 12
P79479
ID P79479 PRELIMINARY; PRT; 39 AA.
AC P79479;
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervioidea; Cervidae;
OC Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.
RA SWABRICK P.A., CRAWFORD A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63082; AAB37782.1; -.
KW MHC.
FT NON_TER 1
   NON_TER 39
SQ SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match
Best Local Similarity 62.1%; Score 36; DB 7; Length 39;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 25 RHNYGVF 31

RESULT 13
O97835
ID O97835 PRELIMINARY; PRT; 78 AA.
AC O97835;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLA-DRB1*N20.2.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovioidea; Bovidae;
OC Caprinae; Ovis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=7407; TISSUE=BLOOD;
RA AIDA Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017207; BAA36764.1; -.
FT NON_TER 1
   NON_TER 78
SQ SEQUENCE 78 AA; 9677 MW; D252D9D CRC32;

Query Match
Best Local Similarity 62.1%; Score 36; DB 6; Length 78;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 72 RHNYGVF 78

RESULT 14

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O97839
ID O97839 PRELIMINARY; PRT; 78 AA.
AC O97839;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLA-DRB1*N2.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Caprinae; Ovis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SUFFOLK BREED AND CORRIDALE BREED; TISSUE=BLOOD;
RA AIDA Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017212; BAA36769.1; -.
FT NON_TER 1
FT NON_TER 78
FT NON_TER 78
SQ SEQUENCE 78 AA; 9430 MW; 2883C99C CRC32;

Query Match 62.1%; Score 36; DB 6; Length 78;
Best Local Similarity 85.7%; Pred. No. 8.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 72 RHNYGVF 78

RESULT 15
O97844
ID O97844 PRELIMINARY; PRT; 78 AA.
AC O97844;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAY-1999 (Tremblrel. 10, Last annotation update)
DE DR BETA-CHAIN ANTIGEN BINDING DOMAIN (FRAGMENT).
GN OLA-DRB1*N8.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Caprinae; Ovis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SUFFOLK BREED; TISSUE=BLOOD;
RA AIDA Y.;
RT "Ovis aries DNA for MHC class II DRB1 exon 2.";
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB017220; BAA36777.1; -.
FT NON_TER 1
FT NON_TER 78
FT NON_TER 78
SQ SEQUENCE 78 AA; 9645 MW; 0A246905 CRC32;

Query Match 62.1%; Score 36; DB 6; Length 78;
Best Local Similarity 85.7%; Pred. No. 8.3;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RHNYGSF 8
Db 72 RHNYGVF 78

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Search completed: May 27, 2000, 19:55:22
Job time: 986 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:50:47 ; Search time 31.68 Seconds
(without alignments)
7.477 Million cell updates/sec

Title: US-09-016-061-98
Perfect score: 58
Sequence: 1 ARHNYGSFYE 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_36.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	58	100.0	10	1 W76039	LM609 grafted anti
2	53	91.4	10	1 W76040	LM609 grafted anti
3	53	91.4	10	1 W76023	LM609 grafted anti
4	49	84.5	10	1 W76027	LM609 grafted anti
5	48	82.8	10	1 W76038	LM609 grafted anti
6	46	79.3	10	1 W76022	LM609 grafted anti
7	46	79.3	10	1 W76024	LM609 grafted anti
8	46	79.3	10	1 W76025	LM609 grafted anti
9	46	79.3	10	1 W76026	LM609 grafted anti
10	46	79.3	10	1 W76028	LM609 grafted anti
11	46	79.3	10	1 W76029	LM609 grafted anti
12	46	79.3	10	1 W76030	LM609 grafted anti
13	46	79.3	10	1 W76010	LM609 grafted anti
14	46	79.3	117	1 W76001	Vitaxin antibody h
15	46	79.3	117	1 W76003	LM609 antibody hea
16	43	74.1	10	1 W76021	LM609 grafted anti
17	41	70.7	10	1 W76037	LM609 grafted anti
18	41	70.7	10	1 W76020	LM609 grafted anti
19	38	65.5	110	1 W84099	Vitronectin alpha
20	38	65.5	117	1 W84093	Murine vitronectin
21	38	65.5	117	1 W84097	Humanised anti-alp
22	37	63.8	86	1 W60938	Streptococcus pneu
23	36	62.1	117	1 R79157	Human IgE receptor
24	36	62.1	117	1 R79155	Human IgE receptor
25	36	62.1	117	1 W7357	Heavy chain variab
26	36	62.1	117	1 W27526	Heavy chain variab
27	36	62.1	117	1 W27354	Heavy chain variab
28	36	62.1	239	1 W73874	Human antiFc epsil
29	36	62.1	242	1 W73876	Human antiFc epsil
30	34	58.6	256	1 R22568	SCFVB18 construct
31	34	58.6	256	1 R22583	SCFVB18 construct
32	34	58.6	256	1 R22584	SCFVB18 construct
33	34	58.6	256	1 R22585	SCFVB18 construct
34	34	58.6	256	1 R22586	SCFVB18 construct

35	34	58.6	256	1	R22587	SCFVB18 construct
36	33	56.9	80	1	R13396	HLA-DRW12a antigen
37	33	56.9	80	1	R13397	HLA-DRW12b antigen
38	33	56.9	270	1	R66551	Cynomolgus Monkey
39	33	56.9	270	1	W81819	M. cynomolgus 2pB
40	33	56.9	566	1	R55207	Human zona pelluci
41	33	56.9	566	1	R81816	Human 2pB protein.
42	33	56.9	715	1	R80481	Recombinant human
43	32.5	56.0	1144	1	R76059	Mycoplasma pirum a
44	32	55.2	11	1	W22700	Peptide sequence #
45	32	55.2	15	1	W25799	Synthetic human S1

ALIGNMENTS

RESULT 1

W76039
ID W76039 standard; Protein; 10 AA.
AC W76039;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #15.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998: U01826.
PR 30-JAN-1997: US-791391.
PA (IXSY-) IXSY INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49876.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
LM609, also related nucleic acid, used to treat, prevent or diagnose
angio genesis or restenosis
PS Claim 62; Page 43; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
LM609 heavy and light chain variable region; LM609 and the antibody
vitaxin bind selectively to integrin alphavbeta3 and can be used to
inhibit binding of alphavbeta3 to a ligand and thus block
integrin-mediated signal transduction. This is useful in the treatment,
prevention and diagnosis of alphavbeta3-mediated disease, specifically
angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
arthritis, macular degeneration, osteoporosis etc.). The antibodies
contain non-murine framework regions so are suitable for use in humans.
Enhanced types of LM609 have affinity more than 90 times greater than
that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 100.0%; Score 58; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00044;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFYE 10
|||||
Db 1 ARHNYGSFYE 10

RESULT 2

W76040
ID W76040 standard; Protein; 10 AA.
AC W76040;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #16.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; 001826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49877.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 43; 129pp; English.
 CC W6007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 91.4%; Score 53; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.003;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFY 9
 Db |||||
 Bb 1 ARHNYGSFY 9

RESULT 3
 ID W76023 standard; Protein; 10 AA.
 AC W76023;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #5.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; 001826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49860.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W6007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 91.4%; Score 53; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.003;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSFY 9
 Db |||||
 Bb 1 ARHNYGSFY 9

RESULT 4
 ID W76027 standard; Protein; 10 AA.
 AC W76027;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #9.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; 001826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49864.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W6007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 84.5%; Score 49; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.014;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ARHNYGSFY 10
 Db |||||
 Bb 1 ARHNYGSFAE 10

RESULT 5
 ID W76038 standard; Protein; 10 AA.

AC W76038;
 DE 02-NOV-1998 (first entry)
 DT LM609 grafted antibody V-H region CDR3 protein fragment #14.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB: V49875.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 43; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 82.8%; Score 48; DB 1; Length 10;
 Best Local Similarity 88.9%; Pred. No. 0.02;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSFV 9
 |||||
 DB 1 ARHNYGSFY 9

RESULT 6
 W76022
 ID W76022 standard; Protein; 10 AA.
 AC W76022;
 DE 02-NOV-1998 (first entry)
 DT LM609 grafted antibody V-H region CDR3 protein fragment #4.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB: V49859.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 79.3%; Score 46; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
 |||||
 DB 1 ARHNYGSF 8

RESULT 7
 W76024
 ID W76024 standard; Protein; 10 AA.
 AC W76024;
 DE 02-NOV-1998 (first entry)
 DT LM609 grafted antibody V-H region CDR3 protein fragment #6.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN WO9833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB: V49861.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;

Query Match 79.3%; Score 46; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
 |||||
 DB 1 ARHNYGSF 8


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RESULT 8
W76025
ID W76025 standard; Protein; 10 AA.
AC W76025;
DE 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #7.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49862.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angio genesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC LM609 heavy and light chain fragments of the grafted monoclonal antibody
CC vitaxin bind selectively to integrin alphavbeta3- and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
CC Sequence 10 AA;
SQ

Query Match 79.3%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
DB 1 ARHNYGSF 8

RESULT 9
W76026
ID W76026 standard; Protein; 10 AA.
AC W76026;
DE 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #8.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49863.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3

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PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angio genesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC LM609 heavy and light chain fragments of the grafted monoclonal antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
CC Sequence 10 AA;
SQ

Query Match 79.3%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
DB 1 ARHNYGSF 8

RESULT 10
W76028
ID W76028 standard; Protein; 10 AA.
AC W76028;
DE 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #10.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI; 98-437472/37.
DR N-PSDB; V49865.
PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angio genesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain fragments of the grafted monoclonal antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
CC Sequence 10 AA;
SQ

Query Match 79.3%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
DB 1 ARHNYGSF 8

Query Match 79.3%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 ARHNYGSF 8
| | | | | | | |
Db 1 ARHNYGSF 8

RESULT 11

W76029 ID W76029 standard; Protein; 10 AA.

AC W76029; DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #11.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DT N-PSDB; V49866.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 79.3%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
| | | | | | | |
Db 1 ARHNYGSF 8

RESULT 12

W76030 ID W76030 standard; Protein; 10 AA.

AC W76030; DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #12.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DT N-PSDB; V49867.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 79.3%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
| | | | | | | |
Db 1 ARHNYGSF 8

RESULT 13

W76010 ID W76010 standard; Protein; 10 AA.

AC W76010; DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #1.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DT N-PSDB; V49847.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Disclosure; Page 40; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 79.3%; Score 46; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.043;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
 Db 1 ARHNYGSF 8

RESULT 14

W76001
 ID W76001 standard; Protein; 117 AA.
 AC W76001;
 DT 02-NOV-1998 (first entry)
 DE Vitaxin antibody heavy chain variable region protein fragment.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 WPI: 98-437472/37.
 DR N-PSDB: V49820.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 1; Fig 1a; 129pp; English.
 CC This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.
 CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions
 CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.
 SQ Sequence 117 AA;

Query Match 79.3%; Score 46; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.54;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
 Db 97 ARHNYGSF 104

RESULT 15

W76003
 ID W76003 standard; Protein; 117 AA.
 AC W76003;
 DT 02-NOV-1998 (first entry)
 DE LM609 antibody heavy chain variable region protein fragment.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.

PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 WPI: 98-437472/37.
 DR N-PSDB: V49820
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 43; Fig 2a; 129pp; English.
 CC This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 SQ Sequence 117 AA;

Query Match 79.3%; Score 46; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.54;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
 Db 97 ARHNYGSF 104

Search completed: May 27, 2000, 19:50:47
 Job time: 1743 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:52:03 ; Search time 29.7 Seconds
(without alignments)
19.741 Million cell updates/sec

Title: US-09-016-061-100
Perfect score: 57
Sequence: 1 ARHNYGSPYS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 168808

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR_63.*

1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	40	70.2	113	2	S26468	Ig heavy chain V r
2	39	68.4	555	2	T21028	hypothetical prote
3	38	66.7	89	2	S38688	MHC class II histo
4	38	66.7	89	2	S38683	MHC class II histo
5	38	66.7	89	2	S38684	MHC class II histo
6	38	66.7	225	2	I47095	MHC class II OVAR-
7	37	64.9	386	2	S51436	probable membrane
8	37	64.9	479	1	F70039	conserved hypothet
9	37	64.9	2288	2	T29999	hypothetical prote
10	36	63.2	82	2	I51106	Major Histocompati
11	36	63.2	446	2	T19625	hypothetical prote
12	36	63.2	470	2	H71667	glutamate--tRNA li
13	36	63.2	575	2	T12094	beta-fructofuranos
14	36	63.2	583	2	S56680	beta-fructofuranos
15	36	63.2	592	2	JQ0991	beta-fructofuranos
16	36	63.2	592	2	S56681	beta-fructofuranos
17	36	63.2	592	2	S61503	beta-fructofuranos
18	36	63.2	593	2	T01575	beta-fructofuranos
19	36	63.2	786	2	S37031	probable succinogl
20	35	61.4	9	2	S36850	Ig heavy chain V r
21	35	61.4	83	2	S21593	Ig heavy chain V r
22	35	61.4	167	2	T16454	hypothetical prote
23	35	61.4	568	2	T28876	hypothetical prote
24	35	61.4	584	2	T06163	beta-fructofuranos
25	35	61.4	660	2	S71276	beta-fructofuranos
26	35	61.4	2295	2	B71621	probable membrane
27	34	59.6	65	2	S17441	hypothetical prote
28	34	59.6	85	2	I59634	MHC class II DR-be
29	34	59.6	89	2	S38676	MHC class II histo
30	34	59.6	89	2	S38680	MHC class II histo

31 34 59.6 89 2 S57512 MHC class II histo
32 34 59.6 98 1 WMBPF72 gene 7 protein - p
33 34 59.6 98 1 WMBPF9 gene 7 protein - p
34 34 59.6 107 2 PL0080 Ig kappa chain V r
35 34 59.6 123 2 C35239 MHC class II histo
36 34 59.6 200 2 D32526 class II histocomp
37 34 59.6 210 1 B69265 conserved hypothet
38 34 59.6 221 2 I45939 MHC cell surface g
39 34 59.6 230 2 S46332 homeotic protein G
40 34 59.6 237 2 C37060 class II histocomp
41 34 59.6 248 2 T14547 beta-fructofuranos
42 34 59.6 266 2 I34287 gene HLA-DRB1 prot
43 34 59.6 266 2 A27618 class II histocomp
44 34 59.6 266 2 I54295 lymphocyte antigen
45 34 59.6 275 2 D71087 probable translati

ALIGNMENTS

RESULT 1

S26468
Ig heavy chain V region - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S26468
R:Kavaler, J. EMBL Data Library, April 1991
submitted to the EMBL Data Library, April 1991
A:Reference number: S26459
A:Accession: S26468
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-113 <KAV>
A:Cross-references: EMBL:X59107; NID:g51944; PIDN:CAA41833.1; PID:g51945
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:11-94/Domain: immunoglobulin homology <IMM>

Query Match 70.2%; Score 40; DB 2; Length 113;
Best Local Similarity 60.0%; Pred. No. 1.8;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ARHNYGSPYS 10
||| ||::||
Db 93 ARHPYGNYYA 102

RESULT 2

T21028
hypothetical protein F16H6.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T21028
R:Matthews, L. EMBL Data Library, November 1996
submitted to the EMBL Data Library, November 1996
A:Reference number: Z19362
A:Accession: T21028
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-555 <WIL>
A:Cross-references: EMBL:Z81506; PIDN:CAB04128.1; GSPDB:GN00023; CESP:F16H6.1
A:Experimental source: clone F16H6
C:Genetics:
A:Gene: CESP:F16H6.1
A:Map position: 5
A:Introns: 123/1; 318/3

Query Match 68.4%; Score 39; DB 2; Length 555;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYS 10
|| |||||
Db 314 HNSGSFYS 321

RESULT 3

MHC class II histocompatibility antigen HLA-DR-08 beta chain - Galago senegalensis (frag
C:Species: Galago senegalensis
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997
C:Accession: S38688
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced
A:Reference number: S38676
A:Accession: S38688
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:227158
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 66.7%; Score 38; DB 2; Length 89;
Best Local Similarity 77.8%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHYGSFYS 10
|||||
Db 75 RHYGVFES 83

RESULT 4

MHC class II histocompatibility antigen HLA-DR-03 beta chain - Galago senegalensis (frag
C:Species: Galago senegalensis
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997
C:Accession: S38683
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced
A:Reference number: S38676
A:Accession: S38683
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:227153
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 66.7%; Score 38; DB 2; Length 89;
Best Local Similarity 77.8%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHYGSFYS 10
|||||
Db 75 RHYGVFES 83

RESULT 5

MHC class II histocompatibility antigen HLA-DR-04 beta chain - Galago senegalensis (frag
C:Species: Galago senegalensis
C:Date: 25-Dec-1994 #sequence_revision 26-Jul-1996 #text_change 16-Feb-1997
C:Accession: S38684
R:Figueroa, F.; O'Huigin, C.; Tichy, H.; Klein, J.
submitted to the EMBL Data Library, November 1993
A:Description: The origin of the primate Mhc-DRB genes and allelic lineages as deduced
A:Reference number: S38676
A:Accession: S38684
A:Molecule type: DNA
A:Residues: 1-89 <FIG>
A:Cross-references: EMBL:227154
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 66.7%; Score 38; DB 2; Length 89;
Best Local Similarity 77.8%; Pred. No. 3.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHYGSFYS 10
|||||
Db 75 RHYGVFES 83

RESULT 6

MHC class II OVAR-DR-beta-3 - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 15-Oct-1996 #sequence_revision 15-Oct-1996 #text_change 23-Jul-1999
C:Accession: I47095
R:Fabbs, S.A.; Maddox, J.F.; Gogolin-Ewens, K.J.; Baker, L.; Wu, M.J.; Brandon, M.R.
Anim. Genet. 24, 249-255, 1993
A:Title: Isolation, characterization and evolution of ovine major histocompatibility
A:Reference number: I47075; MUID:94057592
A:Accession: I47095
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-225 <FAB>
A:Cross-references: GB:L04790; NID:g458880; PIDN:AAA16562.1; PID:g458881
C:Genetics:
A:Gene: OVAR-DRB3
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 66.7%; Score 38; DB 2; Length 225;
Best Local Similarity 77.8%; Pred. No. 8.4;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHYGSFYS 10
|||||
Db 68 RHYGVFES 76

RESULT 7

S51436
probable membrane protein YLR191W - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein L9470.1
C:Species: Saccharomyces cerevisiae
C:Date: 23-Feb-1995 #sequence_revision 12-May-1995 #text_change 06-Feb-1998
C:Accession: S51436
R:Wohlmann, P.
submitted to the EMBL Data Library, November 1994
A:Description: The sequence of S. cerevisiae cosmid 9470.
A:Reference number: S51414
A:Accession: S51436
A:Molecule type: DNA
A:Residues: 1-386 <WOH>
A:Cross-references: EMBL:U17246; NID:g577192; PID:g577193; MIPS:YLR191W
C:Genetics:
A:Gene: SGD:PEX13
A:Cross-references: SGD:S0004181; MIPS:YLR191W
A:Map position: 12R
C:Superfamily: SH3 homology
C:Keywords: transmembrane protein
F:264-280/Domain: transmembrane #status predicted <TMM>
F:313-367/Domain: SH3 homology <SH3>

Query Match 64.9%; Score 37; DB 2; Length 386;
Best Local Similarity 85.7%; Pred. No. 22;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSFY 9
:|||||
Db 117 NNYGSFY 123

RESULT 8
F70039
conserved hypothetical protein yvfw - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: F70039
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C: Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A: Ehrlich, S.D.; Emmerison, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y, M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033
A:Accession: F70039
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-479 <KUN>
A:Cross-references: GB:Z99121; GB:AL009126; NID:g2635827; PID:e1186092; PID:g2635917
A:Experimental source: strain 168
C:Genetics:
A:Gene: yvfw
C:Superfamily: conserved hypothetical iron-sulfur protein HP0138; ferredoxin 2[4Fe-4S] H
F:303-381/Domain: ferredoxin 2[4Fe-4S] homology <FER>

Query Match 64.9%; Score 37; DB 1; Length 479;
Best Local Similarity 75.0%; Pred. No. 27;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 HNYGSFYS 10
Db 332 HSYGSYIS 339

RESULT 9
T29999
hypothetical protein ZC8.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T29999
R:Latreille, P.; Bradshaw, H.
submitted to the EMBL Data Library, July 1996
A:Description: The sequence of C. elegans cosmid zc8.
A:Reference number: Z20719
A:Accession: T29999
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-2288 <LAT>
A:Cross-references: EMBL:U64862; PIDN:AA852624.1; GSPDB:GN00028; CESP:ZC8.4
A:Experimental source: strain Bristol N2; clone ZC8
C:Genetics:
A:Gene: CESP:ZC8.4
A:Map position: 10
A:Introns: 43/2; 80/3; 110/3; 153/2; 274/3; 738/2; 1249/1; 1392/3; 1454/1; 1602/1; 1686/

Query Match 64.9%; Score 37; DB 2; Length 2288;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ARHNGSFY 9
Db 34 SRNGYGFY 42

RESULT 10
I51106
Major Histocompatibility Complex class IIB - ring-necked pheasant (fragment)
C:Species: Phasianus colchicus (ring-necked pheasant)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 23-Jul-1999
C:Accession: I51106
R:Witzell, H.; von Schantz, T.; Zoorob, R.; Auffray, C.
Immunogenetics 39, 395-403, 1994
A:Title: Molecular characterization of three Mhc class II B haplotypes in the ring-ne
A:Reference number: I51103; MUID:94245280
A:Accession: I51106
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-82 <WIT>
A:Cross-references: EMBL:X75406; NID:g496926; PIDN:CAA53160.1; PID:g496927
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 63.2%; Score 36; DB 2; Length 82;
Best Local Similarity 85.7%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RHNYGSF 8
Db 75 RHNYGVF 81

RESULT 11
T19625
hypothetical protein C31H5.6 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T19625
R:Kershaw, J.
submitted to the EMBL Data Library, April 1997
A:Reference number: Z19153
A:Accession: T19625
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-446 <WIL>
A:Cross-references: EMBL:Z93778; PIDN:CAB07846.1; GSPDB:GN00019; CESP:C31H5.6
A:Experimental source: clone C31H5
C:Genetics:
A:Gene: CESP:C31H5.6
A:Map position: 1
A:Introns: 49/2; 85/1; 120/2; 183/3; 218/3; 255/3; 285/2; 331/3; 360/3

Query Match 63.2%; Score 36; DB 2; Length 446;
Best Local Similarity 100.0%; Pred. No. 39;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RHNYGS 7
Db 51 RHNYGS 56

RESULT 12
H71667
glutamate--trna ligase (EC 6.1.1.17) (gltX2) RP623 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 08-Oct-1999
C:Accession: H71667
R:Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark
Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499
A:Accession: H71667
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-470 <AND>
A:Cross-references: GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAA15066.1; PID:e134

A:Experimental source: strain Madrid E

C:Genetics:

A:Gene: gltX2; RP623

C:Superfamily: glutamate--tRNA ligase; glutamine--tRNA ligase homology

C:Keywords: aminoacyl-tRNA synthetase; ligase; protein biosynthesis

Query Match 63.2%; Score 36; DB 2; Length 470;

Best Local Similarity 66.7%; Pred. No. 41;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 ARHNGSFY 9

|||||

Db 31 ARHNGKFF 39

RESULT 13

T12094

beta-fructofuranosidase (EC 3.2.1.26) - fava bean

C:Species: Vicia faba (fava bean)

C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 24-Nov-1999

C:Accession: T12094

R:Weber, H.; Borisjuk, L.; Heim, U.; Buchner, P.; Wobus, U.

Plant Cell 7, 1835-1846, 1995

A:Title: Seed coat-associated invertases of Fava bean control both unloading and storage

A:Reference number: Z17416; MUID:96093423

A:Accession: T12094

A:Status: preliminary; translated from GB/EMBL/DBDJ

A:Molecule type: mRNA

A:Residues: 1-575 <WEB>

A:Cross-references: EMBL:Z35162; NID:g861154; PID:g861155

A:Experimental source: cv. Fribo, seed coat

C:Genetics:

A:Gene: CWINV1

C:Superfamily: beta-fructofuranosidase

C:Keywords: cell wall; glycoprotein; glycosidase; hydrolase

Query Match

Best Local Similarity 63.2%; Score 36; DB 2; Length 575;

Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10

|||||

Db 308 RYDYGNEYA 316

RESULT 14

S56680

beta-fructofuranosidase (EC 3.2.1.26) 3 precursor, cell wall - carrot

N:Alternate names: invertase

C:Species: Daucus carota (carrot)

C>Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 22-Jun-1999

C:Accession: S56680

R:Lorenz, K.; Lienhard, S.; Sturm, A.

Plant Mol. Biol. 28, 189-194, 1995

A:Title: Structural organization and differential expression of carrot beta-fructofuran

A:Reference number: S56680; MUID:95306787

A:Accession: S56680

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-583 <LOR>

A:Cross-references: EMBL:X78423; NID:g468534; PIDN:CAA55188.1; PID:g1020102

C:Genetics:

A:Gene: inv3

A:Introns: 68/1; 71/1; 357/3; 410/3; 493/2; 523/3

C:Superfamily: beta-fructofuranosidase

C:Keywords: cell wall; glycoprotein; glycosidase; hydrolase

F:1-42/domain: signal sequence and propeptide #status predicted <SIG>

F:43-583/product: beta-fructofuranosidase 3, cell wall #status predicted <MAT>

Query Match

63.2%; Score 36; DB 2; Length 583;

Best Local Similarity 55.6%; Pred. No. 50;

Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10

|||||

Db 313 RYDYGNEYA 321

RESULT 15

JQ0991

beta-fructofuranosidase (EC 3.2.1.26) precursor - carrot

N:Alternate names: beta-fructosidase; vacuolar invertase

C:Species: Daucus carota (carrot)

C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 22-Jun-1999

C:Accession: JQ0991

R:Sturm, A.; Chrispeels, M.J.

Plant Cell 2, 1107-1119, 1990

A:Title: cDNA cloning of carrot extracellular beta-fructosidase and its expression in

A:Reference number: JQ0991; MUID:93005650

A:Accession: JQ0991

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-592 <STU>

A:Cross-references: GB:M58362; NID:g167550; PIDN:AAA03516.1; PID:g167551

C:Superfamily: beta-fructofuranosidase

C:Keywords: glycosidase; hydrolase

Query Match

Best Local Similarity 63.2%; Score 36; DB 2; Length 592;

Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10

|||||

Db 321 RYDYGNEYA 329

Search completed: May 27, 2000, 19:52:04

Job time: 1507 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 20:45:30 ; Search time 48.34 Seconds
(without alignments)
6.300 Million cell updates/sec

Title: US-09-016-061-100
Perfect score: 57
Sequence: 1 ARHNYGSFYS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters: 83857

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : SwissProt_38.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	64.9	386	1 PEXD_YEAST	P80667 saccharomyc
2	36	63.2	470	1 SYE2_RICPR	Q9zct8 rickettsia
3	36	63.2	583	1 INV3_DAUCA	Q39693 daucus caro
4	36	63.2	592	1 INV1_DAUCA	P26792 daucus caro
5	36	63.2	592	1 INV2_DAUCA	Q39692 daucus caro
6	36	63.2	786	1 EXPD_RHIME	P33698 rhizobium m
7	34	59.6	65	1 CCSA_PEA	P31172 pisum sativ
8	34	59.6	98	1 VG7_BPPH2	P13848 bacterioph
9	34	59.6	98	1 VG7_BPPH2	P07533 bacterioph
10	34	59.6	275	1 IF2A_PYRHO	O58655 pyrococcus
11	34	59.6	284	1 IPYR_PICPA	O13505 pichia past
12	34	59.6	286	1 IPYR_KLULA	P13998 kluyveromyc
13	34	59.6	286	1 IPYR_YEAST	P00817 saccharomyc
14	34	59.6	328	1 CCSA_ARATH	P56770 arabidopsis
15	34	59.6	361	1 LIM4_MOUSE	P53776 mus musculu
16	34	59.6	512	1 PNFA_HAEIN	P43842 haemophilus
17	34	59.6	683	1 SPF1_YEAST	P24332 saccharomyc
18	34	59.6	1386	1 RPOD_WARPO	P06274 marchantia
19	33	57.9	245	1 GSC_CHICK	P53545 gallus gall
20	33	57.9	313	1 CCSA_TOBAC	P12216 nicotiana t
21	33	57.9	316	1 Y025_NPVAC	P41430 autographa
22	33	57.9	347	1 UL33_HSV6U	P52380 herpes slmp
23	33	57.9	371	1 MNCP_OXYFA	P15798 oxytricha f
24	33	57.9	371	1 MNCP_OXYTR	Q27151 oxytricha t
25	33	57.9	448	1 NCAP_CVHOC	P33469 human coron
26	33	57.9	473	1 SYE_AQUAE	O67271 aquifex aeo
27	33	57.9	494	1 RNH1_CRIFA	Q07762 crithidia f
28	33	57.9	514	1 LIM_HALRO	Q25132 halocynthia
29	33	57.9	590	1 INVA_MAIZE	P49174 zea mays (m
30	33	57.9	642	1 INVA_VICFA	Q43857 vicia faba
31	33	57.9	649	1 INVA_PHAU	P29001 phaseolus a
32	33	57.9	651	1 INVA_PHAU	O24509 phaseolus v
33	33	57.9	715	1 ADSV_BOVIN	Q28046 bos taurus
34	33	57.9	802	1 YGN9_YEAST	P51321 saccharomyc

ALIGNMENTS

RESULT 1
PEXD_YEAST

ID	PEXD_YEAST	STANDARD;	PRT;	386 AA.
AC	P80667;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-OCT-1996 (Rel. 34, Last sequence update)			
DT	15-DEC-1998 (Rel. 37, Last annotation update)			
DE	PEROXISOMAL MEMBRANE PROTEIN PAS20 (PEROXIN-13).			
GN	PEX13 OR PAS20 OR YLR191W OR L9470.1.			
OS	Saccharomyces cerevisiae (Baker's yeast).			
OC	Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;			
OC	Saccharomycetales; Saccharomycetes; Saccharomycetes.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 97011156.			
RA	Elgersma Y., Kwast L., Klein A., Voorn-Brouwer T., van den Berg M.,			
RA	Tabak H.P., Distel B.;			
RT	"The SH3 domain of the Saccharomyces cerevisiae peroxisomal membrane			
RT	protein Pex13p functions as a docking site for Pex5p, a mobile			
RT	receptor for the Import PEX13-containing proteins.";			
RL	J. Cell Biol. 135:97-109(1996).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=S288C / AB972;			
RA	Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,			
RA	Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T.,			
RA	Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,			
RA	Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menezes S.,			
RA	Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L.,			
RA	Talch A., Trevasakis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,			
RA	Wilson R., Waterston R.;			
RL	Submitted (NOV-1994) to the EMBL/GenBank/DBDJ databases.			
RN	[3]			
RP	PARTIAL SEQUENCE, AND CHARACTERIZATION.			
RC	STRAIN=S288C;			
RX	MEDLINE; 97011157.			
RA	Erdmann R., Blobel G.;			
RT	"Identification of Pex13p a peroxisomal membrane receptor for the			
RT	PTS1 recognition factor.";			
RL	J. Cell Biol. 135:111-121(1996).			
CC	-1- FUNCTION: COMPONENT OF THE PEROXISOMAL TRANSLOCATION MACHINERY			
CC	WITH PEX14 AND PEX17. INTERACTS WITH THE PTS1 RECEPTOR			
CC	(PAS10/PEX5).			
CC	-1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. PEROXISOMAL.			
CC	-1- SIMILARITY: CONTAINS 1 SH3 DOMAIN.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; S82971; AAB46885.1; -			
DR	EMBL; U37420; AAA79308.1; -			
DR	EMBL; U17246; AAB67453.1; -			

P14629 xenopus lae
Q05808 anthonomus
P24658 canine dist
P31565 oenothera b
Q60001 salmonella
P37750 escherichia
P01911 homo sapien
P01913 homo sapien
P01912 homo sapien
P01914 homo sapien
P18470 canis famli

35 33 57.9 1196 1 XPG_XENLA
36 33 57.9 1790 1 VIT_ANTGR
37 33 57.9 2184 1 RRPL_CDVO
38 32 56.1 65 1 CCSA_OENBE
39 32 56.1 194 1 PTH_SALTI
40 32 56.1 196 1 WBBJ_ECOLI
41 32 56.1 198 1 HB2G_HUMAN
42 32 56.1 266 1 HB2A_HUMAN
43 32 56.1 266 1 HB2B_HUMAN
44 32 56.1 266 1 HB2C_HUMAN
45 32 56.1 266 1 HB2D_CANFA

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DR EMBL: U14913; AAB67448.1; -.
DR HSP; Q06187; IAW.
DR SGD; L003024; PAS20.
DR PRINTS; PRO0452; SH3DOMAIN.
DR PROSITE; PS00002; SH3; 1.
DR PFAM; PF00018; SH3; 1.
KW Peroxisome; Transport; Protein transport; Transmembrane; SH3 domain.
FT DOMAIN 1 263 LUMENAL (POTENTIAL).
FT TRANSMEM 264 280 POTENTIAL.
FT DOMAIN 281 386 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 306 372 SH3.
SQ SEQUENCE 386 AA; 42706 MW; DBEA9A2372185860 CRC64;

Query Match 64.9%; Score 37; DB 1; Length 386;
Best Local Similarity 85.7%; Pred. No. 8.1;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSFY 9
Db 117 NNYGSFY 123

RESULT 2
SYE2_RICPR
ID SYE2_RICPR STANDARD; PRT; 470 AA.
AC Q9ZCT8;
DT 15-FEB-2000 (Rel. 39, Created)
DT 15-FEB-2000 (Rel. 39, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE GLUTAMYL-TRNA SYNTHETASE 2 (EC 6.1.1.17) (GLUTAMATE--TRNA LIGASE 2)
DE (GLURS 2).
GN GLTX2 OR RP623.
OS Rickettsia prowazekii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MADRID E;
RX MEDLINE; 93039499.
RA Andersson S.G.E., Zomorodipour A., Andersson J.O.,
RA Sichert-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
RA Eriksson A.-S., Winkler H.H., Kurland C.G.;
RT "The genome sequence of Rickettsia prowazekii and the origin of
RT mitochondria".
RL Nature 396:133-140(1998).
CC -1- CATALYTIC ACTIVITY: ATP + L-GLUTAMATE + TRNA(GLU) = AMP +
CC PYROPHOSPHATE + L-GLUTAMYL-TRNA(GLU).
CC -1- SUBUNIT: MONOMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
CC
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CC
DR EMBL: AJ235272; CAA15066.1; -.
DR HSP; P27000; IGLN.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT SIMILAR 10 20 "HIGH" REGION.
FT SIMILAR 239 243 "KMSKS" REGION.
FT BINDING 242 242 ATP (BY SIMILARITY).
SQ SEQUENCE 470 AA; 53696 MW; DFICE5A20B8A9FD CRC64;

Query Match 63.2%; Score 36; DB 1; Length 470;
Best Local Similarity 66.7%; Pred. No. 16;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 1 ARHNYGSFY 9
Db 31 ARHNGKFF 39

RESULT 3
INV3_DAUCA
ID INV3_DAUCA STANDARD; PRT; 583 AA.
AC Q39693;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 3 PRECURSOR (EC 3.2.1.26)
DE (SUCROSE-6-PHOSPHATE HYDROLASE 3) (INVERTASE 3) (CELL WALL BETA-
DE FRUCTOSIDASE 3).
GN INV3.
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. QUEEN ANNE'S LACE;
RX MEDLINE; 95306787.
RA Lorenz K., Lienhard S., Sturm A.;
RT "Structural organization and differential expression of carrot beta-
RT fructofuranosidase genes: identification of a gene coding for a
RT flower bud-specific isozyme.".
RL Plant Mol. Biol. 28:189-194(1995).
CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN PHLOEM UNLOADING AND IN
CC STRESS RESPONSE.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING BETA-D-
CC FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES.
CC -1- SUBCELLULAR LOCATION: IONICALLY BOUND TO THE CELL WALL.
CC -1- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
CC
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CC or send an email to license@isb-sib.ch).
CC
DR EMBL: X78423; CAA55188.1; -.
DR PROSITE; PS00609; GLYCOSYL-HYDROL_F32; 1.
DR PFAM; PF00251; Glyco_hydro_32; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Cell wall; Zymogen; Signal.
FT SIGNAL 1 ? POTENTIAL.
FT PROPEP 7 ? POTENTIAL.
FT CHAIN 7 583 BETA-FRUCTOFURANOSIDASE, INSOLUBLE
FT ISOENZYME 3.
FT CARBOHYD 164 164 POTENTIAL.
FT CARBOHYD 280 280 POTENTIAL.
FT CARBOHYD 303 303 POTENTIAL.
FT CARBOHYD 340 340 POTENTIAL.
FT CARBOHYD 561 561 POTENTIAL.
SQ SEQUENCE 583 AA; 66381 MW; 1DBF591CD94749AF CRC64;

Query Match 63.2%; Score 36; DB 1; Length 583;
Best Local Similarity 55.6%; Pred. No. 20;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
Db 313 RYDIGNFYA 321

RESULT 4
INV1_DAUCA
ID INV1_DAUCA STANDARD; PRT; 592 AA.

```

P26792;
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-FEB-2000 (Rel. 39, Last annotation update)
DE BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 1 (CELL WALL BETA-
DE (SUCROSE-6-PHOSPHATE HYDROLASE 1) (INVERTASE 1) (CELL WALL BETA-
DE FRUCTOSIDASE 1).
GN INV1.
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
RN [1]
RP STURM A., Chrispeels M.J.;
RC STRAIN-CV, QUEEN ANNE'S LACE;
RX MEDLINE; 93005650.
RA "cDNA cloning of carrot extracellular beta-fructosidase and its
RT expression in response to wounding and bacterial infection.";
RL Plant Cell 2:1107-1119(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 94035200.
RA Ramloch-Lorenz K., Knudsen S., Sturm A.;
RT "Molecular characterization of the gene for carrot cell wall beta-
RT fructosidase.";
RL Plant J. 4:545-554(1993).
CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN PHLOEM UNLOADING AND IN
CC STRESS RESPONSE.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING BETA-D-
CC FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES.
CC -1- SUBCELLULAR LOCATION: IONICALLY BOUND TO THE CELL WALL.
CC -1- TISSUE SPECIFICITY: IN LEAVES AND ROOTS OF YOUNG PLANTS.
CC -1- INDUCTION: IN RESPONSE TO WOUNDING AND BACTERIAL INFECTION.
CC -1- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
CC -----
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CC -----
DR EMBL; M58362; AAA03516.1; -.
DR EMBL; X69321; CAA49162.1; -.
DR PIR; JQ0991; JQ0991.
DR PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.
DR PFAM; PF00251; Glyco_hydro_32; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Cell wall; Zymogen; Signal.
FT SIGNAL 1 31 (POTENTIAL).
FT PROPEP 32 48 OR 40 (POTENTIAL).
FT CHAIN 49 592 BETA-FRUCTOFURANOSIDASE, INSOLUBLE
FT ISOENZYME 1.
FT ACT_SITE 74 74 BY SIMILARITY.
FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (COMPLEX).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 311 311 N-LINKED (GLCNAC. . .) (COMPLEX).
FT CARBOHYD 348 348 N-LINKED (GLCNAC. . .) (HIGH MANNOSE).
FT CARBOHYD 570 570 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 133 133 R -> W (IN REF. 2).
FT CONFLICT 133 133 A -> V (IN REF. 2).
FT CONFLICT 487 487
SQ SEQUENCE 592 AA; 6681 MW; E3DF85355D277D0C CRC64;

Query Match 63.2%; Score 36; DB 1; Length 592;
Best Local Similarity 55.6%; Pred. No. 20;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 2 RHNYGSEYS 10
|:|:|:|:
Db 321 RYDYGNEFYA 329

RESULT 5
INV2_DAUCA STANDARD; PRT; 592 AA.
ID Q39692;
AC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DT BETA-FRUCTOFURANOSIDASE, INSOLUBLE ISOENZYME 2 (CELL WALL BETA-
DE (SUCROSE-6-PHOSPHATE HYDROLASE 2) (INVERTASE 2) (CELL WALL BETA-
DE FRUCTOSIDASE 2).
GN INV2.
OS Daucus carota (Carrot).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Asteridae; euasterids II; Apiales; Apiaceae; Daucus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, QUEEN ANNE'S LACE;
RX MEDLINE; 95306787.
RA Lorenz K., Lienhard S., Sturm A.;
RT "Structural organization and differential expression of carrot beta-
RT fructofuranosidase genes: identification of a gene coding for a
RT flower bud-specific isozyme.";
RL Plant Mol. Biol. 28:189-194(1995).
CC -1- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN PHLOEM UNLOADING AND IN
CC STRESS RESPONSE.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL NON-REDUCING BETA-D-
CC FRUCTOFURANOSIDE RESIDUES IN BETA-D-FRUCTOFURANOSIDES.
CC -1- SUBCELLULAR LOCATION: IONICALLY BOUND TO THE CELL WALL.
CC -1- SIMILARITY: BELONGS TO FAMILY 32 OF GLYCOSYL HYDROLASES.
CC -----
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CC -----
DR EMBL; X78424; CAA55189.1; -.
DR PROSITE; PS00609; GLYCOSYL_HYDROL_F32; 1.
DR PFAM; PF00251; Glyco_hydro_32; 1.
KW Hydrolase; Glycosidase; Glycoprotein; Cell wall; Zymogen; Signal.
FT SIGNAL 1 75 (POTENTIAL).
FT PROPEP 75 75 BY SIMILARITY.
FT CHAIN 75 75 BETA-FRUCTOFURANOSIDASE, INSOLUBLE
FT ISOENZYME 2.
FT ACT_SITE 75 75 BY SIMILARITY.
FT CARBOHYD 171 171 POTENTIAL.
FT CARBOHYD 195 195 POTENTIAL.
FT CARBOHYD 310 310 POTENTIAL.
FT CARBOHYD 347 347 POTENTIAL.
FT CARBOHYD 568 568 POTENTIAL.
SQ SEQUENCE 592 AA; 67397 MW; 2734603836709133 CRC64;
Query Match 63.2%; Score 36; DB 1; Length 592;
Best Local Similarity 55.6%; Pred. No. 20;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 2 RHNYGSEYS 10
|:|:|:|:
Db 320 RYDYGNEFYA 328
RESULT 6
EXOP_RHIME STANDARD; PRT; 786 AA.
ID P33698;
AC 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE SUCCINOGLYCAN BIOSYNTHESIS TRANSPORT PROTEIN EXOP.
GN EXOP.
OS Rhizobium meliloti.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Sinorhizobium.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE; 94042869.
RA Glucksmann M.A., Reuber T.L., Walker G.C.;
RT "Family of glycosyl transferases needed for the synthesis of
RT succinoglycan by Rhizobium meliloti";
RL J. Bacteriol. 175:7033-7044(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE; 94042870.
RA Glucksmann M.A., Reuber T.L., Walker G.C.;
RT "Genes needed for the modification, polymerization, export, and
RT processing of succinoglycan by Rhizobium meliloti: a model for
RT succinoglycan biosynthesis";
RL J. Bacteriol. 175:7045-7055(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=2011;
RX MEDLINE; 94067019.
RA Becker A., Kleickmann A., Keller M., Arnold W., Puehler A.;
RT "Identification and analysis of the Rhizobium meliloti exoAMONP genes
RT involved in exopolysaccharide biosynthesis and mapping of promoters
RT located on the exoHKAOMNP fragment";
RL Mol. Gen. Genet. 241:367-379(1993).
CC -!- PATHWAY: EXOPOLYSACCHARIDE BIOSYNTHESIS.
CC -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
CC -!- SIMILARITY: SOME, TO B.SOLANACEARUM EPSB.
CC -----
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CC -----
DR EMBL; L20758; AA16042.1; -.
DR EMBL; Z22636; CAAR0349.1; -.
DR PIR; B49349; B49349.
DR PIR; S37031; S37031.
DR PIR; S39960; S39960.
KW Exopolysaccharide synthesis; Transport; Transmembrane; ATP-binding.
FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 43 66 POTENTIAL.
FT DOMAIN 67 689 PERIPLASMIC (POTENTIAL).
FT TRANSMEM 690 711 POTENTIAL.
FT DOMAIN 712 786 CYTOPLASMIC (POTENTIAL).
FT NP_BIND 583 590 ATP (POTENTIAL).
SQ SEQUENCE 786 AA; 86123 MW; E19E771E31F2030C CRC64;

Query Match 63.2%; Score 36; DB 1; Length 786;
Best Local Similarity 62.5%; Pred. No. 27;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFY 9
DB 768 RHRYGKY 775

RESULT 7
CCSA_PEA
ID CCSA_PEA STANDARD; PRT; 65 AA.
AC P31172;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
CC -----
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DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CYTOCHROME C BIOGENESIS PROTEIN CCSA (FRAGMENT).
GN CCSA.
OS Pisum sativum (Garden pea).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;
OC core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae;
OC Pisum.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. ALASKA;
RX MEDLINE; 9135950.
RA Nagano Y., Ishikawa H., Matsuno R., Sasaki Y.;
RT "Nucleotide sequence and expression of the ribosomal protein L2 gene
RT in pea chloroplasts";
RL Plant Mol. Biol. 17:541-545(1991).
CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
CC HEME ATTACHMENT (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE CCMF/CYCK/CCL1/NRFE/CCSA FAMILY.
CC -----
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CC -----
DR EMBL; X59015; CAA41754.1; -.
DR PIR; S17441; S17441.
KW Cytochrome c-type biogenesis; Chloroplast.
FT NON_TER 1
SQ SEQUENCE 65 AA; 7396 MW; 9E523E0C70B102AA CRC64;

Query Match 59.6%; Score 34; DB 1; Length 65;
Best Local Similarity 75.0%; Pred. No. 4.4;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYS 10
DB 57 HSYGSFTS 64

RESULT 8
VG7_BPPH2
ID VG7_BPPH2 STANDARD; PRT; 98 AA.
AC P13848;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE HEAD MORPHOGENESIS PROTEIN (LATE PROTEIN GP7).
GN 7.
OS Bacteriophage phi-29.
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Podoviridae.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87106857.
RA Vicek C., Paces V.;
RT "Nucleotide sequence of the late region of Bacillus phage phi 29
RT completes the 19,285-bp sequence of phi 29 genome. Comparison with
RT the homologous sequence of phage PZA.";
RL Gene 46:215-225(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87016351.
RA Innis C.A., Garvey K.J., Ito J.;
RT "Nucleotide sequence of phage phi 29 gene 7: structure of intergenic
RT spacer between the major early and late genes.";
RL Nucleic Acids Res. 14:7129-7129(1986).
CC -----
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CC -----

DR EMBL; M14782; AAA32279.1; -;
DR EMBL; X04386; CAA27974.1; -;
DR PIR; A28923; WMBPF9.
KW Late protein.
SQ SEQUENCE 98 AA; 11266 MW; FF2E7985D2266E14 CRC64;

Query Match 59.6%; Score 34; DB 1; Length 98;
Best Local Similarity 77.8%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFVS 10
I | | | | |
Db 33 RVNYGSFVS 41

RESULT 9
VG7_BPPZA STANDARD; PRT; 98 AA.
ID P07533;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-FEB-1998 (Rel. 07, Last sequence update)
DT 01-FEB-1991 (Rel. 17, Last annotation update)
DE HEAD MORPHOGENESIS PROTEIN (LATE PROTEIN GP7).
GN 7.
OS Bacteriophage PZA.
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Podoviridae.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 87031573.
RA Paces V., Vilek C., Urbanek P.;
RT "Nucleotide sequence of the late region of Bacillus subtilis phage
PZA, a close relative of phi 29.";
RL Gene 44:107-114(1986).
CC -----

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CC -----

DR EMBL; M11813; AAA88483.1; -;
DR PIR; A24831; WMBP7Z.
KW Late protein.
SQ SEQUENCE 98 AA; 11281 MW; 444408C39B606A25 CRC64;

Query Match 59.6%; Score 34; DB 1; Length 98;
Best Local Similarity 77.8%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFVS 10
I | | | | |
Db 33 RVNYGSFVS 41

RESULT 10
IF2A_PVRHO STANDARD; PRT; 275 AA.
ID IF2A_PVRHO
AC O38655;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)
DE PROBABLE TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-ALPHA).
CC -----

GN PH0961.
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OT3;
RX MEDLINE; 98344137.
RA Kwarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yanamoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Kuchimura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA RES. 5:55-76(1998).
CC -!- FUNCTION: EIF-2 FUNCTIONS IN THE EARLY STEPS OF PROTEIN SYNTHESIS
CC BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR TRNA
CC (BY SIMILARITY).
CC -!- SUBUNIT: HETEROTRIMER COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
CC CHAIN (BY SIMILARITY).
CC -----

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CC -----

DR EMBL; AP000004; BAA30058.1; -;
DR PIR; PF00575; S1; 1.
KW Initiation factor; Protein biosynthesis.
SQ SEQUENCE 275 AA; 31980 MW; 6AAAD15F10FFB436 CRC64;

Query Match 59.6%; Score 34; DB 1; Length 275;
Best Local Similarity 83.3%; Pred. No. 21;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
I | | | | |
Db 23 HNYGAF 28

RESULT 11
IPYR_PICPA STANDARD; PRT; 284 AA.
ID IPYR_PICPA
AC O13505;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
DE HYDROLASE) (PPASE).
GN IPPI.
OS Pichia pastoris (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC Saccharomycetaceae; Pichia.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-11430;
RX MEDLINE; 99034033.
RA Cosano I.C., Alvarez P., Molina M., Nombela C.;
RT "Cloning and sequence analysis of the Pichia pastoris TRP1, IPPI and
RT HIS3 genes.";
RL Yeast 14:861-867(1998).
CC -!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O -> 2 ORTHOPHOSPHATE.
CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
CC -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.
CC -----

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DR EMBL; AJ0101000; CAA04453.1; -
 DR HSP; P00817; IWGI.
 DR PROSITE; PS00387; PPASE; 1.
 DR PFAM; PF00719; Pyrophosphatase; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 284 AA; 31937 MW; 3DAD2970D775D6 CRC64;

Query Match 59.6%; Score 34; DB 1; Length 284;
 Best Local Similarity 83.3%; Pred. No. 22;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
 |||||
 Db 91 HNYGAF 96

RESULT 12

IPYR_KLUJLA STANDARD; PRT; 286 AA.
 AC P13998;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPP1 OR IPP.
 OS Kluyveromyces lactis (Yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Kluyveromyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89189093.
 RA Stark M.J.R., Milner J.S.;
 RT "Cloning and analysis of the Kluyveromyces lactis TRP1 gene: a
 RT chromosomal locus flanked by genes encoding inorganic pyrophosphatase
 RT and histone H3.";
 RL Yeast 5:35-50(1989).
 RN [2]

RP SIMILARITY TO E.COLI AND YEAST PPASES.

RX MEDLINE; 90254161.
 RA Lahti R., Kolakowski L.F. Jr., Helminen J., Vihtonen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RT "Conservation of functional residues between yeast and E. coli
 RT inorganic pyrophosphatases.";
 RL Biochim. Biophys. Acta 1038:338-345(1990).
 CC -!- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -!- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE PPASE FAMILY.

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DR EMBL; X14230; CAA32446.1; -

DR PIR; S07894; PWVKL.
 DR HSP; P00817; IWGI.
 DR PROSITE; PS00387; PPASE; 1.
 DR PFAM; PF00719; Pyrophosphatase; 1.
 KW Hydrolase; Magnesium.
 FT INIT_MET 0 BY SIMILARITY.
 FT ACT_SITE 56 56 PROBABLE.
 FT BINDING 78 78 INORGANIC PYROPHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 286 AA; 32034 MW; 11647F4ABD916A2F CRC64;

Query Match 59.6%; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 22;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HNYGSF 8
 |||||
 Db 91 HNYGAF 96

RESULT 13

IPYR_YEAST STANDARD; PRT; 286 AA.
 AC P00817;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO-
 DE HYDROLASE) (PPASE).
 GN IPP1 OR PPA1 OR PPA OR YBR011C OR YBR0202.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
 OC Saccharomycetaceae; Saccharomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 89083474.
 RA Kolakowski L.F. Jr., Schloesser M., Cooperman B.S.;
 RT "Cloning, molecular characterization and chromosome localization of
 RT the inorganic pyrophosphatase (PPA) gene from S. cerevisiae.";
 RL Nucleic Acids Res. 16:10441-10452(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN-S288C;
 RA Entian K.-D., Koetter P., Rose M., Li Z., Thermann R., Brendel M.,
 RA Baur A., Boles E., Miosga T., Schaaff-Gerstenschlaeger I.,
 RA Zimmermann F.K.;
 RL Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE.

RX MEDLINE; 78087552.
 RA Cohen S.A., Sterner R., Keim P.S., Heinrikson R.L.;
 RT "Covalent structural analysis of yeast inorganic pyrophosphatase.";
 RL J. Biol. Chem. 253:889-897(1978).
 RN [4]
 RP SEQUENCE OF 25-35 AND 239-251.
 RX STRAIN-S288C;
 RA Garrels J.I., Fletcher B., Kobayashi R., Latter G.I., Schwender B.,
 RA Volpe T., Warner J.R., McLaughlin C.S.;
 RT "Protein identifications for a Saccharomyces cerevisiae protein
 RT database.";
 RL Electrophoresis 15:1466-1486(1994).
 RN [5]

RP SEQUENCE OF 239-249.
 RX STRAIN-ATCC 38531 / Y41;
 RA MEDLINE; 97089742.
 RA Norbeck J., Blomberg A.;
 RT "Protein expression during exponential growth in 0.7 M NaCl medium of
 RT Saccharomyces cerevisiae.";
 RL FEMS Microbiol. Lett. 137:1-8(1996).
 RN [6]
 RP ACTIVE SITE.

RX MEDLINE; 80109718.
 RA Bond M.W., Chiu N.Y., Cooperman B.S.;
 RT "Identification of an arginine important for enzymatic activity
 RL within the covalent structure of yeast inorganic pyrophosphatase.";
 RN Biochemistry 19:94-102(1980).
 [7]
 RA X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RA Arutunian E.G., Terzian S.S., Voronova A.A., Kuranova I.P.,
 RA Smirnova E.A., Valnshtein B.K., Hohne W.E., Hansen G.;
 RT "X-ray diffraction study of inorganic pyrophosphatase from baker's
 RT yeast at the 3-A resolution.";
 RL Dokl. Akad. Nauk SSSR 258:1481-1492(1981).
 RN [8]
 RX X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS).
 RX MEDLINE; 97148342.
 RA Heikinheimo P., Lehtonen J., Baykov A., Lahti R., Cooperman B.S.,
 RA Goldman A.;
 RT "The structural basis for pyrophosphatase catalysis.";
 RL Structure 4:1491-1508(1996).
 RN [9]
 RA X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS).
 RA Swaminathan K., Cooperman B.S., Lahti R., Voet D.;
 RL Submitted (DEC-1997) to the PDB data bank.
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS) OF MUTANTS LYS-78 AND LYS-117.
 RX MEDLINE; 99096888.
 RA Tuominen V., Heikinheimo P., Kajander T., Torkkel T., Hyytia T.,
 RA Kapyla J., Lahti R., Cooperman B.S., Goldman A.;
 RT "The R78K and D117E active-site variants of Saccharomyces cerevisiae
 RT soluble inorganic pyrophosphatase: structural studies and mechanistic
 RT implications.";
 RL J. Mol. Biol. 284:1565-1580(1998).
 RN [11]
 RP SIMILARITY TO E.COLI AND K.LACTIS PPASES.
 RX MEDLINE; 90254161.
 RA Lahti R., Kolakowski L.F. Jr., Heinenen J., Vihinen M., Pohjanoksa K.,
 RA Cooperman B.S.;
 RT "Conservation of functional residues between yeast and E. coli
 RT inorganic pyrophosphatases.";
 RL Biochim. Biophys. Acta 1038:338-345(1990).
 CC -1- CATALYTIC ACTIVITY: PYROPHOSPHATE + H(2)O = 2 ORTHOPHOSPHATE.
 CC -1- COFACTOR: REQUIRES THE PRESENCE OF DIVALENT METAL CATION.
 CC MAGNESIUM CONFERS THE HIGHEST ACTIVITY. IT BINDS UP TO 4 DIVALENT
 CC CATIONS PER SUBUNIT, WITH THREE REQUIRED FOR ACTIVITY.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 CC -----
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 CC -----
 DR EMBL; X13253; CAA31629.1; -;
 DR EMBL; Z35880; CAA84949.1; -;
 DR PIR; S45864; PWBV.
 DR PDB; 1PVP; 15-OCT-91.
 DR PDB; 1YPP; 07-DEC-96.
 DR PDB; 1WGI; 19-NOV-97.
 DR PDB; 1WGU; 19-NOV-97.
 DR PDB; 1HUJ; 08-APR-98.
 DR PDB; 1HUK; 08-APR-98.
 DR PDB; 117E; 23-DEC-98.
 DR PDB; 8PRK; 23-DEC-98.
 DR SWISS-2DPAGE; P00817; YEAST.
 DR YEPD; 7305; -;
 DR SGD; L0000872; IPPL.
 DR PROSITE; PS00387; PPASE; 1.
 DR PFAM; PF00719; Pyrophosphatase; 1.
 KW Hydrolase; Magnesium; 3D-structure.

FT	INIT_MET	0	0
FT	ACT_SITE	56	56
FT	BINDING	78	78
FT	CONFLICT	40	40
FT	CONFLICT	71	71
FT	CONFLICT	74	74
FT	CONFLICT	123	123
FT	CONFLICT	136	136
FT	CONFLICT	186	186
FT	CONFLICT	224	224
FT	CONFLICT	266	266
FT	STRAND	4	7
FT	STRAND	16	20
FT	STRAND	25	25
FT	TURN	28	30
FT	TURN	38	41
FT	STRAND	45	45
FT	STRAND	55	55
FT	STRAND	79	79
FT	TURN	97	98
FT	TURN	111	112
FT	STRAND	121	123
FT	TURN	131	132
FT	STRAND	135	135
FT	STRAND	138	146
FT	STRAND	151	158
FT	TURN	160	161
FT	TURN	165	167
FT	HELIX	172	175
FT	TURN	176	177
FT	TURN	179	180
FT	HELIX	182	197
FT	STRAND	203	203
FT	HELIX	205	207
FT	STRAND	210	210
FT	HELIX	212	230
FT	TURN	231	231
FT	TURN	245	246
FT	TURN	248	249
FT	TURN	251	252
FT	TURN	255	260
FT	TURN	274	275
SQ	SEQUENCE	286 AA;	32184 MW; F29390260B60C8B2 CRC64;

Query Match 59.6%; Score 34; DB 1; Length 286;
 Best Local Similarity 83.3%; Pred. No. 22;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HNYGSF 8
 Db 91 HNYGAF 96

RESULT 14

ID	CCSA_ARATH	STANDARD;	PRT;	328 AA.
DT	15-FEB-2000	(Rel. 39, Created)		
DT	15-FEB-2000	(Rel. 39, Last sequence update)		
DT	15-FEB-2000	(Rel. 39, Last annotation update)		
DE	CYTCHROME C BIOGENESIS PROTEIN CCSA.			
GN	CCSA.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OG	Chloroplast.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;			
OC	core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;			
OC	Arabidopsis.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=CV. COLUMBIA;			
RA	Sato S., Nakamura Y., Kaneko T., Asamizu E., Tabata S.;			

RT "Complete structure of the chloroplast genome of Arabidopsis
 RL thaliana.";
 CC Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: REQUIRED DURING CYTOCHROME BIOGENESIS AT THE STEP OF
 CC HEME ATTACHMENT (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE CCMP/CYCK/CCL1/NRPE/CCSA FAMILY.
 CC -----
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 CC -----
 DR EMBL; AP000423; BAA84436.1; -;
 KW Cytochrome c-type biogenesis; Chloroplast.
 SQ SEQUENCE 328 AA; 37732 MW; C88D1508B2924D6F CRC64;

Query Match 59.6%; Score 34; DB 1; Length 328;
 Best Local Similarity 75.0%; Pred. No. 25;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYS 10
 :|||||
 Db 320 HSYGSFYS 327

RESULT 15
 LIM4_MOUSE
 ID LIM4_MOUSE STANDARD; PRT; 361 AA.
 AC P53776; O08916;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE LIM HOMEOBOX PROTEIN 4 (FRAGMENT).
 GN LHX4 OR GSH4 OR GSH-4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RC SEQUENCE OF 1-190 FROM N.A.
 RC STRAIN=FVB/N; TISSUE=EMBRYO;
 RX MEDLINE; 97432832.
 RA Yamashita T., Moriyama K., Sheng H.Z., Westphal H.;
 RT "Lhx4, a LIM homeobox gene,"
 RL Genomics 44:144-146(1997).
 RN [2]
 RC SEQUENCE OF 130-361 FROM N.A.
 RX MEDLINE; 94298779.
 RA Li H., Witte D.P., Branford W.W., Aronow B.J., Weinstein M., Kaur S.,
 RA Wert S., Singh G., Schreiner C.M., Whitsett J.A., Scott W.J. Jr.,
 RA Potter S.S.;
 RT "Gsh-4 encodes a LIM-type homeodomain, is expressed in the developing
 RT central nervous system and is required for early postnatal
 RT survival.";
 RL EMBO J. 13:2876-2885(1994).
 CC -!- FUNCTION: MAY PLAY A CRITICAL ROLE IN THE DEVELOPMENT OF
 CC RESPIRATORY CONTROL MECHANISMS AND IN THE NORMAL GROWTH AND
 CC MATURATION OF THE LUNG.
 CC -!- SUBCELLULAR LOCATION: NUCLEAR (POTENTIAL).
 CC -!- TISSUE SPECIFICITY: TRANSIENT EXPRESSION IN VENTROLATERAL REGIONS
 CC OF THE DEVELOPING NEURAL TUBE AND HINDBRAIN.
 CC -!- SIMILARITY: TO OTHER HOMEOBOX DOMAINS. BELONGS TO THE LIM
 CC SUBFAMILY.
 CC -!- SIMILARITY: CONTAINS 2 LIM DOMAINS. THE LIM DOMAIN BINDS 2 ZINC
 CC IONS.
 CC -----
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DR EMBL; U89343; AAC53336.1; -;
 DR EMBL; S71659; AAB31260.1; -;
 DR HSP; P02836; IHDD.
 DR MGD; MGI:101776; LHX4.
 DR PROSITE; PS00478; LIM_DOMAIN_1; 2.
 DR PROSITE; PS00023; LIM_DOMAIN_2; 2.
 DR PROSITE; PS00027; HOMEOBOX_1; 1.
 DR PROSITE; PS00071; HOMEOBOX_2; 1.
 DR PFAM; PF00046; homeobox; 1.
 DR PFAM; PF00412; LIM; 2.
 KW Homeobox; DNA-binding; Nuclear protein; Repeat; LIM motif;
 KW Metal-binding; Zinc; Transcription regulation.
 FT NON_TER 1 1
 FT DOMAIN 1 52 LIM.
 FT DOMAIN 60 115 LIM.
 FT DNA_BIND 128 187 HOMEOBOX.
 SQ SEQUENCE 361 AA; 40086 MW; 09535343C7990FED CRC64;

Query Match 59.6%; Score 34; DB 1; Length 361;
 Best Local Similarity 62.5%; Pred. No. 28;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHYGSFY 9
 ||:|
 Db 192 RHRWGQFY 199

Search completed: May 27, 2000, 20:45:30
 Job time: 2284 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:55:22 ; Search time 34.67 seconds
(without alignments)
19.998 Million cell updates/sec

Title: US-09-016-061-100
Perfect score: 57
Sequence: 1 ARHNGSFYS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 225878

Minimum DB seq length: 0
Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : SPTREMBL12:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	40	70.2	89	7	O19495	O19495 gallus gall
2	39	68.4	555	5	Q9XV91	Q9XV91 caenorhabdi
3	39	68.4	611	2	Q9X5S2	Q9X5S2 streptomyce
4	38	66.7	39	7	P79474	P79474 cervus elap
5	38	66.7	39	7	P79477	P79477 cervus elap
6	38	66.7	39	7	P79478	P79478 cervus elap
7	38	66.7	39	7	P79479	P79479 cervus elap
8	38	66.7	82	7	Q30606	Q30606 macaca mula
9	38	66.7	82	7	Q30608	Q30608 macaca mula
10	38	66.7	82	7	Q30637	Q30637 macaca mula
11	38	66.7	82	7	Q30638	Q30638 macaca mula
12	38	66.7	82	7	Q30658	Q30658 macaca mula
13	38	66.7	82	7	Q30659	Q30659 macaca mula
14	38	66.7	82	7	Q30666	Q30666 macaca mula
15	38	66.7	82	7	Q30667	Q30667 macaca mula
16	38	66.7	82	7	Q30668	Q30668 macaca mula
17	38	66.7	82	7	O19287	O19287 macaca mula
18	38	66.7	82	7	O19288	O19288 macaca mula
19	38	66.7	83	7	O98002	O98002 oviss aries
20	38	66.7	85	7	Q30796	Q30796 oviss aries

21	38	66.7	85	7	Q30800	Q30800 oviss aries
22	38	66.7	85	7	Q30803	Q30803 oviss aries
23	38	66.7	85	7	Q30812	Q30812 oviss aries
24	38	66.7	85	7	P79966	P79966 capra aegag
25	38	66.7	85	7	P79967	P79967 capra aegag
26	38	66.7	85	7	P79968	P79968 capra aegag
27	38	66.7	86	7	Q30326	Q30326 bos taurus
28	38	66.7	89	7	O19210	O19210 capra hircu
29	38	66.7	89	7	O19212	O19212 capra hircu
30	38	66.7	89	7	Q30521	Q30521 galago sene
31	38	66.7	89	7	Q30522	Q30522 galago sene
32	38	66.7	89	7	Q30526	Q30526 galago sene
33	38	66.7	89	7	Q30217	Q30217 homo sapien
34	38	66.7	107	7	Q9XRM7	Q9XRM7 phasianus c
35	38	66.7	225	7	Q30844	Q30844 oviss aries
36	38	66.7	232	7	Q9XRM6	Q9XRM6 phasianus c
37	38	66.7	266	7	Q30632	Q30632 macaca mula
38	37	64.9	479	2	O07021	O07021 bacillus su
39	37	64.9	2288	5	Q23081	Q23081 caenorhabdi
40	36	63.2	78	6	O97835	O97835 oviss aries
41	36	63.2	78	6	O97839	O97839 oviss aries
42	36	63.2	78	6	O97844	O97844 oviss aries
43	36	63.2	78	6	O97968	O97968 oviss aries
44	36	63.2	79	7	O19191	O19191 prionalluru
45	36	63.2	79	7	O19192	O19192 prionalluru

ALIGNMENTS

RESULT 1
O19495 PRELIMINARY; PRT; 89 AA.
ID O19495
AC O19495;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE MHC CLASS II BETA 1 DOMAIN (FRAGMENT).
GN B-LBI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
OC Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-15.151-5; TISSUE=BURSA;
RA PHARR G.T., DODGSON J.B., HUNT H.D., BACON L.D.;
RL Immunogenetics 47:350-354(1998).
DR EMBL; U91532; AAC15813.1; .
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.

FT NON_TER 1 1
FT NON_TER 89 89
SQ SEQUENCE 89 AA; 10724 MW; FDAC6024 CRC32;

Query Match 70.2%; Score 40; DB 7; Length 89;
Best Local Similarity 77.8%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNGSFYS 10
| | | | | | | |
Db 75 RHNGGDFES 83

RESULT 2
O9XV91 PRELIMINARY; PRT; 555 AA.
ID O9XV91
AC O9XV91;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
DE F16H6.1 PROTEIN.
GN F16H6.1.

OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditia; Rhabditidae;
 OC Rhabditina; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94150718.
 RA MATTHEWS L.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RL elegans.";
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 94150718.
 RA WILSON R., AINSKOUGH R., ANDERSON K., BAYNES C., BERKS M.,
 RA BONFIELD J., BURTON J., CONNELL M., COPSEY T., COOPER J., COULSON A.,
 RA CRAXTON M., DEAR S., DU Z., DURBIN R., FAVELLO A., FULTON L.,
 RA GARDNER A., GREEN P., HAWKINS T., HILLIER L., JIER M., JOHNSTON L.,
 RA JONES M., KERSHAW J., KIRSTEN J., LAISTER N., LATREILLE P.,
 RA LIGHTNING J., LLOYD C., MCMURRAY A., MORTIMORE B., O'CALLAGHAN M.,
 RA PARSONS J., PERCY C., RIFKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 RA SMALDON N., SMITH A., SONNHAMMER E., STADEN R., SULSTON J.,
 RA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 RA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOHLDMAN P.;
 RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 RL elegans.";
 RL Nature 368:32-38(1994).
 DR EMBL: 281506; CAB04128.1; -;
 SQ SEQUENCE 555 AA; 60401 MW; F0504B72 CRC32;

Query Match 68.4%; Score 39; DB 5; Length 555;
 Best Local Similarity 87.5%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 HNYGSFYS 10
 II IIIII
 Db 314 HNSGSFYS 321

RESULT 3
 ID Q9X5S2 PRELIMINARY; PRT; 611 AA.
 AC Q9X5S2;
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DE 01-NOV-1999 (TReMBLrel. 12, Last annotation update)
 DE MMCD.
 GN MMCD.
 OS Streptomyces lavendulae.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-NRRL 2564;
 RX MEDLINE: 93201491.
 RA MAO Y.Q., VAROGLOU M., SHERMAN D.H.;
 RT "Molecular characterization and analysis of the biosynthetic gene
 cluster for the antitumor antibiotic mitomycin C from Streptomyces
 lavendulae NRRL 2564.";
 RL Chem. Biol. 6:251-263(1999).
 DR EMBL: AF127374; RAD32727.1; -;
 SQ SEQUENCE 611 AA; 68499 MW; C6A3C8E5 CRC32;

Query Match 68.4%; Score 39; DB 2; Length 611;
 Best Local Similarity 77.8%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
 IIIII I
 Db 524 RHNYGFMS 532

RESULT 4
 ID P79474 PRELIMINARY; PRT; 39 AA.
 AC P79474;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DE 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
 OC Cervinae; Cervus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SWARBRICK P.A., CRAWFORD A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U63077; AAB37777.1; -;
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4767 MW; E01AA287 CRC32;

Query Match 66.7%; Score 38; DB 7; Length 39;
 Best Local Similarity 77.8%; Pred. No. 1.7;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
 IIIII I
 Db 25 RHNYGVFES 33

RESULT 5
 ID P79477 PRELIMINARY; PRT; 39 AA.
 AC P79477;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
 OC Cervinae; Cervus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SWARBRICK P.A., CRAWFORD A.M.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U63080; AAB37780.1; -;
 KW MHC.
 FT NON_TER 1 1
 FT NON_TER 39 39
 SQ SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match 66.7%; Score 38; DB 7; Length 39;
 Best Local Similarity 77.8%; Pred. No. 1.7;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
 IIIII I
 Db 25 RHNYGVFES 33

RESULT 6
 ID P79478 PRELIMINARY; PRT; 39 AA.
 AC P79478;
 DT 01-MAY-1997 (TReMBLrel. 03, Created)
 DT 01-MAY-1997 (TReMBLrel. 03, Last sequence update)
 DT 01-AUG-1998 (TReMBLrel. 07, Last annotation update)
 DE MHC CLASS II DRB (FRAGMENT).
 OS Cervus elaphus (Red deer).

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
OC Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.
RA SWARBRICK P.A., CRAWFORD A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63081; AAB37781.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match 66.7%; Score 38; DB 7; Length 39;
Best Local Similarity 77.8%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
Db 25 RHNYGVFES 33
|||||

RESULT 7
P79479 PRELIMINARY; PRT; 39 AA.
AC P79479;
DT 01-MAY-1997 (TREMBlrel. 03, Created)
DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
DT 01-AUG-1998 (TREMBlrel. 07, Last annotation update)
DE MHC CLASS II DRB (FRAGMENT).
OS Cervus elaphus (Red deer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Cervoidae; Cervidae;
OC Cervinae; Cervus.
RN [1]
RP SEQUENCE FROM N.A.
RA SWARBRICK P.A., CRAWFORD A.M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U63082; AAB37782.1; -.
KW MHC.
FT NON_TER 1 1
FT NON_TER 39 39
SQ SEQUENCE 39 AA; 4806 MW; 49B4754A CRC32;

Query Match 66.7%; Score 38; DB 7; Length 39;
Best Local Similarity 77.8%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
Db 25 RHNYGVFES 33
|||||

RESULT 8
Q30606 PRELIMINARY; PRT; 82 AA.
AC Q30606;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE MAJOR HISTOCOMPATIBILITY COMPLEX CLASS II (FRAGMENT).
GN MHC-DRB.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Cercopitheciidae; Cercopitheciinae;
OC Macaca.
RN [1]
RP SEQUENCE FROM N.A.
RA KNAPP L.A., CADAVID L.F., EBERLE M.E., KNECHTLE S.J., BONTROP R.E.,
RA WATKINS D.I.;

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RT "Identification of new mamu-DRB alleles using DGGE and direct
RT sequencing.";
RL Immunogenetics 45:171-179(1997).
DR EMBL; U57948; AAC50981.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 9921 MW; A871F869 CRC32;

Query Match 66.7%; Score 38; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
Db 73 RHNYGVFES 81
|||||

RESULT 9
Q30608 PRELIMINARY; PRT; 82 AA.
AC Q30608;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE MAJOR HISTOCOMPATIBILITY COMPLEX CLASS II (FRAGMENT).
GN MHC-DRB.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Cercopitheciidae; Cercopitheciinae;
OC Macaca.
RN [1]
RP SEQUENCE FROM N.A.
RA KNAPP L.A., CADAVID L.F., EBERLE M.E., KNECHTLE S.J., BONTROP R.E.,
RA WATKINS D.I.;
RT "Identification of new mamu-DRB alleles using DGGE and direct
RT sequencing.";
RL Immunogenetics 45:171-179(1997).
DR EMBL; U57950; AAC50983.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 9880 MW; 84AB3DAA CRC32;

Query Match 66.7%; Score 38; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
Db 73 RHNYGVFES 81
|||||

RESULT 10
Q30637 PRELIMINARY; PRT; 82 AA.
AC Q30637;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).
GN MHC DR-BETA 1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Cercopitheciidae; Cercopitheciinae;
OC Macaca.
RN [1]
RP SEQUENCE FROM N.A.

```

```

RC STRAIN=1KM; TISSUE=BLOOD;
RX MEDLINE; 93123123.
RA SLIERENDREGT B.L., VAN NOORT J.T., BAKAS R.M., OTTING N., JONKER M.,
RA BONTROP R.E.;
RT "Evolutionary stability of transspecies major histocompatibility
complex class II DRB lineages in humans and rhesus monkeys.";
RL Hum. Immunol. 35:29-39(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=1KM; TISSUE=BLOOD;
RA SLIERENDREGT B.L.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; 226140; CAA81141.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 10024 MW; 9D3AA6A2 CRC32;

Query Match 66.7%; Score 38; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
Db ||||| I I
73 RHNYGVFES 81

RESULT 11
ID Q30638 PRELIMINARY; PRT; 82 AA.
AC Q30638;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).
GN MHC DR-BETA 1.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Cercopitheciidae; Cercopitheciinae;
OC Macaca.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1KL; TISSUE=BLOOD;
RA SLIERENDREGT B.L.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; 226161; CAA81162.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 9964 MW; F161DC3E CRC32;

Query Match 66.7%; Score 38; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
Db ||||| I I
73 RHNYGVFES 81

RESULT 12
ID Q30658 PRELIMINARY; PRT; 82 AA.
AC Q30658;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).
GN MHC DR-BETA 5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Cercopitheciidae; Cercopitheciinae;
OC Macaca.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1KL; TISSUE=BLOOD;
RA SLIERENDREGT B.L.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; 226161; CAA81162.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 9964 MW; F161DC3E CRC32;

Query Match 66.7%; Score 38; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
Db ||||| I I
73 RHNYGVFES 81

RESULT 13
ID Q30659 PRELIMINARY; PRT; 82 AA.
AC Q30659;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).
GN MHC DR-BETA 5.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Primates; Catarrhini; Cercopitheciidae; Cercopitheciinae;
OC Macaca.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1ME; TISSUE=BLOOD;
RA SLIERENDREGT B.L.;
RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; 226162; CAA81163.1; -.
DR PFAM; PF00969; MHC_II_beta; 1.
KW MHC.
FT NON_TER 1 1
FT NON_TER 82 82
SQ SEQUENCE 82 AA; 9953 MW; CC45E3FD CRC32;

Query Match 66.7%; Score 38; DB 7; Length 82;
Best Local Similarity 77.8%; Pred. No. 3.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
Db ||||| I I
73 RHNYGVFES 81

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KW MHC.
 FT NON_TER 1 1
 FT NON_TER 82 82
 SQ SEQUENCE 82 AA; 9940 MW; 79205B65 CRC32;

Query Match 66.7%; Score 38; DB 7; Length 82;
 Best Local Similarity 77.8%; Pred. No. 3.7;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
 Db ||||| |
 73 RHNYGVFES 81

RESULT 14

Q30666 ID Q30666 PRELIMINARY; PRT; 82 AA.

AC Q30666; DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
 DE MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).

GN MHC DR-BETA.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae;

OC Macaca.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-IMP; TISSUE=BLOOD;

RX MEDLINE: 93123123.

RA SLIERENDREGT B.L.; VAN NOORT J.T., BAKAS R.M., OTTING N., JONKER M.,

RA BONTROP R.E.;

RT "Evolutionary stability of transspecies major histocompatibility complex class II DRB lineages in humans and rhesus monkeys.";

RL Hum. Immunol. 35:29-39(1992).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-IMP; TISSUE=BLOOD;

RA SLIERENDREGT B.L.;

RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.

DR EMBL; 226170; CAA81171.1; -.

DR PFAM; PF00969; MHC_II_beta; 1.

KW MHC.

FT NON_TER 1 1

FT NON_TER 82 82

SQ SEQUENCE 82 AA; 9881 MW; 2B69C7C0 CRC32;

Query Match 66.7%; Score 38; DB 7; Length 82;
 Best Local Similarity 77.8%; Pred. No. 3.7;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10
 Db ||||| |
 73 RHNYGVFES 81

RESULT 15

Q30667 ID Q30667 PRELIMINARY; PRT; 82 AA.

AC Q30667;

DT 01-NOV-1996 (TReMBLrel. 01, Created)

DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)

DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)

DE MAJOR HISTOCOMPATIBILITY COMPLEX (FRAGMENT).

GN MHC DR-BETA.

OS Macaca mulatta (Rhesus macaque).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;

OC Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecinae;

OC Macaca.

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-IMP; TISSUE=BLOOD;

RX MEDLINE: 93123123.

RA SLIERENDREGT B.L.; VAN NOORT J.T., BAKAS R.M., OTTING N., JONKER M.,

RA BONTROP R.E.;

RT "Evolutionary stability of transspecies major histocompatibility complex class II DRB lineages in humans and rhesus monkeys.";

RL Hum. Immunol. 35:29-39(1992).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN-IMP; TISSUE=BLOOD;

RA SLIERENDREGT B.L.;

RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.

DR EMBL; 226171; CAA81172.1; -.

DR PFAM; PF00969; MHC_II_beta; 1.

KW MHC.

FT NON_TER 1 1

FT NON_TER 82 82

SQ SEQUENCE 82 AA; 9880 MW; FE88E994 CRC32;

Query Match 66.7%; Score 38; DB 7; Length 82;
 Best Local Similarity 77.8%; Pred. No. 3.7;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 RHNYGSFYS 10

Db ||||| |

73 RHNYGVFES 81

Search completed: May 27, 2000, 19:55:22

Job time: 986 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 27, 2000, 19:50:47 ; Search time 31.68 seconds
(without alignments)
7.477 Million cell updates/sec

Title: US-09-016-061-100
Perfect score: 57
Sequence: 1 ARHNYGSPYS 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 188963

Minimum DB seq length: 0

Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	10	1 W76040	LM609 grafted anti
2	53	93.0	10	1 W76039	LM609 grafted anti
3	53	93.0	10	1 W76023	LM609 grafted anti
4	52	91.2	10	1 W76038	LM609 grafted anti
5	48	84.2	10	1 W76024	LM609 grafted anti
6	46	80.7	10	1 W76022	LM609 grafted anti
7	46	80.7	10	1 W76025	LM609 grafted anti
8	46	80.7	10	1 W76026	LM609 grafted anti
9	46	80.7	10	1 W76027	LM609 grafted anti
10	46	80.7	10	1 W76028	LM609 grafted anti
11	46	80.7	10	1 W76029	LM609 grafted anti
12	46	80.7	10	1 W76030	LM609 grafted anti
13	46	80.7	10	1 W76010	LM609 grafted anti
14	46	80.7	117	1 W76001	Vitaxin antibody h
15	46	80.7	117	1 W76003	LM609 antibody hea
16	43	75.4	10	1 W76037	LM609 grafted anti
17	43	75.4	10	1 W76021	LM609 grafted anti
18	41	71.9	10	1 W76020	LM609 grafted anti
19	38	66.7	110	1 W84099	Vitronectin alpha-
20	38	66.7	117	1 W84093	Murine vitronectin
21	38	66.7	117	1 W84097	Humanised anti-alp
22	36	63.2	117	1 R79157	Human IGE receptor
23	36	63.2	117	1 R79155	Human IGE receptor
24	36	63.2	117	1 W27357	Heavy chain variab
25	36	63.2	117	1 W27526	Heavy chain variab
26	36	63.2	117	1 W27354	Heavy chain variab
27	36	63.2	239	1 W73874	Human antiFc epsil
28	36	63.2	242	1 W73876	Human antiFc epsil
29	34	59.6	256	1 R22568	ScFvB18 construct
30	34	59.6	256	1 R22583	ScFvB18 construct
31	34	59.6	256	1 R22584	ScFvB18 construct
32	34	59.6	256	1 R22585	ScFvB18 construct
33	34	59.6	256	1 R22586	ScFvB18 construct
34	34	59.6	256	1 R22587	ScFvB18 construct

35 33 57.9 80 1 R13396 HLA-DRw12a antigen
36 33 57.9 80 1 R13397 HLA-DRw12b antigen
37 33 57.9 270 1 R66551 Cynomolgus Monkey
38 33 57.9 270 1 W81819 M. cynomolgus ZPB
39 33 57.9 566 1 R55207 Human zona pelluci
40 33 57.9 566 1 W81816 Human ZPB protein.
41 33 57.9 715 1 R80481 Recombinant human
42 33 57.9 1471 1 W74585 Calcium independent
43 32 56.1 11 1 W22700 Peptide sequence #
44 32 56.1 15 1 W25799 Synthetic human SI
45 32 56.1 18 1 W27062 Chemically syntheses

ALIGNMENTS

RESULT 1

W76040
ID W76040 standard; Protein; 10 AA.
AC W76040;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #16.
KW Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;
KW LM609; inhibitor; Integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49877.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT Integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim '62: Page 43: 129pp: English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to Integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 100.0%; Score 57; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.00064;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ARHNYGSPYS 10
| | | | | | | | | |
Db 1 ARHNYGSPYS 10

RESULT 2

W76039
ID W76039 standard; Protein; 10 AA.
AC W76039;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #15.
KW Vitaxin; antibody; variable region; heavy chain; light chain; Integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49876.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 43; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 CC Sequence 10 AA;

Query Match 93.0%; Score 53; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0029;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARHNYGSFY 9
 | | | | | | | |
 Db 1 ARHNYGSFY 9

RESULT 3
 W76023
 ID W76023 standard; Protein; 10 AA.

AC W76023;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #5.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49860.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 41; 129pp; English.
 CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block

CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 CC Sequence 10 AA;

Query Match 93.0%; Score 53; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.0029;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARHNYGSFY 9
 | | | | | | | |
 Db 1 ARHNYGSFY 9

RESULT 4
 W76038
 ID W76038 standard; Protein; 10 AA.

AC W76038;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #14.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI; 98-437472/37.
 DR N-PSDB; V49875.
 PT Humanised antibody, Vitaxin, that binds selectively to alphaVbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 62; Page 43; 129pp; English.

CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphaVbeta3 and can be used to
 CC inhibit binding of alphaVbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphaVbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 CC Sequence 10 AA;

Query Match 91.2%; Score 52; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.0043;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 ARHNYGSFYS 10
 | | | | | | | |
 Db 1 ARHNYGSFYS 10

RESULT 5
 W76024
 ID W76024 standard; Protein; 10 AA.

AC W76024;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #6.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49861.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PT Claim 62; Page 41; 129pp; English.
 PS W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;
 Query Match 80.7%; Score 46; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.042;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ARHNYGSF 8
 Db | | | | | | | |
 1 ARHNYGSF 8
 RESULT 7
 ID W76025 standard; Protein; 10 AA.
 AC W76025;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #7.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49862.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PT Claim 62; Page 41; 129pp; English.
 PS W76007-W76040 are protein fragments of the grafted monoclonal antibody
 CC LM609 heavy and light chain variable region. LM609 and the antibody
 CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
 CC inhibit binding of alphavbeta3 to a ligand and thus block
 CC integrin-mediated signal transduction. This is useful in the treatment,
 CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
 CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
 CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
 CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
 CC contain non-murine framework regions so are suitable for use in humans.
 CC Enhanced types of LM609 have affinity more than 90 times greater than
 CC that of parent the parent antibody.
 SQ Sequence 10 AA;
 Query Match 84.2%; Score 48; DB 1; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.02;
 Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 ARHNYGSFYS 10
 Db | | | | | | | | | |
 1 ARHNYGSFAS 10
 RESULT 6
 ID W76022 standard; Protein; 10 AA.
 AC W76022;
 DT 02-NOV-1998 (first entry)
 DE LM609 grafted antibody V-H region CDR3 protein fragment #4.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis; primer; V-H region; CDR;
 KW complementarity determining region.
 OS Mus sp.
 PN W09833919-A2.
 PD 06-AUG-1998.
 PF 30-JAN-1998; U01826.
 PR 30-JAN-1997; US-791391.
 PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49859.
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PT Claim 62; Page 41; 129pp; English.

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RESULT 8
W76026
ID W76026 standard; Protein; 10 AA.
AC W76026;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #8.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1997; US-791391.
PR (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49863.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 80.7%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
Db |||||
1 ARHNYGSF 8

RESULT 10
W76028
ID W76028 standard; Protein; 10 AA.
AC W76028;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #10.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1997; US-791391.
PR (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49865.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically,
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 80.7%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
Db |||||
1 ARHNYGSF 8

RESULT 9
W76027
ID W76027 standard; Protein; 10 AA.
AC W76027;
DT 02-NOV-1998 (first entry)
DE LM609 grafted antibody V-H region CDR3 protein fragment #9.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1997; US-791391.
PR (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR WPI: 98-437472/37.
DR N-PSDB: V49864.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

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QY 1 ARHNYGSF 8
Db 1 ARHNYGSF 8

RESULT 11
W76029
ID W76029 standard; Protein; 10 AA.
AC W76029;
DE 02-NOV-1998 (first entry)
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW LM609; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR N-PSDB; V49867.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Claim 62; Page 41; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 80.7%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
Db 1 ARHNYGSF 8

RESULT 13
W76010
ID W76010 standard; Protein; 10 AA.
AC W76010;
DE 02-NOV-1998 (first entry)
KW LM609 grafted antibody V-H region CDR3 protein fragment #1.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.
PI Glaser SM, Huse WD;
DR N-PSDB; V49847.
PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
PT integrin - and related grafted antibodies based on murine monoclonal
PT LM609, also related nucleic acid, used to treat, prevent or diagnose
PT angiogenesis or restenosis
PS Disclosure; Page 40; 129pp; English.
CC W76007-W76040 are protein fragments of the grafted monoclonal antibody
CC LM609 heavy and light chain variable region. LM609 and the antibody
CC vitaxin bind selectively to integrin alphavbeta3 and can be used to
CC inhibit binding of alphavbeta3 to a ligand and thus block
CC integrin-mediated signal transduction. This is useful in the treatment,
CC prevention and diagnosis of alphavbeta3-mediated disease, specifically
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC angiogenesis and restenosis (but also e.g. (non-)immune inflammation,
CC diabetic retinopathy, neovascular glaucoma, cancer, psoriasis, rheumatoid
CC arthritis, macular degeneration, osteoporosis etc.). The antibodies
CC contain non-murine framework regions so are suitable for use in humans.
CC Enhanced types of LM609 have affinity more than 90 times greater than
CC that of parent the parent antibody.
SQ Sequence 10 AA;

Query Match 80.7%; Score 46; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.042;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
Db 1 ARHNYGSF 8

RESULT 12
W76030
ID W76030 standard; Protein; 10 AA.
AC W76030;
DE 02-NOV-1998 (first entry)
KW LM609 grafted antibody V-H region CDR3 protein fragment #12.
KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
KW macular degeneration; osteoporosis; primer; V-H region; CDR;
KW complementarity determining region.
OS Mus sp.
PN WO9833919-A2.
PD 06-AUG-1998.
PF 30-JAN-1998; U01826.
PR 30-JAN-1997; US-791391.
PA (IXSY-) IXSYS INC.

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Query Match 80.7%; Score 46; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.042;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
 |||||
 Db 1 ARHNYGSF 8

RESULT 14

W76001
 ID W76001 standard; Protein; 117 AA.

AC 02-NOV-1998 (first entry)
 DE Vitaxin antibody heavy chain variable region protein fragment.
 KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;
 KW LM609; inhibitor; integrin-mediated signal transduction; treatment;
 KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;
 KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;
 KW macular degeneration; osteoporosis.

OS Mus sp.

PN W09833919-A2.

PD 06-AUG-1998.

PF 30-JAN-1998; U01826.

PR 30-JAN-1997; US-791391.

PA (IXSY-) IXSYS INC.

PI Glaser SM, Huse WD;

DR WPI: 98-437472/37.

DR N-PSDB; V49820.

PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3

PT integrin - and related grafted antibodies based on murine monoclonal

PT LM609, also related nucleic acid, used to treat, prevent or diagnose

PT angiogenesis or restenosis

PS Claim 1; Fig 1a; 129pp; English.

CC This sequence represents a fragment of the vitaxin antibody variable
 CC heavy chain region. Vitaxin and the antibody LM609 bind selectively to
 CC integrin alphavbeta3 and can be used to inhibit binding of alphavbeta3
 CC to a ligand and thus block integrin-mediated signal transduction. This is
 CC useful in the treatment, prevention and diagnosis of alphavbeta3-mediated
 CC disease, specifically angiogenesis and restenosis (but also e.g.

CC (non-)immune inflammation, diabetic retinopathy, neovascular glaucoma,
 CC cancer, psoriasis, rheumatoid arthritis, macular degeneration,
 CC osteoporosis etc.). The antibodies contain non-murine framework regions

CC so are suitable for use in humans. Enhanced types of LM609 have affinity
 CC more than 90 times greater than that of parent the parent antibody.

SQ Sequence 117 AA;

Query Match 80.7%; Score 46; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.51;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
 |||||
 Db 97 ARHNYGSF 104

RESULT 15

W76003
 ID W76003 standard; Protein; 117 AA.

AC W76003;

DT 02-NOV-1998 (first entry)

DE LM609 antibody heavy chain variable region protein fragment.

KW Vitaxin; antibody; variable region; heavy chain; light chain; integrin;

KW LM609; inhibitor; integrin-mediated signal transduction; treatment;

KW diagnosis; angiogenesis; restenosis; inflammation; diabetic retinopathy;

KW neovascular glaucoma; cancer; psoriasis; rheumatoid arthritis; murine;

KW macular degeneration; osteoporosis.

OS Mus sp.

PN W09833919-A2.

PD 06-AUG-1998.

PF 30-JAN-1998; U01826.

PR 30-JAN-1997; US-791391.

PA (IXSY-) IXSYS INC.
 PI Glaser SM, Huse WD;
 DR WPI: 98-437472/37.
 DR N-PSDB; V49820
 PT Humanised antibody, Vitaxin, that binds selectively to alphavbeta3
 PT integrin - and related grafted antibodies based on murine monoclonal
 PT LM609, also related nucleic acid, used to treat, prevent or diagnose
 PT angiogenesis or restenosis
 PS Claim 43; Fig 2a; 129pp; English.
 CC This sequence represents the LM609 antibody variable heavy chain region.
 CC LM609 and the antibody vitaxin bind selectively to integrin alphavbeta3
 CC and can be used to inhibit binding of alphavbeta3 to a ligand and thus
 CC block integrin-mediated signal transduction. This is useful in the
 CC treatment, prevention and diagnosis of alphavbeta3-mediated disease,
 CC specifically angiogenesis and restenosis (but also e.g. (non-)immune
 CC inflammation, diabetic retinopathy, neovascular glaucoma, cancer,
 CC psoriasis, rheumatoid arthritis, macular degeneration, osteoporosis
 CC etc.). The antibodies contain non-murine framework regions so are
 CC suitable for use in humans. Enhanced types of LM609 have affinity more
 CC than 90 times greater than that of parent the parent antibody.
 SQ Sequence 117 AA;

Query Match 80.7%; Score 46; DB 1; Length 117;
 Best Local Similarity 100.0%; Pred. No. 0.51;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ARHNYGSF 8
 |||||
 Db 97 ARHNYGSF 104

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